

# thurj

the harvard undergraduate  
research journal

Fall 2020  
Vol. 13, Issue 1

## **NATIVE MAIZE, TRANSGENIC CONTAMINATION, AND INTELLECTUAL PROPERTY RIGHTS:**

The Case of San Miguel del Valle,  
Oaxaca, Mexico

North Korea's Exposure to  
World Commodity Prices

From Hyper-Surveillance  
to Sudden Abandonment

Regulation and  
Transcription of Chromatin  
Structure



*Congratulations to*  
**Adele**  
**Woodmansee**  
*for winning*  
*Best Manuscript*

Adele Woodmansee is a 2020 graduate of Harvard College, where she studied Integrative Biology and Social Anthropology. She conducted thesis research about small-scale maize agriculture in the town of San Miguel del Valle, Oaxaca, Mexico from 2017-2019. She combined genetic investigation to test for transgenic contamination in locally grown, native maize varieties with ethnographic research about seed systems and the impacts of climate change and economic policies on maize production. She spent ten months living in the community to conduct maize sample collection, participant observation, interviews in Spanish and Zapotec, and linguistic analysis of Zapotec agricultural vocabulary. She carried out genetic analyses in the Davis lab at the Harvard Herbaria. Her article, *Native Maize, Transgenic Contamination, and Intellectual Property Rights: The Case of San Miguel del Valle, Oaxaca, Mexico*, is adapted from the fifth chapter of her thesis and describes the genetic work she did in conjunction with a social discussion of transgenic contamination.

*December 2020*

Dear Harvard Community,

We are delighted to present the Fall 2020 issue of The Harvard Undergraduate Research Journal (THURJ), Harvard's sole peer-reviewed student-run biannual publication dedicated to showcasing outstanding research from the Harvard undergraduate community. For over ten years, we have been proud to publish high-quality, original research from a wide range of disciplines. In light of this year's particularly difficult circumstances, we are proud of the tremendous work, collaboration, and commitment that THURJ members have put into making this electronic issue possible. In this issue, our authors explore topics as far-ranging as evaluating North Korea's international trading presence, to a scientific and ethnographic understanding of transgenic contamination of Mexican maize.

Every year, we work to increase THURJ's visibility in the Harvard community and strengthen our reputation as a professional-quality journal. Despite the virtual setting, this year we are proud to have recruited many incoming first-years to our organization—the most out of any recent year—and we hope that they are empowered to continue promoting the sharing of scholarly research on campus. In our efforts to promote undergraduate research, THURJ continues to be a leader in the larger national scientific community by working with research journals at our peer undergraduate institutions and lending our expertise to help students at schools worldwide establish their own undergraduate research journals. This semester, we have collaborated with undergraduates from Georgetown and Yale, helping them spearhead the creation of their own undergraduate research journals.

This work would not be possible without the incredible insight, dedication, and support of our faculty advisory board. We would like to thank our student and faculty reviewers, staff writers, and designers for their immense efforts in creating, editing, and polishing this issue. We would also like to extend our unwavering gratitude to our faculty advisor Professor Guido Guidotti for his guidance and wise counsel. Additionally, we are tremendously grateful for continued support from FAS Dean Claudine Gay, FAS Dean of Science Christopher Stubbs, FAS Dean of Social Sciences Lawrence Bobo, Harvard College Dean Rakesh Khurana, Provost Alan Garber, Vice Provost for Research Richard McCullough, HMS Dean George Daley, Harvard Catalyst, the Office of the President, Harvard SEAS and Harvard College.

We are incredibly excited and proud to present our newest issue and to share this outstanding research with the Harvard community. Enjoy!

Sincerely,



Mohamed El-Abtah  
Co-Editor-in-Chief



Matthew Hirschfeld  
Co-Editor-in-Chief

Submit your research to

# thurj

The Harvard Undergraduate Research Journal

---

---

THURJ is the *only* campus publication that showcases peer-reviewed *undergraduate* student research.

Circulation to dorms, departments, libraries, and scientific institutions.

Submit your research, manuscript or thesis!

Email [contact@thurj.org](mailto:contact@thurj.org) or visit our website at: [www.thurj.org](http://www.thurj.org) for submission guidelines.

THURJ accepts submissions that reflect original research in all disciplines!\*

## \$500 for Top Manuscript!

For more info, including our latest issues, email [contact@thurj.org](mailto:contact@thurj.org) or visit our website at: [www.thurj.org](http://www.thurj.org)

\*Including the formal sciences, natural sciences, applied sciences, engineering, social sciences, and humanities.

# Contents

## Research

11 From Hyper-Surveillance to Sudden Abandonment: On Reconfiguring Black Motherhood in the Fourth Trimester  
*Sandra Ojeaburu*

21 The Part of Our World: North Korea's Exposure to World Commodity Prices  
*Sewon Park*

29 Native Maize, Transgenic Contamination, and Intellectual Property Rights: The Case of San Miguel del Valle, Oaxaca, Mexico  
*Adele Woodmansee*

40 Regulation of Transcription and Chromatin Structure by Spt6 and Elf1 in Yeast  
*Ann Yang*

## Features

49 Challenges of Oceanic Plastic Pollution Today  
*Serena Zhao*

54 A Failing Educational System  
*Ramon Rivera*

58 Utilizing Linguistics to Develop Novel Retrosynthesis Pathways for Drug Development  
*Dianelis Lopez*

61 Challenges of Coronavirus Epidemiological Modeling  
*Andrea Rivera*

## Executive Board

### Managing Editor of Peer Review

William Ho '21

### Co-Editors-in-Chief

Mohamed El-Abtah '21

Matthew Hirschfeld '21

### Managing Editor of Design

Daniel Mendoza '21

### Managing Editor of Content

Andrea Rivera '22

### Business Manager

Sreekar Mantena '22

## Board

### Peer Review

#### Associate Editors

Andrea Rivera '22

Edward Lee '22

#### Peer Reviewers

Mythri Ambatipudi '22

Brandon Gong '22

Michael Kielstra '22

Yuen Ting Chow '23

Catherine Gallori '23

Simon Levien '23

#### Peer Reviewers

Tyler Masuyama '23

Seo-Hyun Yoo '23

David Aley '24

Rubaiya Emran '24

Josh Josephy-Zack '24

Jai Khurana '24

Taylor Larson '24

Jailene Ramos '24

Serena Zhao '24

### Design

#### Designers

Yuen Ting Chow '23

Rubaiya Emran '24

### Content

#### Writers

Andrea Rivera '22

Dianelis Lopez '22

Ramon Rivera '24

Serena Zhao '24

## Our Supporters



**HARVARD**

Faculty of Arts and Sciences



**HARVARD  
CATALYST**

**THE  
COOP**

## Faculty Reviewers

Thomas Baranga, Ph.D.

Undergraduate Advisor and Lecturer in the  
Economics Department, Harvard University

Jennifer Carballo, Ph.D.

Research Associate, Peabody Museum of  
Archaeology

Stephen Chaudoin, Ph.D.

Assistant Professor in the Government  
Department, Harvard University

Arthur Dempster, Ph.D.

Professor Emeritus of Statistics, Harvard  
University

Brian D. Farrell, Ph.D.

Professor of Organismic and Evolutionary  
Biology, Harvard University

Pierre Jacob, Ph.D.

Associate Professor in the Department of  
Statistics, Harvard University

Rima Jolivet, Ph.D.

Senior Research Associate, Women & Health  
Initiative and Global Health & Population  
Department, Harvard T.H. Chan School of  
Public Health

David S. Jones Ph.D.

A. Bernard Ackerman Professor of the Culture  
of Medicine and Professor of Epidemiology,  
Harvard T.H. Chan School of Public Health

Elena Kramer, Ph.D.

Bussey Professor of Organismic and  
Evolutionary Biology, Harvard University

Alexander McQuown

Graduate Student, Harvard MCB Denic Lab

John de la Parra Ph.D.

Research Associate, Harvard University  
Herbaria

Kevin Struhl, Ph.D.

David Wesley Gaiser Professor in the  
Department of Biological Chemistry and  
Molecular Pharmacology, Harvard Medical  
School

Gabriela Soto, Ph.D.

Professor of the History of Science, Harvard  
University

Dustin Tingley, Ph.D.

Professor of Government, Harvard University

Amanda Whipple, Ph.D.

Assistant Professor in the Department of  
Molecular and Cellular Biology, Harvard  
University

Alexander Young, Ph.D.

Undergraduate Advisor and Lecturer in the  
Department of Statistics, Harvard University

## Faculty Advisory Board

Alán Aspuru-Guzik, Ph.D.  
Professor of Chemistry & Chemical Biology

Paul Bamberg, Ph.D.  
Senior Lecturer in Mathematics

Michael Brenner, Ph.D.  
Glover Professor of Applied Mathematics & Applied Physics

Myron Essex, D.V.M., Ph.D.  
Mary Woodward Lasker Professor of Health Sciences

Brian Farrell, Ph.D.  
Professor of Biology

Jeffrey Flier, M.D.  
Dean, Harvard Medical School & George C. Resiman Professor of Medicine

Steven Freedman, M.D., Ph.D.  
Chief of the Division of Translational Research & Professor of Medicine, Harvard Medical School

Guido Guidotti, Ph.D.  
Higgins Professor of Biochemistry

David Haig, Ph.D.  
George Putnam Professor of Organismic & Evolutionary Biology

Dudley Herschbach, Ph.D.  
Frank B. Baird Jr. Research Professor of Science

John Hutchinson, Ph.D.  
Abbot & James Lawrence Professor of Engineering & Gordon McKay Professor of Applied Mechanics

Efthimios Kaxiras, Ph.D.  
John Hasbrouck Van Vleck Professor of Pure & Applied Physics

George Lauder, Ph.D.  
Professor of Biology & Alexander Agassiz Professor of Zoology

Richard Losick, Ph.D.  
Maria Moors Cabot Professor of Biology

Lakshminarayanan Mahadevan, Ph.D.  
Lola England Professor of Applied Mathematics, Professor of Organismic and Evolutionary Biology & Professor of Physics

David Mooney, Ph.D.  
Robert P. Pinkas Family Professor of Bioengineering

Hongkun Park, Ph.D.  
Professor of Chemistry & Physics

Steven Pinker, Ph.D.  
Johnstone Family Professor of Psychology

Tobias Ritter, Ph.D.  
Associate Professor of Chemistry & Chemical Biology

Eugene Shakhnovich, Ph.D.  
Professor of Chemistry & Chemical Biology

Irwin Shapiro, Ph.D.  
Timken University Professor

Zhigang Suo, Ph.D.  
Allen E. & Marilyn M. Puckett Professor of Mechanics & Materials

David Weitz, Ph.D.  
Mallinckrodt Professor of Physics & Applied Physics

## Contact

**General:** [contact@thurj.org](mailto:contact@thurj.org)

**Advertising:** [advertising@thurj.org](mailto:advertising@thurj.org)

**Subscribing:** [subscriptions@thurj.org](mailto:subscriptions@thurj.org)

**Submissions:** [submissions@thurj.org](mailto:submissions@thurj.org)

**Website:** [www.thurj.org](http://www.thurj.org)

**Copyright © 2020 The Harvard Undergraduate Research Journal**

We abide by the Creative Commons BY-NC-ND 3.0 license. Commercial uses and derivative works are prohibited. Material appearing in this publication may be redistributed providing that articles in their entirety are reproduced. Rights of photographs may only be granted by the photographer. The opinions expressed in this magazine are those of the contributors and are not necessarily shared by the editors. All editorial rights are reserved.

## About Us

The Harvard Undergraduate Research Journal (*THURJ*) showcases peer-reviewed undergraduate student research from all academic disciplines. As a biannual publication, *THURJ* familiarizes students with the process of manuscript submission and evaluation. Moreover, it provides a comprehensive forum for discourse on the cutting-edge research that impacts our world today.

At its core, *THURJ* allows students to gain insight into the peer review process, which is central to modern scientific inquiry. All *THURJ* manuscripts are rigorously reviewed by the Peer Review Board (consisting of Harvard undergraduates), and the top manuscripts that they select are further reviewed by Harvard graduate students, post-doctoral fellows, and professors. This process not only stimulates faculty-student collaboration and provides students with valuable feedback on their research, but also promotes collaboration between the College and Harvard's many graduate and professional schools. In addition to publishing original student research papers, *THURJ* is also an important medium for keeping the Harvard community updated on research-related news and developments.

## About the Cover

This Cover image represents the native landraces of maize cultivated in Oaxaca, Mexico using the *milpa* agriculture system. This varied landscape is indicative of transgenic Maize used, the topic of the best manuscript *Native Maize, Transgenic Contamination, and Intellectual Property Rights: The Case of San Miguel del Valle, Oaxaca, Mexico*.

Image sources: [pixabay.com](http://pixabay.com)

**From Hyper-Surveillance to Sudden Abandonment:  
On Reconfiguring Black Motherhood  
in the Fourth Trimester**  
by Sandra Ojeaburu '20

11

The nexus of maternal health disparities and structural racism has become a greater focus in recent years. Further research has identified startling trends in maternal and infant mortality rates for Black mothers. While childbirth is often the focus of healthcare initiatives, given this is a time of high risk for Black mothers, postpartum care after childbirth has been awarded minimal attention. The topic of postpartum care is a unique period that can act as an indicator of the psychosocial support Black mothers get in medical establishments and in their communities. This paper investigates the political connotations of breastfeeding and legacies of wet nursing that have produced misinformation around breastfeeding in Black communities in Mississippi. At the structural level, it aims to decipher how bridging healthcare settings with mothers' homes, families and communities can ultimately narrow breastfeeding disparities for Black mothers.



21

**Part of Our World:  
North Korea's Exposure to World Commodity Prices**  
by Sewon Park '21

Contrary to popular belief, North Korea is not a “hermit kingdom” and since the late 1990s has developed global trade networks through a variety of state companies despite international conditions. How integrated North Korean industries really are to the world economy, however, remains unknown – particularly from an empirical standpoint. This paper uses satellite nighttime lights data and IMF reported world commodity prices to present three main findings. First, production intensity in coal-producing counties in North Korea is considerably responsive to increases in global coal prices. The same pattern is revealed for steel. This empirically confirms how the North Korean regime has strategically aligned its coal and steel production activity with global coal and steel price fluctuations, respectively. North Korea is and has been considerably intertwined with and connected to world markets and coal/steel prices. Second, our findings suggest that luminosity may reflect trade with China as well. Third, there is no relationship between Chinese producer prices and luminosity in commodity-specific producing regions. This indicates that the DPRK-Chinese relationship is far less market-driven and more characterized by geopolitical factors instead. These results demand a recalibration of our understanding of how North Korea maintains its regime, nuclear activities, and evades sanctions through its integrated economy and trade activity.



29

## Native Maize, Transgenic Contamination, and Intellectual Property Rights: The Case of San Miguel del Valle, Oaxaca, Mexico

by Adele Woodmansee '20

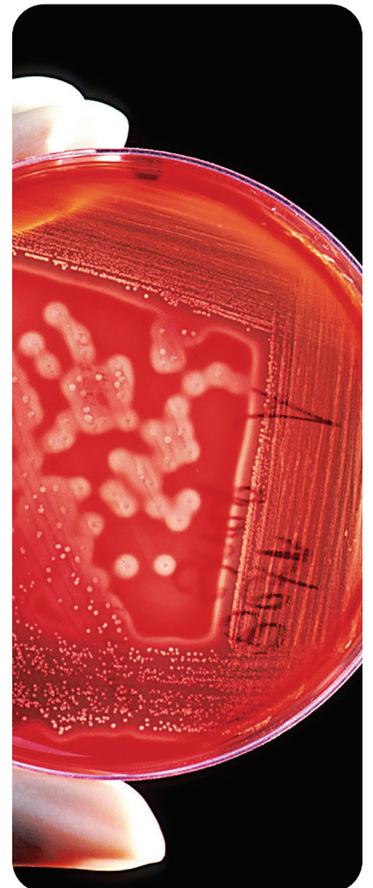
Mexico is the geographical center for the origin and diversity of maize (*Zea mays*). Native maize diversity in Mexico is tied to small-scale farmers' livelihoods, which are threatened as economic policies and climate change. The issue of transgenic contamination, or mixture between genetically modified maize and native maize varieties, has become a major point of debate in Mexico. Biopiracy of genetic material conserved by indigenous farmers is also an ongoing issue. In this paper, I combine scientific, political, and ethnographic perspectives on native maize diversity and transgenic contamination of native Mexican maize. I focus on the town of San Miguel del Valle, where I conducted ethnographic and genetic research, and I situate this case study within national debates about native maize. I argue that native maize seeds are politically powerful and reflect the uncertainty and importance of smallholder agricultural livelihoods in the context of neoliberal policies, climate change, and intellectual property law.

## Regulation of Transcription and Chromatin Structure by Spt6 and Elf1 in Yeast

by Ann Yang '22

40

In this paper, I summarize and discuss studies that use the budding yeast *Saccharomyces cerevisiae* to study eukaryotic transcription. This paper is framed around how the role of chromatin structure, the system of DNA packaging in eukaryotes, in regulating transcription by affecting DNA accessibility to transcribing proteins. The main focus of this paper is on studies that investigate the roles of the protein factors Spt6 and Elf1 in affecting chromatin structure and transcription. Major questions that are highlighted include: what are the mechanisms operating behind Spt6-mediated control of chromatin structure?, what are the consequences of that control for transcription?, and what is the relationship between Spt6 and Elf1, if any? My motivations for this paper are from experimental research started in Fall 2019 that was directed toward identifying mutations in the gene encoding Elf1 that suppress phenotypes a mutant allele of the gene encoding Spt6. I reviewed the literature surrounding these two proteins for a deeper understanding of their individual roles as well as their dependence on other cellular proteins. I also conducted this literature research to better inform future experiments that may be done to further elucidate the roles of Spt6 and Elf1 in transcription.



# Research

# From Hyper-Surveillance to Sudden Abandonment: On Reconfiguring Black Motherhood in the Fourth Trimester

Sandra Ojeaburu  
Harvard College '20

Black infants face disparities in breastfeeding initiation and duration that ultimately increase their risk of future health complications. In Mississippi, Black mothers face unique structural and sociocultural barriers to breastfeeding including discrimination in health facilities, first food deserts, and limited familial and community support. This project aims to understand how sociocultural and historical barriers affect Black Mississippians breastfeeding practices. With an understanding of these norms, it aims to uncover solutions that exist at the intersection of community-based postpartum care and science-based evidence and answer the question: How do Black mother support groups in Mississippi bridge gaps in breastfeeding initiation and duration? To address this question, I conducted ethnographic research in Jackson, Greenville, Clarksdale, and Indianola, Mississippi from June-August 2019. Out of interviews with 50 study participants, five main themes emerged explaining sociocultural barriers to breastfeeding initiation and duration amongst Black mothers: (1) Misinformation in the Black community (2) Perception of breastfeeding as “nasty,” (3) Perception of breastfeeding as an indicator of poverty, (4) Breakdown of familial support in breastfeeding and (5) The positive impact of “Baby Friendly Designations” at daily institutions. Findings showed that postpartum initiatives that focus on normalizing breastfeeding are most effective when they ensure that daily institutions are “Baby Friendly.” Moreover, community support groups are crucial in empowering Black mothers to initiate and continue breastfeeding.

## Introduction

“I think certain things like breastfeeding need to be pushed, especially if they are beneficial. The hospital does not do this enough. I do not think they really care. They rush us up out of the hospital after birth and they’re like, ‘take the baby, bye!’”

Thus, laments Rhonda, a Black mother from Mississippi on the dichotomy between the maternal healthcare in prenatal visits and the abrupt absence of postpartum care. Similar to Rhonda, many mothers highlight the paradoxical and fearful nature of this transitional period after birth. Known as the fourth trimester, this time often goes unnoticed and is battled with in silence—a stark contrast for mothers that had constant prenatal check-ups and visits with their OB/GYNs. This period has complex challenges, especially for single mothers. These include navigating the rocky and unequal terrain of childcare, hormonal changes that can often manifest in postpartum depression and for some mothers, all of these challenges lie atop a seemingly insurmountable buttruss—breastfeeding.

In Mississippi, health disparities exacerbate these challenges for Black mothers. Mississippi has ranked 50th in states with the most health challenges faced by women, infants and children (United Health Foundation, 2019). More specifically, breastfeeding initiation and duration rates in Mississippi rank amongst the lowest in the nation (CDC, 2018). According to the most recent Breastfeeding Report Card released by the CDC, on average 70% of all infants in Mississippi initiate breastfeeding while only 38.6% continued breastfeeding at 6 months. Compared to nationwide rates of 84.1% infants starting breastfeeding and 58.3% breastfeeding at 6 months—Mississippi rates are low (CDC, 2018). For Black infants, the disparities worsen, in Mississippi white infants are breastfed at a rate, 25 percentage points higher than that of Black infants (Merewood 2019). In addition to factors associated with race, low income, receiving Special Supplemental Nutrition program for

Women, Infants and Children (WIC), and earning less than a college education, all decrease mothers’ likelihood of breastfeeding their infants (Thomson, 2017). Geographic disparities are also evident, as women living in the South have lower rates of breastfeeding initiation (Thomson, 2017). This is an especially significant problem because breastfeeding can offer health advantages that address health disparities in Black communities (Anstey, 2017). For example, epidemiological evidence indicates that breastfeeding offers benefits for infants including reduced risk for ear, respiratory, and gastrointestinal infections and decreased likelihood to develop asthma, obesity, and diabetes. In addition, benefits for mothers include lower risk for developing type 2 diabetes, hypertension, and breast and ovarian cancers (American Academy of Pediatrics, 2012). Given the wealth of benefits, it’d seem as though breastfeeding should be more common—so why is it not?

While most women in the US are aware that breastfeeding is the best source of nutrition for almost all infants, they lack knowledge about its specific benefits. In Black communities, the underlying factors associated with low breastfeeding rates are complex. In addition to this lack of knowledge on the health benefits, factors deterring initiation include structural racism, discrimination against Black women in health facilities, distrust of the medical system by Black communities, cultural deterrents/stigma, and limited familial and community support (US Department of Health and Human Services, 2011).

This paper explores these aforementioned factors in order to understand how sociocultural and historical barriers affect Black Mississippians breastfeeding practices. Moreover, through tracing breastfeeding norms in Black communities, this paper will demonstrate how medical recommendations can create implicit value judgements and assign moral pathologies to Black mothers’ bodies. It aims to uncover solutions that exist at the nexus of community-based postpartum care and science-based evidence.

Through juxtaposing community-based care with the fissures and discontinuities that exist in Black maternal care within the healthcare system, I explore further the sociocultural barriers within Mississippi that result in lower breastfeeding initiation and duration amongst Black mothers. Ultimately, I answer the question: How do Black mother support groups in Mississippi bridge gaps in breastfeeding initiation and duration?

## Background

The American Academy of Pediatrics (AAP) recommends exclusive breastfeeding for at least 6 months after birth. Institutional neglect of the fourth trimester combined with distrust of healthcare professionals force many Black mothers to rely primarily on their families or friends for support while breastfeeding. This support often consists of education on breastfeeding techniques, how to ensure babies are sufficiently fed, how to feed babies that have difficult latching onto mother's breasts and how to pump breastmilk. However, when breastfeeding is not widely represented in mothers' communities, women that choose to breastfeed can face stigmatization and ultimately discouragement. Thus, the politics of breastfeeding in both Black communities and the way they collide, intersect, and align with recommendations in the healthcare systems must be analyzed. The following section unpacks this literature on the structural and institutional associated with barriers to breastfeeding for Black women.

### Political connotations of breastfeeding

Before analyzing the healthcare statistics or cultural views surrounding breastfeeding, it is necessary to identify the two lenses by which breastfeeding can be viewed. Professor of the sociology of gender, Linda Blum theorizes that breastfeeding is at the intersection of "corporeal" and "cultural" (Blum, 1999). Differentiating between these terms elucidates the way political meanings have been inscribed on Black women's bodies.

The term "corporeal bodies" refers to physical bodies. Medicine utilizes indications of symptoms or abnormalities that can be pathologized and then associated with illness. There is a standard of care since what is healthy is determined by medical evidence. Corporal bodies are not imbued with value judgements. However, the term "cultural body" is more abstract and highlights that health choices or recommendations can be obfuscated by often invisible, yet structural biases shaped by culture (Blum, 1999). Cultural bodies are saturated with value-judgements, political implications and sometimes moral pathologies. For Black mothers, in many hospital settings in the United States, their bodies have been labeled, even subconsciously, with cultural and political judgements that impact the medical treatment of their bodies. Often, Black mothers in the United States are unable to simply receive treatment for their corporeal bodies, as their care is often tinged by racist perceptions of this cultural body.

Black mothers in the United States have been associated with stereotypes that implicitly assign moral value to their bodily choices. In *Birthing a Slave*, Marie Schwartz outlines the use of doctors and medicine to monitor enslaved women's reproduction and also conduct medical experiments. These experiments subsequently reproduced racist notions about pain, and obstetrical hardness that deemed Black women's bodies as more durable, less susceptible to feeling pain, more fertile (Schwartz, 2006). Medical experimentation

from slavery era to Jim Crow era and targeted sterilization and hysterectomies onwards produced incorrect medical observations that only promoted a racist notion of Black mother's bodies. While medical experimentation and slavery were the most salient representations of the way racial inferiority was reinforced by medical practice, recent studies show the manifestations of these modes of thought in healthcare practices today. A study by Cynthia Prather, out of the CDC National Center for HIV, Hepatitis, STD and TB Prevention, found current disparities in socioeconomic status, education and limited access to health continue to affect access to support for Black women (Prather et. al, 2018). In addition, unconscious notions and tropes that Black women are "hypersexual," contribute to the way many are not supported as mothers (Prather et. al, 2018). Linda Blum articulates the lack of support can also be attributed to the bias that since Black mothers are incorrectly viewed as hyper fertile, they are seen as naturals at breastfeeding, not needing of breastfeeding support (Blum, 1999). This underlying assumption is dangerous and only decreases the support Black mothers get in learning to breastfeed and even care for their children.

Historical evidence and current practices suggest that stereotypes continue to impact Black mothers' medical treatment and ultimately shape the support they receive from doctors or nurses in formal medical institutions. The next sections articulate the discriminatory practices in hospital rooms that occur immediately after childbirth.

### Discrimination against Black women in health facilities

As the main location for new mothers to gain health education, hospitals play a pivotal role in destigmatizing breastfeeding. Yet, these same locales often exacerbate chronic stress or traumatic encounters in hospital room. Mothers' distrust stems from mistreatment that increases risk of health complications, decreases beneficial medical recommendations. On average, Black women report higher levels of physician distrust than White counterparts due to the unequal treatment (Armstrong, Ravenell, et. al, 2007). These bastions of care for many Black women become places imbued with fear or terror.

This distrust is grounded in both historic and present mistreatment. For instance, mothers that deliver at hospitals that serve high numbers of Black people are more likely to have serious complications including infections, birth-related embolisms and emergency hysterectomies — than mothers who deliver at institutions that serve fewer Black women (Creanga, 2014). In addition, for many Black mothers, racism and prejudice by healthcare workers, even subconscious, impact the way Black women's pain is perceived (Adams, 2017). In a study done by the World Health Organization analyzing mistreatment in maternity care in the US, Black mothers were more likely than white counterparts to experience mistreatment within hospitals such as loss of autonomy, being shouted at, scolded or threatened, ignored, refused or receiving no response to requests for help in delivery rooms (Vedam, 2019). These experiences of trauma impact postnatal mental health and family relationships (Reed, 2017).

In addition, disparities in medical interventions during childbirth increase risk of postpartum care complications amongst Black mothers. Black mothers are more likely to face complications in pregnancy that ultimately result in c-sections (Roeder, 2019). Consequently, medical interventions during birth, such as c-sections, increase the likelihood of formula feeding postpartum

and decrease mother's opportunity for immediate skin-to-skin contact with their child.

An added complication is that burgeoning research shows a link between increased c-section rates and the labor and delivery nurse patients assigned to mothers (Edmonds, 2017). Consequently, any bias that nurses have towards Black mothers can increase mothers' rates of c-section and therefore adversely affect breastfeeding initiation, milk supply and infant breastfeeding receptivity compared to vaginal deliveries (Hobbs, 2016). Therefore, greater risk of c-sections in Black births decreases mothers' breastfeeding likelihood.

Overall, this discrimination against women translates into decreased breastfeeding recommendations in hospitals. Anthropologist and law professor Khiara Bridges emphasizes the greater implications for this systematic discrimination through identifying the role healthcare professionals have in framing and defining risk in healthcare settings. She posits that the "risky population" often deemed as low-income, single Black mothers are objects and effect of regulation and management rather than recipients of sufficient care (Bridges, 2011). Bridges links medical staffs' negligence in encouraging breastfeeding to discriminatory practices that reduce Black women's agency (Bridges, 2011). She decries the judgment that many single Black mothers face in systems that label them as welfare queens that take advantage of social safety nets, or even selfish for daring to have children that healthcare professionals assume they cannot care for. In other words, these stereotypes aim to control Black mothers' behavior and bodily autonomy.

Consequently, anthropologist Dana-Ain Davis suggests medical treatment has become void of actual care and rather it has become intermingled with "racialized risk"<sup>1</sup> that intensifies surveillance and monitoring of infant safety, rather than mother's safety (Davis, 2019). It paints Black women as both being "at risk and they are risk" (Bigo, 2002; Davis, 2019). Therefore, despite healthcare professionals' presumable noble intentions, the unconscious bias and omissions of health recommendations may have detrimental effects on mother's perceptions of their own health.

### Structural Racism and the Abundance of First Food Deserts in Mississippi

In addition, due to structural racism, redlining, and unequal distribution of resources in Black communities, Black mothers are more likely to live in first food deserts in which the availability of lactation, birthing and childcare resources are limited. First food deserts are geographic areas where social and economic dynamics unequally constrain breastfeeding when compared with other locations (Seals Allers, 2017). Similar to food deserts in which a city's infrastructure can make it difficult to purchase nutritious and affordable food, first food deserts are infrastructural inadequacies in which there is no access to breastfeeding support.

A study done by the Kellogg Foundation in Jackson, New Orleans, and Birmingham—found trends in racial and economic disparities, childcare support, and cultural beliefs (Seals Allers,

2017). The study found that major characteristics of first food deserts in these regions were no "Baby-Friendly hospitals" within 35 minute commute, 50% or more of employers have no breastfeeding policy or places to nurse/express milk; 30% or more of childcare facilities were untrained to handle expressed milk; 50% or more of the public reports feeling uncomfortable when seeing a woman breastfeed; and there is a persistent and widespread lack of culturally relevant healthcare support, peer support, and public spaces that facilitate breastfeeding (Seals Allers, 2017). Overall, these structural barriers make breastfeeding initiation difficult for Black mothers, even for those that desire to breastfeed.

In the United States, the rate of implementation of evidence-based maternity care practices supportive of breastfeeding is lower among maternity care facilities in neighborhoods with larger black populations. While hospitals have recommended maternity care practices known as Baby Friendly Hospital initiatives, hospitals serving Black people are less likely to implement these practices (Lind 2014). Baby Friendly standards outline ways hospitals can encourage mothers to breastfeed. Listed in Figure 1, these guidelines require standard recommendation of breastfeeding for mothers.

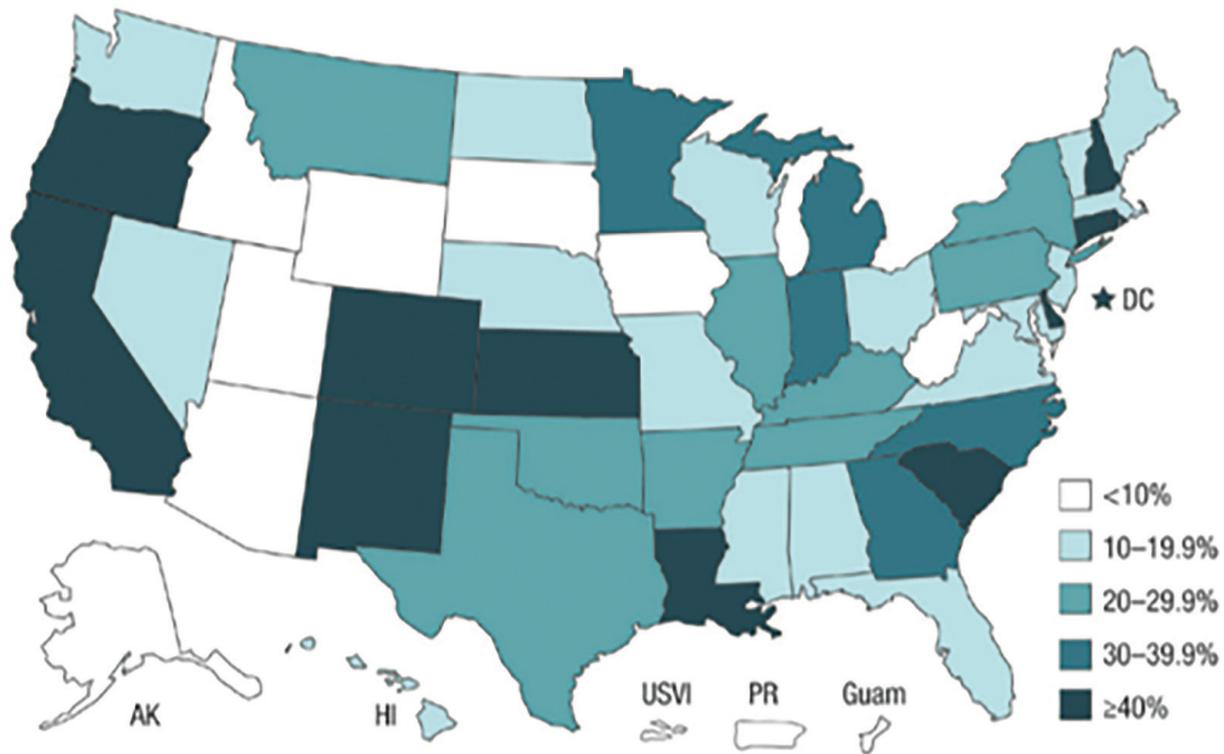
**Figure 1. Ten Steps to Successful Breastfeeding**

1. Have a written breastfeeding policy that is routinely communicated to all health care staff.
2. Train all health care staff in the skills necessary to implement this policy.
3. Inform all pregnant women about the benefits and management of breastfeeding.
4. Help mothers initiate breastfeeding within one hour of birth.
5. Show mothers how to breastfeed and how to maintain lactation, even if they are separated from their infants.
6. Give infants no food or drink other than breast milk, unless medically indicated.
7. Practice rooming in – allow mothers and infants to remain together 24 hours a day.
8. Encourage breastfeeding on demand.
9. Give no pacifiers or artificial nipples to breastfeeding infants.
10. Foster the establishment of breastfeeding support groups and refer mothers to them on discharge from the hospital or birth center.

However, there are racial disparities in access to these recommended maternity care practices. Comparing maternity facilities serving primarily non-Black patients with those serving Black patients, facilities with primarily non-Black patients were about two times more likely to have practices related to early initiation of breastfeeding, limited use of breastfeeding supplements and allowing mothers and infants to remain together after birth (Lind, 2014). These recommendations all make non-Black patients more supported in breastfeeding education. Moreover, these structural disparities for Black mothers worsen by state. As indicated in Figure 2, a map of the percentage of births that take place in Baby-friendly facilities, show the number of hospitals nationwide that sufficiently promote breastfeeding is particularly low in Mississippi with only 12.5% of births occurring in Baby-friendly facilities (CDC, 2018).

Worse yet, these same locations have higher rates of infant formula distribution. In *Skimmed*, legal scholar Andrea Freeman outlined hospitals historic practice of dispensing free formula and discharging mothers before they can receive guidance and support for nursing their newborns for incentives (Freeman, 2020). Historically, infant formula manufacturers partnered with doctors, hospitals, and WIC in predominantly, Black and low-income areas to provide mothers with infant formula at higher rates in order to gain funding in return (Freeman, 2020, 11; Blum, 1999). Therefore, even Black mothers that desire to breastfeed, depending

1. "Racialized Risk" is a term Davis uses to identify the unique way risk has been racialized and gendered. She yields political theorist Didier Bigo's conception of a type of surveillance that targets specific identities of people to draw parallels to the way some doctors and nurses manage and surveil Black mothers' bodies instead of caring for their overall wellbeing.



**Figure 2. Percentages of births at Baby-Friendly facilities in 2018, by state (CDC, 2018)**

on their environment already face structural barriers in their own communities.

### Cultural deterrents to breastfeeding in Black communities

While aforementioned structural barriers decrease breastfeeding initiation rates, cultural barriers also create environments in which breastfeeding is uncommon, and stigmatized. Previous research on breastfeeding norms in Black communities identify cultural deterrents such as the stigma associated with breastfeeding, lack of family and social support in communities, and embarrassment. These cultural deterrents are among barriers that are “modifiable” along with lack of knowledge, social norms, lactation problems, and employment and childcare (US Department of Health and Human Services, 2011). Further research is needed to understand the way specific cultural barriers to breastfeeding manifest in Mississippi’s unique landscape.

For some Black mothers in the US South, breastfeeding is uniquely stigmatized because it conjures memories and legacies of wet nurses during slavery and Jim Crow era. The significance of intergenerational trauma in the discussion of breastfeeding is important in understanding the way the practice of breastfeeding education is passed down from grandmother to mother and mother to child. In *Granny Midwives and Black Women Writers*, literary scholar Valerie Lee recounts this painful history through an analysis of slave narratives that recall “female slaves bearing the pain of swollen breasts, not permitted to nurse their offspring due to laboring elsewhere on the plantation” (Lee, 1996, 75). She further connects this history to the way Black writers such as Angela Davis depict Black women’s milk as “flowing [alongside] blood” and Toni Morrison who discusses the commodification of mother’s milk and resistance to this commodification by displaying characters who reclaim their right to breastfeed only their own children (Lee, 1996,

75-76; Davis, 1983, 9). This commodification of Black mothers’ milk during slavery and wet nursing contribute to trauma and stigma surrounding breastfeeding practices. Legacies of wet nursing imbue breastfeeding practices with negative feelings and may impact breastfeeding initiation and duration.

Moreover, tropes that stereotype Black mothers as having natural abilities to breastfeed only decrease the support that mothers have when learning how to breastfeed their children. Tropes with origins dating back to slavery and Jim Crow era contribute to racial bias surrounding Black mother’s ability to breastfeed. The “Aunt Jemima” and “Black Mammy”<sup>2</sup> caricatures both suggest Black mothers were viewed as naturally being good at breastfeeding and family centered (Davis, 2019). These tropes are dangerous as they create an impression that Black mothers do not need support in breastfeeding which is not the case. In fact, this directly contradicts the low rates of breastfeeding initiation and duration among Black women. When Black mothers are stereotyped as being “naturals” at breastfeeding they are more likely to be given less psychosocial and physical support in learning how to feed their infants.

Historically, doulas<sup>3</sup> have been effective in providing psychosocial support that Black mothers. Doulas help reduce the rate of c-sections, interventions during childbirth, and increase the rate of breastfeeding (Rab, 2019). Moreover, they alleviate some of the socioeconomic factors that contribute to poor maternal health, such as limited access to education or social support networks. Even yet, there is minimal research on the viewpoints of midwives and

2. The “Mammy” caricature arose as a depiction of the Black woman as a loyal servant in White households forced to care for White children and ultimately neglect her own (Clinton 1982).

3. Doulas are trained companions who are not healthcare professionals and who support individuals through health-related experiences

doulas on support mothers in breastfeeding. In this paper, while midwives and doulas often work within medical establishments, this study garners their voices and places them as belonging at a unique intersection where the healthcare system and mothers' home lives meet.

In addition, research on breastfeeding initiation and duration highlights that minimal research has been done to acknowledge these aforementioned sociohistorical factors that impact breastfeeding rates amongst Black mothers (De-Vane Johnson, 2018). Therefore, the goal of this research is to further unpack these sociocultural and historical deterrents to breastfeeding for Black Mississippians and the way social support networks motivate mothers to breastfeed their children.

## Research Methods

### Study Design and Recruitment

From June to August 2019, I conducted an ethnographic study that began in Jackson, Mississippi and ultimately spread to the cities of Greenville, Clarksdale, and Indianola, Mississippi. Participants were recruited informally through word of mouth after establishing connections with grassroots reproductive justice advocates, doulas and a local Baby Cafe primarily serving women on Medicaid/WIC and working with a grassroots political campaign. Inclusion criteria for this study included: Black mothers at least 18 years of age; grassroots organization or non-profits that supported prenatal or postnatal maternal care, healthcare providers, reproductive justice advocates, doulas, and/or midwives. These criteria ensured an understanding of the role of community-based organizations outside the purview of healthcare systems and medical establishments and the role doctors have in breastfeeding recommendations. Furthermore, doulas and midwives were included in this sample population because a key element of this research included analyzing the displacement of traditional birth workers. Data from study participants were collected as part of ethnographic fieldwork with the purpose of understanding barriers to breastfeeding initiation and duration in Black birthing communities.

### Data Collection

An ethnographic approach to generating data was chosen including the use of life history methods, participant observation and unstructured interviews. This approach was employed in the present study because qualitative methods focus on mothers' unique breastfeeding and postpartum experiences and perceptions of maternal healthcare while garnering the unspoken and often encoded meaning surrounding Black birth stories that go unheard. Detailed field notes were taken in each observation session. To supplement observational data gathered in community settings, in-depth unstructured in person interviews were conducted with 50 study participants in Mississippi to assess women's attitudes, beliefs, and perceived support of breastfeeding amongst Black community members. These interviews were all recorded and detailed notes were taken during each. Interview questions aimed to understand how Black mother support groups in Mississippi and bridge gaps in breastfeeding initiation and duration. Example interview questions included: What location do you go for maternal health location? How do you define satisfactory maternal care? Where do you get maternal care that is satisfactory? How do you family members support postpartum care? Further questions

probed mothers' experiences gaining maternal health education and overall experiences in the birthing process.

### Setting and Participants

More specifically, this ethnographic field research was conducted in the cities of Jackson, Greenville, and Clarksdale, Mississippi. Through a mix of participant observation, site visits, and interviews, this study observed locales in which Black mothers seek psychosocial support during pregnancy and postpartum care. Ethnographic fieldwork was conducted in 4 types of locations: Participants' homes, Baby Cafes in Jackson, Greenville and Indianola, Diaper Bank of the Mississippi Delta in Clarksdale, and Hypno-birthing yoga studios. Much of data collection came from interviews and in-depth notes taken during weekly attendance of Baby Cafe breastfeeding and birthing support groups in which predominantly Black mothers on WIC/Medicaid met weekly to gain free resources and education on birthing, breastfeeding and motherhood. 50 people were interviewed for approximately 1 hour, in either home settings, Baby Cafes, local gathering spaces such as coffee shops or the Jackson Medical Mall.

### Ethical considerations

This study was subject to ethical review and approval through the Harvard Institutional Review Board (IRB) of the Harvard University-Area Committee on the Use of Human Subjects under IRB protocol case number IRB19-0862. Participation was voluntary and based on informed consent, with confidentiality and anonymity assured unless specifically requested. To request full identification, participants were given the option to opt-in to use their real name on the informed consent form. This was particularly important in Mississippi, given the history of research, especially health related research in which Black individuals were not given the opportunity to consent to experimentation or were not attributed ownership over their own narratives. Moreover, given the sensitivity around reproductive justice and pregnancy care, support services including social worker contact numbers were kept on file at each interview in the case of emotional distress caused by discussion of birthing experiences. Finally, all interviews were audio-recorded, and notes were taken through password protected software.

### Data Analysis

The audio recordings were transcribed verbatim following each interview and checked with field and interview notes for accuracy. The material was read through several times and then coded. The codes were further collapsed into themes, allowing construction of an exploratory theoretical framework. Moreover, to undergird research, data was analyzed with anthropological theory based primarily in the works of medical anthropologists with a focus on Black feminist theory.

Moreover, each participant was given their individual interview recordings after interviews and were given the opportunity to read anonymized data analysis and provide feedback. Moreover, in August 2019, all participants were included in an in-person read out and presentation of findings based on their interviews. They were given the opportunity for further discussion in this presentation and to verify accuracy of these findings. By July 2020, participants were given all data and analysis collecting in this study to share feedback and distribute in their communities. This was particularly important given the sacredness of each individuals' story and to combat the often-extractive nature of research.

## Results

Analysis of the interview transcripts revealed 5 main themes affected to breastfeeding initiation and duration. Three themes addressed barriers to breastfeeding initiation and two themes addressed barriers to breastfeeding duration. Themes that arose pertaining to breastfeeding initiation included (1) Misinformation in the Black community that configured breastfeeding as dangerous, (2) Perception of breastfeeding as “nasty,” and (3) Perception of breastfeeding as an indicator of poverty in Black communities. While the themes related to breastfeeding duration were (4) Breakdown of familial support in breastfeeding and (5) The positive impact of “Baby Friendly Designations” at daily institutions. The themes are highlighted and discussed through the use of direct quotations and responses from participants.

### Theme 1: Misinformation on the dangers of breastfeeding

This theme encompasses two main subcategories that contributed to this configuration of breastfeeding as a dangerous act: first discriminatory health recommendations for Black women by healthcare professionals that discouraged or omitted breastfeeding education; as a result, misinformation in Black communities passed down intergenerationally.

First, all 50 participants interviewed shared negative experiences they have witnessed with healthcare professionals. One mother in particular was Chanel, a Black single mother on WIC who was a client of Shanina, a Black certified lactation counselor (CLC). In 2018, Shanina received an unexpected call from Chanel, who was hysterically crying, saying the hospital was not letting her see her newborn baby. Shanina remembered getting off the phone and thinking, “what, that makes absolutely no sense.” Confused but enraged, Shanina immediately drove to the hospital to assist Chanel. After interrogating nurses and hospital staff, she discovered that, “the nurse on staff the night of Chanel’s birth ‘was just being lazy,’” according to another nurse Shanina spoke with. Chanel had a c-section and several health issues post-pregnancy that made breastfeeding difficult, but because of what she’d learned at Baby Cafe support sessions, she still wanted to breastfeed her child. The delivery nurse would have had to supervise Chanel and teach her to breastfeed for a few days and did not want to. Shanina even found that nurses had been giving formula to Chanel’s baby. This instance shows clear negligence and indifference in a healthcare setting. However, it seems that the hospital staff was more than simply incompetent. Why would medical professionals do everything in their power to prevent Chanel from breastfeeding her child when both breastfeeding and skin-to-skin contact are medically recommended? The hospital staff’s disregard for a scientifically-grounded medical necessity, suggest the low rates of breastfed Black infants is more complex than neglect.

For another Black mother named Latisha the answer to the aforementioned question is bias towards Black mothers. Latisha said that she “was never asked if she wanted to breastfeed and was never given this option after her delivery.” Nurses even assumed she was on WIC, despite Latisha’s direct response that she did not qualify and also did not include her husband on her child’s original birth certificate. They incorrectly assumed Latisha was a Black single mother on WIC. Latisha’s experiences suggest the immediate assumptions that some healthcare professionals have when they have Black female patients. Another mother of four named Rhonda

experienced this trend firsthand and said, “in hospitals, they want the easy way out, so they give babies bottles,” alluding to the limited attention or psychosocial support mothers receive after birth. Overall mothers found even if they wanted to breastfeed, when healthcare professions do not recommend breastfeeding or support it in delivery rooms, initiation becomes increasingly difficult. Postpartum care immediately after birth, impacts infants’ lives and mothers’ future ability to feed their children.

One participant echoed the insidious nature of discrimination in postpartum care and the way it propagates economic injustice. Alex works at a nonprofit that addresses food insecurity in the Mississippi Delta. He said, “in rural areas, such as Sunflower County they have no access to baby formula, yet when they go to the nearest birthing hospital which is more than 100 miles away, they are told not to breastfeed and are recommended baby formula.” Though breastfeeding after birth is the most inexpensive option and the most physically accessible option for mothers, hospitals still opt for recommending formula. This practice is both discriminatory and dangerous as it leads to food scarcity for children, as buying infant formula in existing food deserts is unsustainable.

While 49/50 participants outlined the instances of discrimination and mistreatment they or birthing clients have faced in medical establishments, one woman pointed to the greater culture of bias in the medical field. Black mother and Black gynecologist at the University of Mississippi Medical Center named Dr. Jones, argued “the problem is, Mississippi just has so many sick patients. People with diabetes, obesity, hypertension, and first place in heart disease. These are all illnesses that complicate pregnancy. You also see more medical roles and resources in a single cubicle in Boston or New Haven than here. It’s just hard.” While she admitted to knowing many doctors and nurses with strong racial prejudice, Dr. Jones added that the hospital is a place where racial bias can manifest in health guidance, especially when hospitals are understaffed and resourced. The limited resources combined with a greater culture within “risk-management” removes the psychosocial support that Black mothers need to validate their concerns and desires.

Many Black participants acknowledged that they internalized these recommendations that promote infant formula over Black mother’s own breastmilk. Several mothers noted that the fact that doctors and nurses did not support their breastfeeding practices in the hospital, which made mothers question how safe their bodies were for their own children. Mothers interpreted these medical recommendations against breastfeeding as their own moral failings. Consequently, many mothers avoid breastfeeding because they thought the very act of breastfeeding their child was “dangerous for their children”. Participants noted this misinformation was passed down intergenerationally. For instance, Jameyshia, the director of the Mississippi Birth Coalition said, “breastfeeding began to become popular amongst African American mothers in 2015 in Mississippi. The norms were that in hospitals, doctors would not give Black mothers skin to skin time with their infants, so mothers were not used to that and mothers were not given the option to breastfeed, so they did not think breastfeeding or skin to skin were natural. Before, mothers would have to ask for skin-to-skin—fight for it.” This example of health recommendations’ impact is momentous and has the potential to shape birthing epistemologies on what is perceived as “natural” to Black mothers about their own bodies.

Finally, amongst participants, the phrase “trust” was used in 12 different interviews, primarily when comparing the way mothers

were treated in hospital settings and in support networks like the Baby Cafe. The dialectic of trust and distrust existed hand in hand within every interaction participant had with medical establishments. There was inconsistency in the message that is being sent to these mothers on the topic of breastfeeding and this primarily comes from their doctors and nurses that have been the authority on maternal health. As a result, mothers begin to internalize negative perceptions of their own bodies and their relationship to newborns. Misinformation about breastfeeding within communities made mothers less likely to breastfeed and without correction by doctors or nurses in hospital settings, many mothers continued to view breastfeeding as abnormal.

### **Theme 2: Perceptions of breastfeeding as “nasty”**

While all participants acknowledged the health benefits of breastfeeding and would quote a common mantra, “breast is best,” more than half of study participants noted the pervasiveness of negative perception of breastfeeding in their communities as nasty, risky or unnatural. Jackie, a Black mother and founder of a Black mother’s support group discussed the perilous nature of including breastfeeding in the name of her initiative, she said “I named my support group, ‘Let’s talk...baby’ because I knew no one would come if I said, ‘Let’s talk about breastfeeding. Women don’t breastfeed for so many reasons. Some think it is nasty... the history of breastfeeding here is one where women just don’t want to take the chances.’” Jackie outlined the several reasons for low breastfeeding initiation rates in Black communities but highlighted the points of it being “nasty” and a risk to Black mothers. This perception was further grounded by several Black mothers’ experiences of harassment when they decided to breastfeed.

At a Baby Cafe session, a Black mother named Taya expressed that she felt discouraged by family and friends who thought breastfeeding was “nasty.” She exclaimed, “if you see horses, giraffes, dogs they breastfeed, why can’t we?” Another mother named Julia described how she heard a Black employer tell a woman she could not breastfeed in public, though the employer herself was a clinician and a woman. She added, “people are only against displaying breasts when it is for breastfeeding, but you don’t see them telling ‘Ms. Cha Cha’ over there to stop and cover up.” Both mothers raise the ways the sexualization of women’s bodies has created a complicated dilemma for Black mothers. In a conservative state such as Mississippi, breastfeeding in public, while a legal right, is still viewed with judgement. Black mothers that dare breastfeed incur greater social stigma both in public settings and even in private settings with family and friends.

### **Theme 3: Breastfeeding as a symbol of poverty in Black communities**

While the aforementioned themes were most associated with misinformation on the benefits of breastfeeding, the theme of poverty is particularly insidious because the link between poverty and breastfeeding is based in cultural lore, historic wounds and present-day classism.

Kandiss, a Black mother of two children and pharmacist talked about how low breastfeeding rates, “date back to slavery times when women were wet nurses and cared for other people’s kids. So now [breastfeeding] is a symbol of poverty.” She unpacked Black women’s reception to coercive and racist infant formula marketing techniques that targeted Black mothers and said, “Black mothers buy formula

just to show that they can take care of their kids. Even though we know that it is healthier for our kids.” Kandiss concluded, “because we don’t need to breastfeed, we don’t.” Kandiss unpacked how the stigma associated with breastfeeding has led to its association with poverty. Michelle, a Black doula and reproductive justice advocate expressed empathy towards Black mothers that choose formula. She said, “due to the trauma that they have faced, since historically, Black women who breastfed, had to feed master’s child before they fed their own, many grandmothers did not breastfeed their children.” Michelle’s account illuminated the nuances in breastfeeding that connect trauma and memory to Black mothers breastfeeding rates in present day Mississippi. This intergenerational trauma that is unspoken between mothers and daughters manifests itself in discouragement of breastfeeding and tension between daughters who want to breastfeed and mothers who discourage it.

### **Theme 4: Breakdown of familial support in breastfeeding**

Amongst my study participants, those that overcame barriers to breastfeeding initiation were met with obstacles when garnering familial support while breastfeeding. They found that on many occasions their home environments were discouraging and derailed their progress. Therefore, breastfeeding while balancing jobs and convincing family members not to feed their newborns infant formula all decreased breastfeeding duration. One woman named Charnice said, “When I first had my daughter Elicora stay with my mother, while I was at work, she gave her formula even though I told her not to. I stopped letting Elicora stay with her after that.” Similarly, another participant named Maggie, who was the director of a Baby Cafe in Greenville, acknowledged this norm in a support group meeting. She said, “Black women need to breastfeed more or find these support groups because often it can feel like we are the only one in our family breastfeeding—but you’re not alone.” This reassurance was important to the 16 women at the meeting because when each woman was asked if they had an environment outside of the Baby Cafe that was supportive of breastfeeding, the response was a resounding, “No.” Many stated that their mothers and relatives were not aware of the health benefits associated with breastfeeding and tried to feed the newborns baby formula.

One participant named Ruth, the director of the Baby Cafe in Jackson, provided an explanation for this generational divide and extra hurdle that present-day mothers are facing in Mississippi. She said, “there is a whole generation without breastfeeding because it stopped being promoted in the 1960s. The worst part is, people think it’s sexual or incestual, but this just is not true. The solution is changing the culture of how people look at breastfeeding.” Participants, especially single mothers who depended on family members for childcare, emphasized the specific difficulty of having unsupportive mothers. Breastfeeding while balancing work was difficult, but it was near impossible to make sure that family members respected their wishes not to feed their children baby formula. Only one mother in this study found breastfeeding continuation easy. When Kira was asked about the reason for her success she said, “I didn’t have a choice but to breastfeed.” She explained that her mother and grandmother had all breastfed their children, so it is something that was a given for her. This divergent and rare occurrence amongst study participants reiterated the impact familial support has on breastfeeding duration and the reason many depend on a community of like-minded mothers for support.

### Theme 5: Positive impact of Baby Friendly designation at daily institutions

Baby Friendly designated institutions, though increasingly ubiquitous, are burgeoning developments in Mississippi that aim to normalize a culture that supports breastfeeding mothers. These are institutions with specific areas for mothers to express milk. In the Baby Cafe of Jackson, the director Ruth ensured that mothers knew the breastfeeding mandates in their workplaces. She would ask every single mother in each session, “does your workplace have a place to express milk because it is required by law that they do.” If the answer was no, Ruth would make calls right after the session to employers and send emails to ensure that the workplace was compliant. Mothers that attended the Baby Cafe were particularly grateful and one mother name Carey said, “the Baby Cafe reaches out to businesses and my work to make sure they are baby-friendly, which is great.” Ensuring that Black mothers had a space that was supportive of breastfeeding was particularly important for Ruth who understood the gravity of spaces for Black women. She spoke of her childhood and mentioned, “my mother and father always told me that own your own space. They did what they could and owned their own house and plot of land in the Delta. I learned it from them that to change anything and be in control of outcomes, it’s all about space.” Ruth alludes to the particular gravity of land ownership and autonomy in the context of Mississippi with legacies of slavery, Jim Crow, and other ways land ownership has not always been a right for Black populations. Ruth linked this concept of spatial ownership to a feeling of belonging. She knew that mothers were more likely to continue breastfeeding if they had peer, familial supports and workplaces spaces for expressing milk.

Participants aligned on this aforementioned point and agreed that to promote Black motherhood, it is important to normalize breastfeeding in commonly attended institutions such as churches, schools, classrooms, grocery stores and other places of daily life. One mother named Charnice said “I really enjoyed when we went to the museum as a group during MOB (Mothers out Breastfeeding). I felt confident with other mothers.” MOB is a program that allowed Black women to breastfeed in public areas from museums to grocery stores and while many faced criticisms, they began to destigmatize this practice and encourage community support for mothers. The significance of normalizing culture around Black mothers breastfeeding is particularly important in rural areas of Mississippi Delta. One mother at a Baby Cafe in Greenville noted that “the church is not helpful when it comes to this because they are judgmental.” She talked about how she grew up in an AME (African Methodist Episcopal) church and that “they judge people and do not promote breastfeeding. But the church is a public institution since it is state funded, so it should be treated that way, and they should have to promote breastfeeding and healthy practices.” Her point introduces an approach to promoting healthy motherhood at the nexus of daily life and healthcare institution.

Another breastfeeding advocate named Jamila echoed this sentiment and said, “we operate in tribes in the Black community. We are just not very trusting of different cultures or people we do not know. And rightfully so, we have a history of people we cannot trust in the healthcare system.” Jamila emphasized that medical institutions are not the only locales of care to blame, but also women’s own families who judge breastfeeding and perpetuate stigma.

Instead, groups such as the Baby Cafe bring scientific

evidence-based education to supportive culturally grounded communities of Black mothers. The Baby Cafe also provided education that made mothers feel confident in their decisions for their children. For example, many mothers stated that they did not have much exposure to breastfeeding before the Baby Cafe and enjoyed the following topics the most: health benefits of breastfeeding for mothers and infants, breastfeeding as birth control, breastfeeding positions, baby sleeping positions, latching positions, birthing positions in labor, hospitals do’s and don’ts, and baby CPR. One mother named Jule in particular said at the Baby Cafe, “I learned to advocate for myself and be firm in whatever decision I have for my child.” In the auspices of the Baby Cafe, mothers noted that they felt at “home.” Another mother named Kim said, “before this group, when I was pregnant, I felt alone. I was told by my sperm donor that he wished something bad happened to my baby...As a single parent, it is lonely, so this place gave me the support I needed and gave me hope.” While another mother praised the Baby Cafe and said, “I am grateful for a community of people I can rely on to make sure my baby and I feel okay.” Finally, Charnice, the mother who has enjoyed the MOB trip said, “The Baby Cafe, provides more than breastfeeding—it’s like therapy.” Overall, there was astounding support for Baby Cafes in changing the culture around motherhood for participants and making it an experience bolstered with psychosocial support and a community of peers.

Jackie, founder of the “Let’s Talk—Baby” support group, echoed the significance of these support groups succinctly, “there are so many conversations that we can have that doctors do not hear because women do not tell their doctors. They rely on fellowship with one another and gain advice from discussing with each other.” Given this history and inaccessibility of healthcare Jackie proposed for a turn to community based psychosocial care. She said that there’s a saying she heard, “anything that you need, you’ll find it in the community.” Indeed, the knowledge and expert support combined with culturally relevant and relatable dialogue helped mothers feel informed, engaged and empowered.

### Discussion

This paper emphasized the necessity for structural changes to postpartum care and cultural changes in Black mothers’ daily sectors of life. The utility of the Baby Café and Baby Friendly institution designations aligns with previous research that shows integrated models of maternal care are effective in long-term improvements in population health (Reis-Reilly, 2018). Specifically, integrated public health interventions that use a socioecological model to identify systems-level factors that affect both individual and community health have been shown to be most effective in creating sustainable organizational and community shifts in maternal health care (Reis-Reilly, 2018). In other words, campaigns that designate daily spaces such as classrooms, workplaces, hospitals, churches, and grocery stores as Baby Friendly, work to address these community level barriers to breastfeeding and successfully shift cultural practices. Ultimately, both grassroots support groups such as Baby Cafes and daily institutions that give mothers spaces to express milk or teach breastfeeding education, can help to normalize breastfeeding amongst Black mothers.

Furthermore, these findings bolster previous research that show inadequacies in focusing solely on individual health behavior in addressing the needs of communities (Reis-Reilly, 2018).

This research illuminated the multifaceted barriers that Black mothers face in breastfeeding initiation and duration including discrimination in hospitals, misinformation in communities, cultural beliefs around breastfeeding and lack of support. These barriers all focus on the way Black mothers in Mississippi interact with their local healthcare professionals, family members, breastfeeding landscape, and respond to stressors and disparities in care, as opposed to their own individual beliefs. In this way, this research focuses primarily on changing systems and community norms as opposed to individual beliefs. Consequentially, this work provided a lens into the different elements of Black Mississippians' maternal health landscape that make psychosocial support while breastfeeding often unattainable.

Finally, this research presented distinct and nuanced relationships between intergenerational trauma, legacies of wet nursing and historical perceptions of breastfeeding that deterred Black mothers from breastfeeding. This discourse bridged gaps in existing literature that acknowledge the need for studies on Black breastfeeding practices to pay particular attention to the embodied experience of historical trauma (De-Vane Johnson, 2017). This work emphasizes the need for sensitive and culturally relevant approaches to both research and public health interventions.

Overall, mothers' postpartum experiences must be fully integrated and accepted by their communities. Breastfeeding must be openly discussed in Black mothers' workplaces, gathering spaces and day to day lives. Given the mistreatment in hospitals by doctors and nurses, mothers must seek other methods of gaining the lactation education and support they need. Instead, community spaces need to normalize mothers out breastfeeding and more programs that embrace public and unapologetic breastfeeding and other aspects of mothering.

The depth of participant interviews and analysis of perceptions of breastfeeding are some of the study's greatest strengths as these rich anecdotes allowed for documentation of shifts in cultural norms. However, several limitations bear mentioning as well, particularly the small sample size that spanned across multiple cities in Mississippi. Data collection offered a wide variety of socioeconomic status, but given participants were recruited word of mouth, this method self-selected for mothers with similar birthing experiences that were often negative. Finally, the variability in familial support amongst participants may limit the generalizability of these study results given mothers depend on these institutions to different extents given their family background.

## Conclusion

These findings point to the significance of grassroots spaces embedded in Black mothers' daily lives that allow for peer support during breastfeeding. While disparities faced within hospitals are necessary areas of improvement, expansion of Baby Friendly Initiatives in institutions nationwide holds great promise for normalizing breastfeeding and advocating for mothers.

Future work would include the disparities faced by Black mothers in attaining childcare services and workplace policies on breastfeeding. The same structural inadequacies within workplaces that do not offer sufficient maternal leave or financial assistance for childcare plans also minimize the ability of mothers to breastfeed for the full recommended 6 months to 1 year. In addition, it is critical that workplace dynamics be explored further. Through encouraging

breastfeeding in everyday spaces, this signals to communities that Black motherhood is important and must constantly be acknowledged, embraced and accepted. Ultimately, hospitals must begin by standardizing breastfeeding recommendations across all patients and daily institutions must continue the work to normalize supporting new Black mothers in communities.

## Acknowledgements

I thank all study participants for their willingness to share such intimate and sacred stories, especially the Baby Café of Jackson where I spent my time once a week for 3 months. I also thank Dr. Carter and Dr. Kleinman from the Anthropology department and Dr. Susan Lipson from the Human Evolutionary Biology department for their support in editing, scoping, and development of this project that is an excerpt from senior thesis research. Special thanks to Courtney DeLong for her shrewd edits, for which I am so grateful. In addition, I thank the Center for American Political Studies and the Harvard College Research Program for funding this research project.

## References

- Adams, R. 2017. Study Suggests Reason Why Black Mothers Breastfeed Less Than White Moms. *Huffington Post*. [https://www.huffpost.com/entry/black-mothers-breastfeedi\\_n\\_5721316](https://www.huffpost.com/entry/black-mothers-breastfeedi_n_5721316)
- American Academy of Pediatrics. (2012). Breastfeeding and the use of human milk. *Pediatrics*.
- Anstey, E. H. (2017). Racial and Geographic Differences in Breastfeeding—United States, 2011–2015. *MMWR. Morbidity and Mortality Weekly Report*, 66. <https://doi.org/10.15585/mmwr.mm6627a3>
- Armstrong, K., Ravenell, K. L., McMurphy, S., & Putt, M. (2007). Racial/ethnic differences in physician distrust in the United States. *American journal of public health*, 97(7), 1283–1289. <https://doi.org/10.2105/AJPH.2005.080762>
- Bigo, D. (2002). Security and Immigration: Toward a Critique of the Governmentality of Unease. *Alternatives*, 27(1\_suppl), 63–92. <https://doi.org/10.1177/03043754020270S105>
- Blum, L. (1999). *At the breast: Ideologies of breastfeeding and motherhood in the contemporary United States*. Boston: Beacon Press.
- Bridges, Khiara M. (2011). *Reproducing Race: An Ethnography of Pregnancy as a Site of Racialization*. Berkeley: University of California Press.
- Center for Disease Control. (2018). Breastfeeding Report Card United States 2018. <https://www.cdc.gov/breastfeeding/pdf/2018breastfeedingreportcard.pdf>.
- Clinton, C. (1982). *The plantation mistress: Woman's world in the old South*. New York: Pantheon Books.
- Creanga, A. A., Bateman, B. T., Mhyre, J. M., Kuklina, E., Shilkrut, A., & Callaghan, W. M. (2014). Performance of racial and ethnic minority-serving hospitals on delivery-related indicators. *American journal of obstetrics and gynecology*, 211(6). <https://doi.org/10.1016/j.ajog.2014.06.006>
- Davis, D. (2019). *Reproductive injustice: Racism, pregnancy, and premature birth (Anthropologies of American medicine)*. New York: New York University Press.
- Davis, A. (1983). *Women, race & class*. New York: Vintage Books
- DeVane-Johnson, S., Gisco, C. W., Williams, R., 2nd, Fogel, C., & Thoyre, S. (2018). A Qualitative Study of Social, Cultural, and Historical Influences on African American Women's Infant-Feeding Practices. *The Journal of perinatal education*, 27(2), 71–85. <https://doi.org/10.1891/1058-1243.27.2.71>
- Edmonds, J.K., O'Hara, M., Clarke, S.P., Shah, N.T. (2017). Variation in

- Cesarean Birth Rates by Labor and Delivery Nurses. *J Obstet Gynecol Neonatal Nurs.*;46 (4) :486-493.
- Fraser, G. (1998). *African American midwifery in the South: Dialogues of birth, race, and memory.* Cambridge, Mass.: Harvard University Press.
- Freeman, A. (2020). *Skimmed: Breastfeeding, race, and injustice.* Stanford, California: Stanford University Press.
- Hobbs, A.J., Mannion, C.A., McDonald, S.W. et al. (2016). The impact of caesarean section on breastfeeding initiation, duration and difficulties in the first four months postpartum. *BMC Pregnancy Childbirth* 16, 90. <https://doi.org/10.1186/s12884-016-0876-1>
- Lee, V. (1996). *Granny midwives and Black women writers: Double-dutched readings.* New York: Routledge.
- Lind, J., Perrine, C. et.al. (2011). Racial Disparities in Access to Maternity Care Practices That Support Breastfeeding — United States, 2011. *MMWR. Morbidity and Mortality Weekly Report.* <https://www.cdc.gov/mmwr/preview/mmwrhtml/mm6333a2.htm>
- Merewood, A. (2019). Addressing Racial Inequities in Breastfeeding in the Southern United States. *Pediatrics.* <https://pediatrics.aappublications.org/content/143/2/e20181897>
- Prather, C., Fuller, T. et.al. 2018. *Health Equity.* Dec 2018. 249-259. <http://doi.org/10.1089/heq.2017.0045>
- Rab, L. (2019). The Secret to Saving the Lives of Black Mothers and Babies. *Politico.* <https://www.politico.com/news/magazine/2019/12/15/black-mothers-matter-079532>
- Reed, R., Sharman, R. & Inglis, C. (2017). Women's descriptions of childbirth trauma relating to care provider actions and interactions. *BMC Pregnancy Childbirth* 17, 21. <https://doi.org/10.1186/s12884-016-1197-0>
- Reis-Reilly, H., Fuller-Sankofa, N., & Tibbs, C. (2018). Breastfeeding in the Community: Addressing Disparities Through Policy, Systems, and Environmental Changes Interventions. *Journal of human lactation: official journal of International Lactation Consultant Association*, 34(2), 262–271. <https://doi.org/10.1177/0890334418759055>
- Roeder, A. (2019). America is Failing its Black Mothers. *Harvard Public Health Magazine.* [https://www.hsph.harvard.edu/magazine/magazine\\_article/america-is-failing-its-black-mothers/](https://www.hsph.harvard.edu/magazine/magazine_article/america-is-failing-its-black-mothers/)
- Schwartz, M. (2006). *Birthing a slave: Motherhood and medicine in the antebellum South.* Cambridge, Mass.: Harvard University Press  
Armstrong, Ravenell, et. al, 2007)
- Seals Allers, K. (2017). *The Big Letdown: How Medicine, Big Business, and Feminism Undermine Breastfeeding.* St. Martin's Press.
- Thomson, J. L., Tussing-Humphreys, L. M., Goodman, M. H., Landry, A. S., & Olender, S. E. (2017). Low rate of initiation and short duration of breastfeeding in a maternal and infant home visiting project targeting rural, Southern, African American women. *International breastfeeding journal*, 12, 15. <https://doi.org/10.1186/s13006-017-0108-y>
- United Health Foundation. (2019). *America's Health Rankings.* <https://www.americashealthrankings.org/about/methodology/our-reports>
- U.S. Department of Health and Human Services. (2011). *The Surgeon General's Call to Action to Support Breastfeeding.* Washington, DC: U.S. Department of Health and Human Services, Office of the Surgeon General.
- Vedam, S., Stoll, K., Taiwo, T.K. et al. (2019). The Giving Voice to Mothers study: inequity and mistreatment during pregnancy and childbirth in the United States. *Reprod Health* 16, 77. <https://doi.org/10.1186/s12978-019-0729-2>
- World Health Organization. (2005). *Baby Friendly Hospital Initiative.* World Health Organization. <https://www.who.int/nutrition/bfhi/en/>

# Part of Our World: North Korea's Exposure to World Commodity Prices

Sewon Park  
*Harvard College '21*

This paper explores how responsive North Korean production activity is to global commodity prices. I use satellite nighttime lights data, IMF reported world commodity prices, and data from the 38 North Digital Atlas over 1992-2013 to present three main findings. First, luminosity (a proxy for economic activity) in coal-producing counties in North Korea is considerably responsive to increases in global coal prices. The same pattern is revealed for steel. I estimate a 0.957 world price elasticity of coal production and a 2.652 world price elasticity of steel production in North Korea, both statistically significant at the 1% level. This empirically confirms how the North Korean regime has strategically aligned its coal and steel production activity with global coal and steel price fluctuations, respectively. Second, our study finds statistically significant, positive relationships between North Korean coal/steel exports to China and luminosity in coal/steel-producing regions, potentially suggesting that luminosity reflects trade with China as well. Third, I found no statistically significant nonzero relationship between Chinese producer prices and luminosity in commodity-specific producing regions. This indicates that the DPRK-Chinese relationship is far less market-driven and more characterized by geopolitical factors instead. These results demand a recalibration of our understanding of how North Korea maintains its regime, nuclear activities, and evades sanctions through its integrated economy and trade activity.

## I. Introduction

In this paper, I examine how movements in global commodity prices impacted production intensities of corresponding goods in North Korea from 1992-2013. This time period marks a transformative time in North Korean economic history: The Soviet Union collapsed, the country fell into a mass famine, sparking marketization from below, the government began to allow some level of market activity, and critical economic and political linkages with China formed. Contrary to popular belief, North Korea is not a “hermit kingdom” and since the late 1990s has developed global trade networks through a variety of state companies. The North Korean government has taken active steps to increase North Korea’s international trading presence, albeit with a limited number of countries given the nation’s nuclear development activities. How integrated North Korean industries really are to the world economy, however, remains unknown. This limits our understanding of how connected the new North Korean economy is to the rest of the world. Knowing how exposed North Korean markets, production capabilities and export activities are to global prices in turn allows us to better analyze how to implement effective, targeted sanctions measures. I explore how integrated the North Korean economy is with the rest of the world economy by analyzing how North Korean production behavior changes based on fluctuations in corresponding world commodity prices.

This paper presents three main findings. First, production intensity in coal-producing counties in North Korea is considerably responsive to increases in global coal prices. The same pattern is revealed for steel. This empirically confirms how the North Korean regime has strategically aligned its coal and steel production activity with global coal and steel price fluctuations, respectively. North Korea is and has been considerably intertwined with and connected to world markets and coal/steel prices. Second, my findings suggest that luminosity may reflect trade with China as well. Third, there is no statistically significant nonzero relationship between Chinese

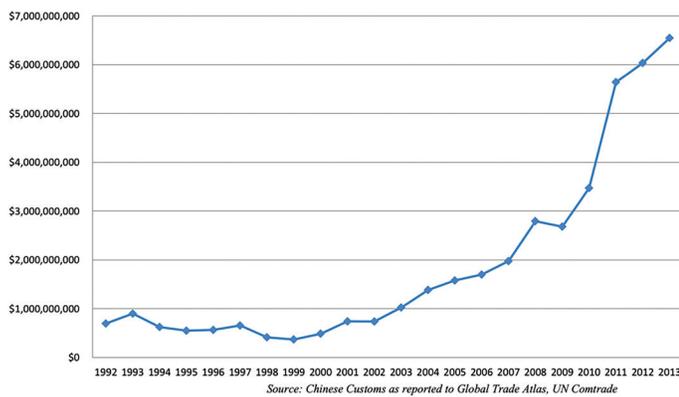
producer prices and luminosity in commodity-specific producing regions. This indicates that the DPRK-Chinese relationship is far less market-driven and more characterized by geopolitical factors instead. I hypothesize that as global prices of coal/steel increased, China bought more North Korean coal/steel because it was offered at lower prices. This illustrates how the North Korean economy has been closer/more intertwined with the rest of the world than we might think: global changes in coal prices impact Chinese importing decisions, which lead to changes in North Korean production and export activities.

For the majority of North Korea’s economic history, the *juche* ideology of nationalist self-reliance has demonized international trade. The country’s external economic relations were historically brittle as the centrally planned state economy and *juche* rhetoric prevented much international trade (Haggard and Noland, 2017). With the disintegration of the Soviet Union in the 1980s, however, North Korea lost its primary trading partner, which had devastating economic and social consequences. Combined with the failure of its public distribution system, a series of natural disasters, and a mass famine, the North Korean economy collapsed in the 1990s (Park, 2003). It was out of this context that the North Korean economy went through a massive transformation. The country underwent two major changes: the formation of state trading companies that operated on an international scale, and the rise of free market activity within the DPRK’s internal economy. Indeed, in the wake of the famine, collapse of the Soviet bloc, and later on, international sanctions, state trading companies were formed to bring the country out of its downward economic spiral. The DPRK government switched from a “self-sufficient economy” model to a “trade-first policy” to generate foreign currency and secure funds for their own operating budget (Park, 2009). Domestically, given that the public distribution system collapsed and people could no longer rely on the government for basic needs, individuals began to engage in barter and trade for their daily livelihoods. In the following years, the government also provisioned “special economic

zones” for limited amounts of market activity and trade. As such, since the late 1990s, even though the North Korean economy was by no means an open international trading partner and still run under a central state-planned system, it had established international state trading companies and supported some level of domestic private market activity.

Starting in the 1990s, the Chinese-North Korean political and economic relationship truly began to take form. Figure 1 shows DPRK-PRC total trade from 1992-2013. Initially, in May 1996, Chinese premier Li Peng and North Korean vice premier Hong Song-nam signed an agreement establishing high-level contacts, promising a widening of economic cooperation, and providing large commitments of food aid (Park, 2003). China paid “friendship prices” in buying North Korean goods, translating to implicit food and/or energy aid estimated at nearly \$6 billion by 2002 (Park, 2003). Over time, this relationship evolved, with the PRC today importing goods such as coal or steel from North Korea at cheaper prices, given their lower quality and international sanctions limiting North Korea’s available trade partners. Political relationships between the two nations and their working parties have also fluctuated throughout history, impacting economic relations over time. In all, the major trading relationship with China developed over this period, leading to China being by far and away North Korea’s largest trading partner today.

Figure 1: DPRK-PRC Total Trade (Exports + Imports)



Source: Chinese Customs as reported to Global Trade Atlas, UN Comtrade

Graph source: Pavone and Sun, “Coal Diplomacy: The Political Economy of North Korean Coal.”

Research on North Korea’s economy has yielded insights into North Korea’s political and economic relationship with China. However, the majority of prior work has been qualitative and anecdotal in nature. Park found through a series of interviews with ROK firms/Chinese businessmen operating ventures in North Korea and North Korean defectors who previously worked in DPRK state trading companies, that sanctions meaning to harm the economy and limit access to WMD-related materials have not worked effectively (Park, 2009). This is because through a variety of trade networks, many involving China, state trading companies have been able to generate funds maintaining the loyalty of North Korean elites and an operating budget to keep the regime afloat (Park, 2009). Despite its international isolation and pressures, the regime is able to survive and cope due to these state trading companies. The trade relationship between China and North Korea has also been carefully analyzed by 38 North, the Korea Economic Institute of America, and other organizations that outline import/export behavior over time, as well as the dependency of the DPRK economy on China. Specific studies on certain commodities, like coal, have tracked how the regime has used trade and exports of that good for sanctions

evasion. Pavone and Sun provide a comprehensive analysis of the coal trade and Chinese-North Korean relations as it pertains to coal as a means of sanctions evasion (Pavone and Sun, 2014).

Indeed, empirical work on North Korea’s economy and its exposure to the world is limited. The methodologies in the aforementioned studies were primarily empirical and focused on trade reports and expert interviews. Very few papers on the North Korean economy as it pertains to global trade are entirely empirical in nature, to my knowledge. Notably, Lee examined the effect of international sanctions on the regional distribution of economic activity in North Korea over time (Lee, 2017). Using a sanctions index he developed and nighttime lights data from The National Oceanic and Atmospheric Administration under the Defense Meteorological Satellite Program (DMSP), he reported that an increase in sanctions was associated with luminosity increases in the capital city, trade hubs near China, and manufacturing cities. He reveals how China has offset the trade restrictions imposed by other countries and regional inequality has increased as a result of these sanctions (Lee, 2017).

## II. Data

For my luminosity measure, I used Lee’s nighttime lights data. Light intensity is reported in digital numbers ranging from 0 to 63 for each pixel. The data provides a luminosity measure over the years 1992-2013 for around 180 different *sigungu* (counties). Summary statistics for the luminosity measure are shown in Table 1, with the  $\Delta$ luminosity variable indicating the change in luminosity from the prior year. Lee points to a study by Henderson et al. (2012) which found that “nighttime lights are correlated with GDP with an elasticity of about 0.3” and “nighttime lights is a good proxy for economic output when subnational data are not available” (Lee, 2017).

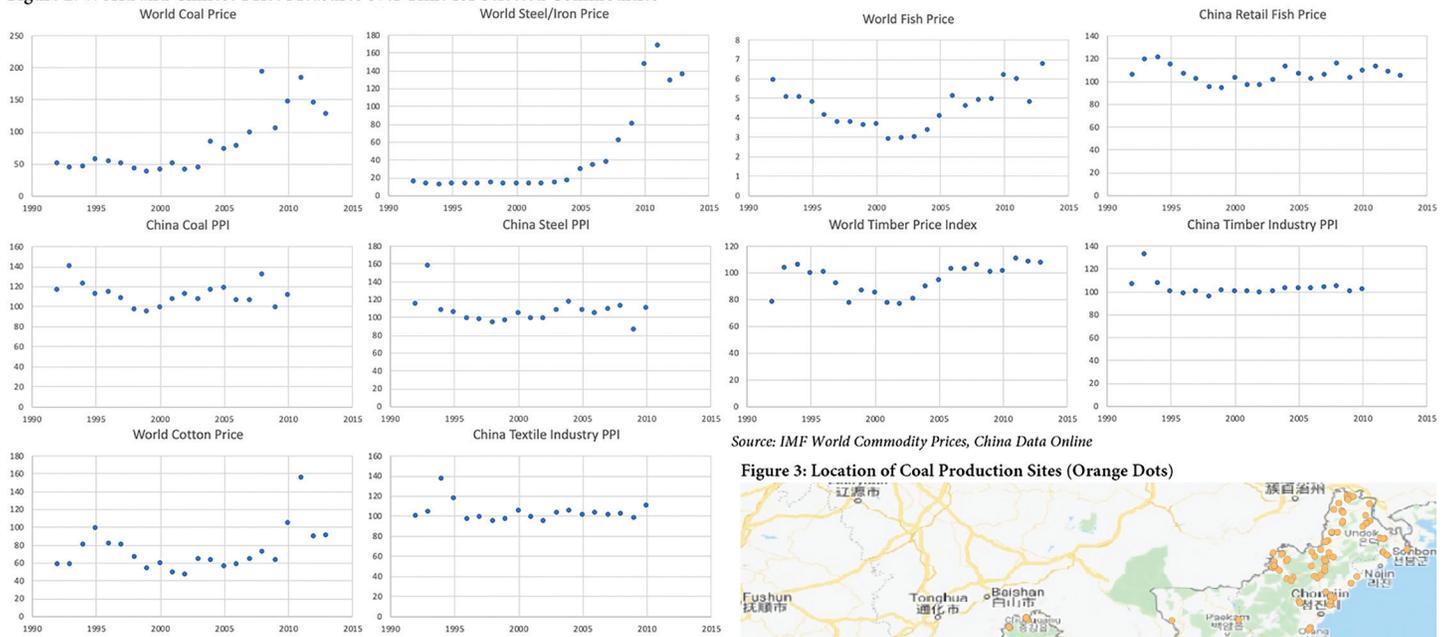
Table 1: Summary Statistics, 1992-2013

	Observations	Mean	Std. Dev	Min	Max
Luminosity	4,048	0.565	3.187	0	60.75
$\Delta$ Luminosity	3,864	0.043	2.269	-43.25	43.25
Number of Coal Mines	4,005	0.802	2.331	0	17
World Coal Price	4,048	80.597	47.388	37.313	192.189
Chinese Coal PPI	3,496	111.142	11.172	94.8	139.7
Number of Iron Production Facilities	4,048	0.125	0.455	0	3
World Steel Price	4,048	44.929	50.369	11.45	167.79
Chinese Steel PPI	3,496	13.268	48.788	0	472.5

Then, I used IMF Global Commodity Price Data to get world prices of commodities over time, and China Data Online to get Chinese retail prices and producer price indices of commodities as well. I analyzed a total of nine commodities: coal, steel/iron, soybeans, cotton/textiles, cement, natural gas, timber, fish, and poultry. Chinese prices on soybeans were limited, so that regression is omitted. Figure 2 shows world and Chinese commodity price indicators over time.

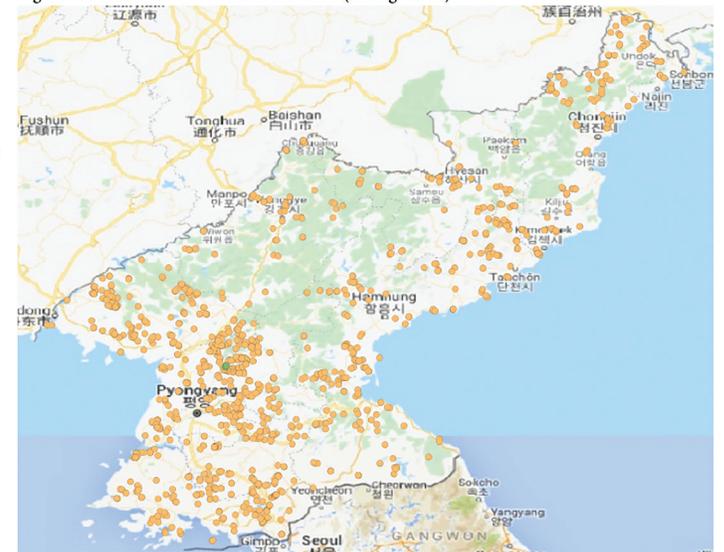
To get a measure of how exposed output in a certain *sigungu* might be to changes in world commodity prices, I then recorded the number of production sites in each *sigungu* for each of the nine commodities. For this data, I used the 38 North Digital Atlas’s information on where specific commodities are produced regionally in North Korea. Figure 3 shows the regional distribution of coal

Figure 2: World and Chinese Price Measures over Time for Selected Commodities



Source: IMF World Commodity Prices, China Data Online

Figure 3: Location of Coal Production Sites (Orange Dots)



Source: 38 North Digital Atlas, Mining Layer

mines in North Korea. Sponsored by the Stimson Center, their digital atlas is arguably the most comprehensive and authoritative public geospatial dataset on production facilities in North Korea. I used their mining, manufacturing/production and agriculture layers, which provides names, descriptions and coordinate locations of different facilities. I matched each facility to its nearest *sigungu* using QGIS software. From information in the names/descriptions of facilities in the 38 North data, as well as other sources like CIA reports on major energy production facilities in North Korea and USGS surveys, I was able to record the number of coal, steel, cement, soybean, natural gas, textiles, timber, fish, and poultry producing facilities in each *sigungu*. This data was matched to the luminosity and price data, with each *sigungu* having the same number of facilities for each commodity throughout the time frame 1992-2013. Because 38 North's Digital Atlas provided production facilities as seen at a snapshot in time, we do not account for changes over time in building/removal of facilities.

Lastly, I used the UN Comtrade dataset to find mirror statistics of North Korean exports to China through reported Chinese imports from the DPRK. This data was limited to only a select few commodities.

### III. Methodology

The base regression that examines how commodity prices over time affect the luminosity of regions in North Korea is:

$$\Delta \ln(Luminosity_{it}) = \beta_0 + \beta_1 \Delta \ln(Price_{jt} Exposure_{ij}) + \delta_y + \delta_c + \epsilon_{it} \quad (1)$$

with  $i$  being region,  $t$  being time,  $j$  being commodity, and Exposure referring to the exposure measure, which in my case is the number of commodity-specific production facilities in that *sigungu*. This is essentially a measure of the elasticity, as I regress the percent change in luminosity on the percent change in price. I interact the change in price with that exposure measure in a *sigungu* to analyze how the relationship between change in price and change in luminosity differs for any additional commodity-specific production facility in a specific region. For instance, if a place has no coal mines, its luminosity measure should not change with coal prices. I use year fixed effects,  $\delta_y$ , to control for factors that

vary across time for the whole country, such as sanctions pressure, global recessions, nation-wide political turmoil, or nation-wide famines. I use county fixed effects,  $\delta_c$ , to control for factors that vary across different counties but remain constant over time, like certain regional economy characteristics, geographical proximity to China, region-specific politics, and the like. By taking the year-on-year log differences, I control for any time trends in both luminosity and prices. In addition, I clustered standard errors by county. I ran this base regression for all eight commodities (coal, steel, fish, timber, textiles, natural gas, soybeans, and poultry), regressing both global and Chinese prices separately.

I then included both world and Chinese prices to isolate and

$$\Delta \ln(Luminosity_{it}) = \beta_0 + \beta_1 \Delta \ln(WorldPrice_{jt} Exposure_{ij}) +$$

$\beta_2 \Delta \ln(ChinesePrice_{jt} Exposure_{ij}) + \beta_3 ChinaExportShare + \delta_y + \delta_c + \epsilon_{it} \quad (2)$   
 separate the effects of each from one another and added the Chinese share of North Korean commodity-specific exports in each year as a control to account for changes in Chinese-North Korean trade patterns. Figure 4 shows how this number has changed over time.

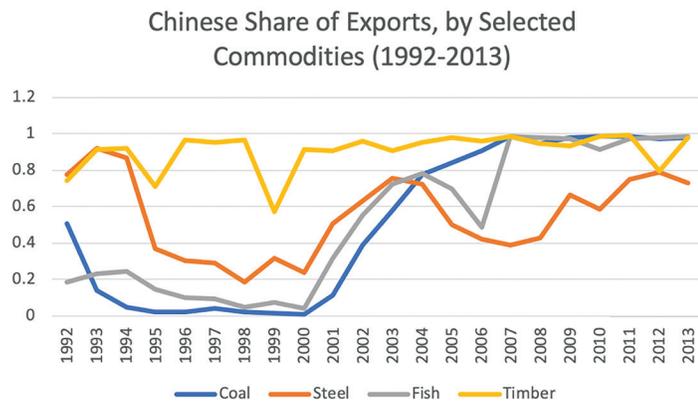
$$\Delta \ln(Luminosity_{it}) = \beta_0 + \beta_1 \Delta \ln(WorldCoalPrice_{jt} Exposure_{ij}) +$$

$$\beta_2 \Delta \ln(ChineseCoalPrice_{jt} Exposure_{ij}) + \beta_3 ChinaCoalExportShare +$$

$$\beta_4 \Delta \ln(WorldIronPrice_{jt} Exposure_{ij}) + \beta_5 \Delta \ln(ChineseSteelPrice_{jt} Exposure_{ij}) +$$

$$\beta_6 ChinaSteelExportShare + \delta_y + \delta_c + \epsilon_{it} \quad (3)$$

Figure 4: Chinese Share of Exports, by Selected Commodities



Furthermore, I estimate the same coefficients here but include both coal and steel commodities' price-exposure interactions. This specification responds to the possibility that counties' response to a steel price shock is confounded by the fact that global coal prices are correlated with global steel prices. Moreover, given that coal is an input into steel production, an increase in global coal prices could impact North Korean steel production independently of changes in global steel prices.

$$\Delta Luminosity_{it} = \beta_0 + \beta_1 \Delta TradeValue_{jt} Exposure_{ij} + \delta_y + \delta_c + \epsilon_{it} \quad (4)$$

Lastly, I tested how reflective the luminosity measure was as a measure of trade with China by regressing the change in luminosity on the change in commodity-specific trade value with China over time.

#### IV. Results

How sensitive is North Korean commodity production to the world and Chinese prices of commodities? Table 2 reports the effect of world coal prices on luminosity in counties with coal production facilities. All columns include the Chinese share of North Korean coal exports as a control. Column 1 reports the impact of world coal prices on luminosity independently of the Chinese coal price and Column 2 reports the impact of Chinese coal prices on luminosity independently of the world coal price. The coefficient in Column 1 is 0.216, statistically significant at the 1% level. A percent increase in the world coal price is associated on average with a 0.216 percent increase in luminosity in counties containing coal mines. As such, we can interpret this as the world price elasticity of production being

**Table 2: Effect of Coal Prices on Luminosity in Coal-Producing Regions, 1992-2013**

	(1)	(2)	(3)
	$\Delta \ln(\text{Luminosity})$		
$\Delta \ln(\text{WorldCoalPrice} \times \text{NumCoalMines})$	0.216** (0.073)	--	0.31** (0.095)
$\Delta \ln(\text{ChineseCoalPrice} \times \text{NumCoalMines})$	--	0.11 (0.178)	-0.362 (0.237)
Chinese Share of NK Coal Exports	-0.119* (0.066)	0.053 (0.068)	0.008 (0.067)
County FE	Y	Y	Y
Year FE	Y	Y	Y
Intercept	0.12** (0.046)	0.079* (0.048)	0.118* (0.05)
R <sup>2</sup>	0.019	0.02	0.024
Root MSE	0.491	0.485	0.484
Observations	3,822	3,276	3,276

Notes: Table 2 reports results of OLS regressions examining the relationship between world coal prices (*WorldCoalPrice*), interacted with the number of coal production facilities in a county (*NumCoalMines*), and luminosity. *ChineseCoalPrice* measures the price of coal in China and *Chinese Share of NK Coal Exports* intends to account for changes in Chinese-North Korean trade patterns. All variables except for the control *Chinese Share of NK Coal Exports* are measured as the change in logs, such that coefficients can be interpreted as elasticities. All regressions include county and year fixed effects, and standard errors are presented in parentheses and are clustered at the county level. Coefficients are individually statistically significant at the \*10%, \*\*5%, \*\*\*1% significance levels.

0.216. North Korean coal production, as measured by luminosity, is indeed sensitive to changes in the world price. The coefficient in Column 2 is not significant, indicating that there is no nonzero relationship between Chinese coal prices and luminosity in coal producing regions. Column 3 includes both world and Chinese coal prices in the regression and yields a coefficient of 0.31 on the regressor world coal price, statistically significant at the 1% level. Here, the world price elasticity of coal production is estimated to be 0.31, a ~43% increase from the coefficient in Column 1, which excludes Chinese coal prices in the specification. The inclusion of Chinese coal prices, along with world coal prices isolates each's impact on luminosity and increases the magnitude of the world price elasticity of coal production estimate. Still, Column 3 does not yield statistically significant results for the relationship between Chinese coal prices and luminosity.

We see a similar trend in Table 3, which reports the relationship between world iron prices and Chinese steel prices on luminosity in steel-producing counties in North Korea. Once again, all columns include the Chinese share of North Korean steel exports as a control. The specification in Column 1 measures the impact of world iron prices, Column 2 measures the impact of Chinese steel prices, and Column 3 includes both world and Chinese prices. The coefficient on world iron prices in Column 1 is 0.533 and is statistically significant at the 1% level, indicating a precisely estimated world price elasticity of North Korean steel production of 0.533. This elasticity estimate decreases slightly in magnitude to 0.497 but remains statistically significant at the 1% level in Column 3, with the inclusion of Chinese prices in the regression equation. Similar to in Table 2, the results for the coefficient on Chinese steel prices are not statistically significant.

I performed similar analyses on world and Chinese prices and luminosity in counties with commodity-specific production facilities for fish, timber, textiles, natural gas, soybeans, and poultry. Table 4 shows that none of these commodities yielded statistically significant, nonzero relationships between price and luminosity, indicating that the price elasticity of production, as measured by luminosity, for these commodities is not distinguishable from zero in our dataset. Data availability was also limited for a number of these other commodities.

In Table 5, I include all regressors from Table 2 and Table 3 together and analyze the impact of world coal and steel prices on luminosity in coal and steel producing counties, respectively. I estimate the same coefficients as in Table 2 and Table 3, but now include both commodities' price-exposure interactions. Column 3

**Table 3: Effect of Steel/Iron Prices on Luminosity in Steel/Iron-Producing Regions, 1992-2013**

	(1)	(2)	(3)
	$\Delta \ln(\text{Luminosity})$		
$\Delta \ln(\text{WorldIronPrice} \times \text{NumIronProductionFacilities})$	0.533** (0.192)	--	0.497** (0.172)
$\Delta \ln(\text{ChineseSteelPrice} \times \text{NumIronProductionFacilities})$	--	0.975* (0.178)	0.905* (0.526)
Chinese Share of NK Steel Exports	0.512* (0.289)	-0.179 (0.162)	-0.088 (0.157)
County FE	Y	Y	Y
Year FE	Y	Y	Y
Intercept	-0.367 (0.241)	0.228* (0.132)	0.157 (0.126)
R <sup>2</sup>	0.021	0.02	0.032
Root MSE	0.491	0.485	0.481
Observations	3,864	3,312	3,312

Notes: Table 3 reports results of OLS regressions examining the relationship between world iron prices (*WorldIronPrice*), interacted with the number of iron production facilities in a county (*NumIronProductionFacilities*), and luminosity. *ChineseSteelPrice* measures the price of steel in China and *Chinese Share of NK Steel Exports* intends to account for changes in Chinese-North Korean trade patterns. All variables except for the control *Chinese Share of NK Steel Exports* are measured as the change in logs, such that coefficients can be interpreted as elasticities. All regressions include county and year fixed effects, and standard errors are presented in parentheses and are clustered at the county level. Coefficients are individually statistically significant at the \*10%, \*\*5%, \*\*\*1% significance levels.

**Table 4: Effect of Commodity Prices on Luminosity in Commodity Specific Production Regions, 1992-2013**

	$\Delta \ln(\text{Luminosity})$					
	(1) Fish	(2) Timber	(3) Textiles	(4) Natural Gas	(5) Soybean	(6) Poultry
$\Delta \ln(\text{WorldCommodityPrice} \times \text{ProductionFacilities})$	-0.075 (0.125)	0.929 (0.604)	48.467 (49.786)	-0.192 (0.175)	-0.018 (0.072)	-0.488 (0.455)
$\Delta \ln(\text{ChineseCommodityPrice} \times \text{ProductionFacilities})$	-0.018 (0.253)	0.489 (1.48)	342.952 (451.723)	0.397 (0.471)	--	--
Chinese Share of NK Commodity Exports	-0.094 (0.074)	--	--	--	--	--
County FE	Y	Y	Y	Y	Y	Y
Year FE	Y	Y	Y	Y	Y	Y
Intercept	0.11* (0.054)	-0.858 (0.734)	1,072.37 (1,412.164)	0.089* (0.038)	0.094* (0.038)	0.099* (0.04)
R <sup>2</sup>	0.017	0.024	0.017	0.021	0.017	0.017
Root MSE	0.491	0.483	0.491	0.483	0.491	0.491
Observations	3,864	3,312	3,864	3,312	3,864	3,864

Notes: Table 4 reports results of OLS regressions examining the relationship between world commodity prices (*WorldCommodityPrice*), interacted with the number of coal production facilities in a county (*ProductionFacilities*), and luminosity. *ChineseCommodityPrice* measures the price of commodities in China and *Chinese Share of NK Commodity Exports* intends to account for changes in Chinese-North Korean trade patterns. All variables except for the control *Chinese Share of NK Commodity Exports* are measured as the change in logs, such that coefficients can be interpreted as elasticities. All regressions include county and year fixed effects, and standard errors are presented in parentheses and are clustered at the county level. Coefficients are individually statistically significant at the \*10%, \*5%, \*\*1% significance levels.

**Table 5: Effect of Prices on Luminosity in Commodity-Producing Regions, Combined Coal and Steel, 1992-2013**

	(1)	(2)	(3)
	$\Delta \ln(\text{Luminosity})$		
$\Delta \ln(\text{WorldCoalPrice} \times \text{NumCoalMines})$	0.44' (0.257)	--	0.957** (0.346)
$\Delta \ln(\text{ChineseCoalPrice} \times \text{NumCoalMines})$	--	-0.409 (0.711)	-1.91* (0.892)
Chinese Share of NK Coal Exports	0.323 (1.27)	-2.008* (1.075)	-1.702 (1.075)
$\Delta \ln(\text{WorldIronPrice} \times \text{NumIronProductionFacilities})$	3.226* (1.597)	--	2.652* (1.333)
$\Delta \ln(\text{ChineseSteelPrice} \times \text{NumIronProductionFacilities})$	--	5.058* (3.007)	4.704 (2.92)
Chinese Share of NK Steel Exports	4.167 (7.437)	-6.068* (3.169)	-4.435 (3.136)
County FE	Y	Y	Y
Year FE	Y	Y	Y
Intercept	-3.485 (6.96)	6.046* (3.067)	4.668 (3.031)
R <sup>2</sup>	0.028	0.034	0.043
Root MSE	2.307	1.894	1.885
Observations	3,822	3,276	3,276

Notes: Table 5 reports results of OLS regressions with all covariates from Table 1 and Table 2 included. All regressions include county and year fixed effects, and standard errors are presented in parentheses and are clustered at the county level. Coefficients are individually statistically significant at the \*10%, \*5%, \*\*1% significance levels.

reports that the world price elasticity of coal production is 0.957 and statistically significant at the 1% level when I include the world price, Chinese price and Chinese export share of steel. This is a notable increase from the same coefficient in Table 2, which estimated an elasticity of 0.31. Once steel-related variables are controlled for, the sensitivity of coal production to global coal prices increases considerably. Interestingly, Column 3 also reports that the world price elasticity of steel production is now 2.652 and statistically significant at the 5% level, once controlling for coal-related variables. This is a marked increase from the estimate in Table 2, which was 0.533. This specification reveals that North Korean steel production is remarkably sensitive to global iron prices once coal-related variables are controlled for.

To contextualize these elasticity estimates, I compare our regression coefficients to literature on countries' price elasticity of supply for coal and steel. To my knowledge, such studies are limited. Still, one paper estimates that the supply of US coal has a short run annual elasticity of 0.61 and a long run elasticity of 1.31 (Dahl). The fact that our elasticity estimates come close to this range illustrates that the North Korean coal and steel world price elasticity of production is remarkably high. This is because Dahl's study estimates the sensitivity of US coal production to US

**Table 6: Luminosity as a Measure of Trade with China (Limited by Data Availability): Relationship Between Commodity Trade Value with China and Regional Distribution of Economic Activity, 1992-2013**

	$\Delta \ln(\text{Luminosity})$			
	(1) Coal	(2) Steel/Iron	(3) Timber	(4) Fish
$\Delta \ln(\text{TradeValue} \times \text{NumProductionFacilities})$	.033** (0.011)	0.148* (0.078)	0.031 (0.075)	-0.012 (0.019)
Intercept	0.109** (0.039)	0.08* (0.036)	0.093* (0.038)	0.092* (0.038)
R <sup>2</sup>	0.017	0.02	0.017	0.017
Root MSE	0.491	0.491	0.491	0.491
Observations	3,822	3,864	3,864	3,864

Notes: Table 6 reports results of OLS regressions examining the relationship between commodity trade value with China and regional distribution of economic activity as measured by luminosity, for commodities coal, steel, timber, and fish. *TradeValue* measures North Korean exports to China through reported Chinese imports from the DPRK, and *NumProductionFacilities* measures the number of commodity-specific production facilities in a county. Both the dependent and independent variables are measured as the change in logs, such that coefficients can be interpreted as elasticities. All regressions include county and year fixed effects, and standard errors are presented in parentheses and are clustered at the county level. Coefficients are individually statistically significant at the \*10%, \*5%, \*\*1% significance levels.

prices, which intuitively is very elastic given that domestic coal production is likely highly responsive to domestic coal prices. That North Korean coal and steel production is similarly responsive in magnitude to world prices of these commodities is thus exceptional.

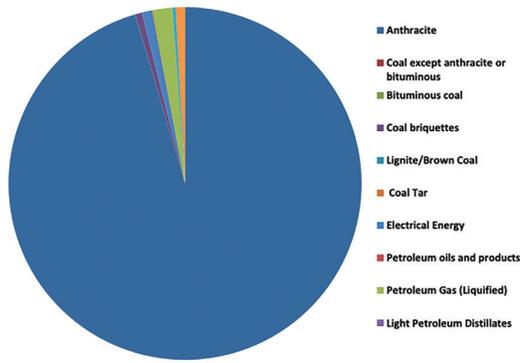
In Table 6, I take a step back and test a more fundamental assumption of this paper. Here, I regress luminosity on commodity-specific trade values with China again for counties with varying numbers of production facilities for that specific commodity. I run this regression to test to what extent luminosity reflects production intensity insofar as it pertains to export activity to China. Due to limited data availability, I only ran regressions for coal, steel and fish. Column 1 reports that a percent increase in North Korean exports of coal to China is associated on average with a 0.033 percent increase in luminosity in coal-producing regions, statistically significant at the 1% level. This result supports the assumption that luminosity can appropriately proxy for economic production activity for coal. Similarly, Column 2 shows that a percent increase in steel exports to China is associated on average with a 0.148 percent increase in luminosity in steel-producing regions, but this result is only statistically significant at the 10% level. This provides somewhat weaker evidence for the idea that luminosity is an effective indicator of production and economic activity in steel. Columns 3 and 4 show that there is no relationship between luminosity and trade value for areas producing timber and fish.

## V. Discussion

North Korea is heavily dependent on coal and steel for both domestic energy production and external trade. Indeed, North Korea holds around \$6tn, or even \$10tn according to some estimates, of untapped deposits in the form of around 200 different minerals (Vella). The coal industry specifically is of particular importance given that the North Korean regime has been using the coal trade to survive despite international sanctions (Pavone and Sun, 2014). Figure 5 shows the fraction of anthracite coal in total DPRK energy exports to China from 1992-2013, and Figure 6 shows DPRK anthracite exports to PRC as a fraction of total production.

I found that production intensity in coal-producing regions is highly responsive to global coal prices, with an estimated world price elasticity of coal production of 0.957. A likely interpretation is that coal production intensity has increased because an increase in global coal prices pushes China to purchase cheaper coal from North Korea. This is confirmed by other studies and in-depth analyses of the coal trade with China over this time period that show how China has developed this trade network to exploit cheaper resource

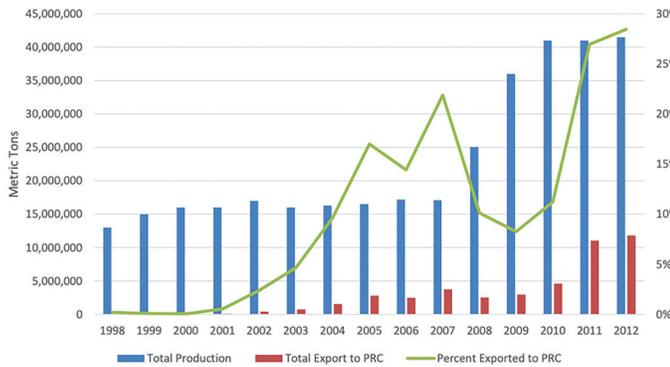
Figure 5: Total DPRK Energy Exports to China from 1992-2013 (revenue)



Source: Chinese Customs as reported to Global Trade Atlas, UN Comtrade

Graph source: Pavone and Sun, "Coal Diplomacy: The Political Economy of North Korean Coal."

Figure 6: DPRK Anthracite Exports to PRC as a Fraction of Total Production



Source: U.S. Geological Survey, "Chinese Customs as reported to Global Trade Atlas"

Graph source: Pavone and Sun, "Coal Diplomacy: The Political Economy of North Korean Coal."

deposits in North Korea when other sources internationally become too expensive (Pavone and Sun, 2014). It could also simply be that global coal prices rose during this time period, and this coincided with the growth of the Chinese-North Korean trade relationship, spurring production. Still, because we exploit regional variation in coal production activity within North Korea and use region fixed effects, we control for the evolving relationship between China and North Korea insofar as it affects all the regions the same way. Yes, there may be differences in how the Chinese-North Korean relationship impacted different regions in the DPRK, but I assume that I have sufficient regional variation in the dataset, and the graphical representation of coal mines in North Korea (Figure 2) roughly tell us that the mines are not concentrated around one specific area and are rather spread out.

Research on the coal trade in literature primarily identifies North Korea trading cheap coal to China as a relatively recent phenomenon. The most comprehensive report on North Korea and coal, a Harvard Kennedy School report by Gregory Pavone and Jin Sun, points to how the North Korean regime has in recent years used coal "in tremendously sophisticated and strategic ways to thrive despite economic sanctions" (Pavone and Sun, 2014). The authors' main puzzle is that since 2008, there has been a substantial increase in DPRK-PRC coal trade that coincides with North Korea's nuclear tests in 2006, 2009, and 2013, as well as the 2010 sinking of the Cheonan (Pavone and Sun, 2014). They explain that this increasing commercial activity came at a strategic time, indicating

that North Korea has begun to use the coal trade to evade sanctions as they come. In this sense, the coal trade is a reactionary measure developed relatively recently as a tool of regime survival in difficult times. Indeed, their driving question is: "How is trade increasing dramatically in the midst of destabilizing actions and targeted sanctions" (Pavone and Sun, 2014)? The cheap coal trade with China is described as North Korea's recent vehicle to evade sanctions and is now a key strategic resource for the regime.

My results reveal, however, that the DPRK started increasing production intensity for coal long before 2008, which is when absolute numbers of coal exports to the PRC increased substantially. Moreover, rather than just being a reactionary tool against sanctions, it seems the DPRK has been more deliberate and strategic with its coal trade starting from the 1990s. North Korea increased coal production intensity *as global coal prices increased*, revealing that since 1992, the regime has strategically raised and lowered production intensity of coal based on a) its world price itself, or b) Chinese demand for cheap coal, which rose with world coal prices. Option a) shows us how strategic, sophisticated and internationally integrated the North Korean regime/economy is, and option b) demonstrates how global coal prices affect North Korean production decisions through Chinese demand. Rather than simply being a relatively recent, new strategy of dealing with geopolitical shocks and international pressure, it seems the North Korean regime has been focusing on coal production for a while, adjusting intensity based on global coal prices and/or Chinese demand for cheap coal. The current trends may be just the tip of the iceberg; a small piece of a larger trend that goes further back – by which the North Korean regime strategically adjusts its coal production. My results illustrate that even though the North Korean economy does not react to world markets the same way that a typical free market, open economy does, it is indirectly affected by global economic factors, like world commodity prices. The mechanism by which global prices affect North Korean production might be increasing Chinese demand for lower cost coal. In this sense, the North Korean economy is closer to international markets than we might think: the DPRK is indirectly intertwined in the world economy and alters its production intensity for coal based on global coal prices, which affect Chinese demand. The implications of this finding are vast: it is empirically proven that North Korea is not a "hermit kingdom." Fluctuations in global commodities markets actually affect the North Korean economy as well. Furthermore, this study empirically confirms that early sanctions in this time have been ineffective in deterring production and economic activity in the DPRK, particularly with respect to coal.

A similar interpretation can be applied to my finding on steel, where the world price elasticity of steel production is estimated to be 2.652. North Korean steel production is remarkably sensitive to global steel prices. While less research on the North Korean steel trade exists, to my knowledge, it is likely that the underlying mechanics are similar to that of the coal trade given the similarities between the commodities in North Korean abundance and trade. Again, it is plausible that North Korea has strategically adjusted its steel production in response to global steel prices, responding to the world market or Chinese demand for steel reflected in those global prices. This finding on steel further indicates that the North Korean economy is very much responsive to the global coal and steel commodities markets.

My findings based on Chinese prices are more puzzling – I found

North Korea Economy

no statistically significant nonzero relationships between prices and luminosity for all eight commodities (coal, steel, fish, timber, textiles, natural gas, soybeans, and poultry). First, my results could be insignificant because of the inherent unreliability of Chinese price data. While China Data Online is a reputable source, the Chinese government is notorious for not publishing accurate price data. The fact that Chinese producer price indices for these commodities are seemingly not associated with production intensity in North Korea for those goods is not consistent with what we know/understand about the North Korean-Chinese trade relationship. Or, it may simply be that the Chinese-North Korean trade relationship is far less driven by market forces than, perhaps, the North Korean-rest of the world trade relationship is. While North Korean production and markets may be sensitive to global commodity prices, the nature of the Chinese-North Korean trading partnership is so driven by internal political factors, domestic politics in both countries, and other non-market decisions that our results are not capturing. It may be that the Chinese government has different reasons for placing restrictions on imports to boost domestic production that might be affecting production intensity in North Korea. China also has other major import partners like Australia, Malaysia, and Indonesia (in the case of coal) to support its domestic demand, so the effect of its import demand on North Korea might be smaller than we thought.

In future studies, it will be worthwhile to expand the duration of our dataset. Much of North Korea's economic opening up and increased trade activity has come after 2013, and with a new round of sanctions as well it may be that the North Korean economy has only become fully susceptible to changes in global prices in more recent years. Further analysis including years until the present would therefore add much to my work.

Table 6 reports that there was a positive relationship between luminosity in coal producing regions and coal exports from North Korea to China, statistically significant at the 1% level. Although this result is simply a correlation, not proof of causation, it may suggest that luminosity can appropriately proxy for trade with China. The fact that there is a statistically significant relationship between North Korean exports in coal and steel, respectively, and luminosity in coal and steel producing regions may provide evidence for North Korea's export relationship with China. In this case, it could be that the relationship between global coal prices and luminosity was driven by greater Chinese demand for cheap North Korean coal/steel when those commodities get more expensive globally. The observed increase in luminosity as a result of global coal prices might truly be reflective of increased trade with China. While such a relationship has frequently been discussed anecdotally and qualitatively in other research, this empirical relationship is notable given its statistical significance. Again, however, it is important to keep in mind that we have merely identified a correlation and cannot establish causality between luminosity and exports to China.

Additionally, trade data between North Korea and China is unreliable. I used mirror statistics, inferring North Korea's commodity exports to China based on Chinese data on imports. There are many problems with using this data -- it is unlikely that the Chinese government properly reports their trade statistics with North Korea, given that the DPRK is heavily sanctioned by the international community. There are most certainly a substantial amount of trade dealings that the Chinese government does not report, and there may even be transactions that North Korean state trading companies make with private Chinese businessmen, who

do not inform the government either. With the existence of illegal dealings at the border, under-the-table transactions, and more, it is likely that the trade data I used in the regressions in Table 6 is flawed. Still, in addition to our results, our assumption that production intensity is a sufficient indicator of economic activity and/or increased trade with China is acceptable given that coal is North Korea's primary export to China, its largest trading partner by far.

## VI. Conclusion

North Korea's place in the global economy has transformed greatly since the 1990s. Much research has been done on North Korea's nuclear weapons program and its evasion of international sanctions, but there is still considerable uncertainty around just how exposed and integrated the North Korean economy is with world markets. This paper uses nighttime lights data and IMF reported world commodity prices to find that production intensity in regions with coal mines and steel production facilities is remarkably responsive to increases in global coal and steel prices, respectively. I estimate a 0.957 world price elasticity of coal production and a 2.652 world price elasticity of steel production in North Korea. This reveals how the North Korean regime has strategically aligned its coal and steel production activity with global coal and steel price fluctuations in a way that is advantageous to its export of such commodities. Based on Chinese demand for cheap coal and steel, that also depends on global commodity prices, North Korea has been able to adapt and alter its production intensity accordingly. This reveals how North Korea is and for a while has been considerably intertwined and connected with world markets and commodity prices. This demands a recalibration of our views of how North Korea maintains its regime, nuclear activities, and evades sanctions through its integrated economy and trade with China. Our study also finds statistically significant, positive relationships between North Korean coal exports to China and our luminosity measure in coal-producing regions, potentially suggesting that luminosity reflects trade with China as well. A similar positive relationship is found for steel, but is only statistically significant at the 10% level. Still, causation has yet to be established, and there are many data limitations, especially regarding trade statistics reported by China. Based on research, we can reasonably link much of North Korea's coal and steel producing activities to export with the PRC. Our analysis of the impact of Chinese producer prices on production intensity yielded no statistically significant results for all eight commodities (coal, steel, fish, timber, textiles, natural gas, soybeans, and poultry). Perhaps this indicates that the DPRK-Chinese relationship is far less market-driven and more characterized by geopolitical factors instead. Chinese price data may also be unreliable.

Academic research has for the most part moved away from assuming North Korea to be a "hermit kingdom" and in general a greater understanding of the North Korean regime's strategic nature has been perpetuated in recent years. Still, my findings suggest that the regime's coal and steel industry strategies are far older and deeper than we might have already imagined -- since the 1990s, the DPRK has been responsive to global coal and steel price fluctuations and adapted its production intensity accordingly. The regime's exposure to international markets and its ability to adjust to them shows just how sophisticated the regime has been and will likely continue to be even in the face of great geopolitical pressure.

Puzzles regarding the relationship with Chinese producer prices remain, but likely reflect the more political, non-market nature of the trade relationship with the PRC. In any case, deepening our understanding of how responsive the North Korean economy is to world/Chinese price movements helps us understand the strategies and capabilities of the DPRK and, consequently, how to most effectively impose sanctions or other diplomatic measures.

## References

- Dahl, Carol, "Energy Demand and Supply Elasticities," Golden, CO, Colorado School of Mines, <http://www.eolss.net/sample-chapters/c08/e3-21-02-04.pdf>.
- Haggard, Stephen, and Marcus Noland, "North Korea's External Economic Relations, 1990–2016," *North Korea and Northeast Asia: New Patterns of Conflict and Cooperation*, February 1, 2017, <https://doi.org/10.11126/stanford/9781503600362.003.0003>.
- Lee, Yong Suk, "International Isolation and Regional Inequality: Evidence from Sanctions on North Korea," Stanford, CA, Stanford University, November 14, 2017.
- Park, John, "North Korea, Inc: Gaining Insights into North Korean Regime Stability from Recent Commercial Activities," Washington, DC, United States Institute of Peace, April 22, 2009, <https://www.usip.org/sites/default/files/North%20Korea%2C%20Inc.PDF>.
- Park, Soo-Bin, "The North Korean Economy: Current Issues and Prospects," Ottawa, Carleton University, October 2003, <https://carleton.ca/economics/wp-content/uploads/cep04-05.pdf>.
- Pavone, Gregory A., and Jin Sun, "Coal Diplomacy: The Political Economy of North Korean Coal," Cambridge, Harvard University John F. Kennedy School of Government, 2014.
- Vella, Heidi, "Opening the lid on North Korea's untapped mineral reserves," [https://mine.nridigital.com/mine\\_sep18/opening\\_the\\_lid\\_on\\_north\\_korea\\_s\\_untapped\\_mineral\\_reserves](https://mine.nridigital.com/mine_sep18/opening_the_lid_on_north_korea_s_untapped_mineral_reserves).

# Native Maize, Transgenic Contamination, and Intellectual Property Rights: The Case of San Miguel del Valle, Oaxaca, Mexico

Adele Woodmansee  
Harvard College '20

Mexico is the geographical center for the origin and diversity of maize (*Zea mays*). This diversity is threatened as economic policies and climate change limit the ability of small-scale farmers to continue agricultural production. I conducted ethnographic research on maize agriculture in San Miguel del Valle, a Zapotec town in Oaxaca state, in conjunction with a study for transgenic contamination in maize planted and sold in the community. Genetic analyses did not detect transgenic contamination in maize grown or sold in San Miguel; local seed saving practices and environmental conditions may have contributed to this lack of detected contamination. San Miguel farmers' perspectives on native maize conservation reflect the ties between maize diversity and the cultural and social survival of farming communities. Understanding farmers' perspectives on their seeds and the issue of transgenic contamination is essential in considering the implications and routes of transgene flow. Native maize seeds are politically powerful and reflect the uncertainty and importance of smallholder agricultural livelihoods in the context of neoliberal policies, climate change, and intellectual property law.

## Introduction



Figure 1: A *milpa* in San Miguel del Valle.

A typical field in San Miguel del Valle (San Miguel) contains maize plants of varied heights. Squash plants blanket the soil, and bean plants spread up and around the maize. Among these crops grows a diversity of weeds, many of which are in fact *quelites* (edible herbs). This is *milpa* agriculture, a dynamic system of intercropping whereby maize, beans and squash are planted together along with other crops and herbs. It is characterized by diversity. Maize plants are of a range of shapes and sizes, due to genetic diversity within maize varieties and varied moisture content. The *milpa* system fosters a strong insect and micro-organism community, providing for natural pest control.

An essential foundation for the *milpa* system is native maize. There are 35 native landraces (cultivars / varieties) of maize cultivated in Oaxaca (Aragón Cuevas, 2011). They vary from the short, drought resistant varieties grown in San Miguel, which can produce ears in dry conditions when only a few feet in height, to the

*olotón* landrace grown in the Mixe region, which can grow up to 20 feet high with plentiful rains due to its ability to fix its own nitrogen. Maize landraces have been developed over the course of thousands of years using informal breeding methods, and they are adapted to localized and often stressful climatic and ecological conditions (Camacho Villa et al., 2005). Because of their genetic variability and adaptation to diverse environments, maize landraces are an important global genetic resource for adaptation to new conditions and pathogens (Arteaga et al., 2016, p. 38). Their nutritional value also tends to be high compared to formally bred varieties (Azeez, Adubi & Durodola, 2018, p. 14).

The *milpas* of small-scale Oaxacan farmers contrast dramatically with what one might observe in a field of commercially produced maize in the U.S. or other parts of Mexico, where maize plants grow to precisely the same size and are planted on their own, with virtually no weed growth due to use of herbicides. Mexico imports ten million tons of maize annually, making up one third of its total needs (Unión de Científicos Comprometidos con la Sociedad, 2017). The majority of these imports come from the U.S., where nearly all maize grown is transgenic<sup>1</sup> and there are no requirements for the separation or labeling of transgenic maize (Fitting, 2011, p. 1). In Mexico, planting of transgenic maize is currently suspended, but its importation is not, and there remains strong pressure from agribusiness corporations for the removal of restrictions because Mexico represents an enormous potential market for transgenic seeds (Wise, 2014).

Transgenic contamination has been found since 2001 in native landraces in several parts of Oaxaca state and other states in Mexico. Transgene flow from genetically modified (GM) crops to native landraces raises important biosafety concerns. The process has four components – seed flow, pollen flow, hybridization, and introgression (Soleri & Cleveland, 2006, p. 27). Introgression, the final step, occurs if the transgene becomes stabilized in the host genome (Agapito-Tenfen & Wickson, 2017, p. 540). Transgenic maize can enter Mexican communities through grain imported from the

<sup>1</sup> Transgenic is a synonym for genetically modified (GM), and I use these terms interchangeably.

U.S., contaminated maize imported from elsewhere in Mexico, or seeds brought back by migrants. If farmers mix transgenic seeds into their seed supply, transgenes can spread into neighboring fields via pollen carried by the wind.

Mexico is the only country in the world where transgenic contamination in native crop varieties has been found at the geographical center of a crop's origin and diversity (Commission for Environmental Cooperation, 2004). There remains a lack of information about transgene prevalence and the extent to which transgenes have introgressed into native landraces, due to insufficient studies and great variation in methodology and results among the studies that have been conducted. A significant social movement has developed around the issue of transgenic maize, and Oaxaca has been at the center of this movement (Agapito-Tenfen & Wickson, 2017).

I spent a cumulative nine months conducting fieldwork on maize agriculture in San Miguel del Valle from 2017-2019. In addition to conducting ethnographic research in Spanish and Zapotec, I collected maize samples to complete a genetic study for transgenic contamination. I later presented the results to farmers. San Miguel del Valle is a town of approximately 2500 inhabitants located one hour from the capital city of Oaxaca state, Mexico. It is governed by *usos y costumbres*, a semi-autonomous indigenous form of government used in some parts of Mexico based on obligatory service, reciprocity, and prestige. Most San Miguel residents are bilingual in Spanish and Zapotec but speak Zapotec as a first language. All land is held communally, and non-mechanized subsistence agriculture remains an important part of the economy, but production is limited by severe droughts (exacerbated by climate change) and lack of effective governmental supports. Other primary economic activities include craft production of wool rugs and migration to the U.S., primarily undocumented migration of men who send back remittances to their families. As in many parts of rural Mexico, migration levels in San Miguel have increased drastically since the North American Free Trade Agreement (NAFTA) was implemented in 1994. Economic and political changes contributed to the decreased ability of farmers to earn a living from agriculture (Stephen, 2007; Wohlgenuth, 2014).

Genetic analyses that I completed did not detect transgenes in any of the maize samples that I collected in San Miguel. In this paper, I discuss the research that I conducted in San Miguel in the context of larger political, social, and scientific issues in order to situate the perspectives and practices of San Miguel farmers. By combining discussion of both genetic and ethnographic elements of my research, I seek to portray the interdisciplinary implications of native maize diversity and small-scale farmers' livelihoods. I argue that native maize seeds are politically powerful and reflect the uncertainty and importance of smallholder agricultural livelihoods.

## The Significance of the Transgenic Maize Debate in Mexico

Despite narratives of high-yielding hybrid and transgenic crop varieties as the solution to global hunger, native maize varieties currently represent the best way in most parts of Mexico to improve self-sufficiency, as much of the land where maize is planted in the country is not suitable for available modern varieties (MVs)<sup>2</sup>

2. I use the term "modern varieties" (MVs) to describe maize varieties

(Cleveland, Soleri, & Smith, 2000). Many of the potential impacts of transgenic maize on native maize diversity may differ little from patterns already occurring with other MVs, including genetic erosion, the loss of genes and genotypes that can result from partial or complete replacement of traditional varieties like landraces with MVs (Heerwaarden, 2007). There are some potential consequences specific to transgene flow that warrant further research, such as the possibility for linking of transgenes associated with increased fitness to maladaptive alleles (Soleri, Cleveland, & Aragón Cuevas, 2006, p. 510).

However, a full understanding of why transgenic contamination has become such a charged topic in Mexico requires consideration of social, political, and scientific factors together. Transgenic maize is associated with increased privatization and concentration of agricultural markets by agribusiness corporations and commercial farmers. This contributes to its perceived threat in Mexico, where small-scale maize agriculture remains predominant in much of the country. Farmers' perspectives on transgenic crops (which have not been extensively investigated) could have important implications, particularly if farmers choose to abandon seed stock that they think to be contaminated (Soleri et al., 2006). Transgenic contamination could also have legal implications for farmers. Although there have been no cases so far of lawsuits against Mexican farmers for planting contaminated seeds of patented crop varieties, the potential implementation of UPOV 91 (discussed in the next section) could make such cases more likely.

Even within the commercial seed sector in countries like the U.S., where seed is purchased annually and pollen flow occurs only within a single generation, it has been difficult to prevent intermixing of transgenic and non-transgenic seeds (Heerwaarden, 2007). The challenges for managing transgene flow in small-scale maize farming systems are much greater – such farmers save their own seeds annually and acquire seeds through informal networks. Individual maize populations within a community are thus linked into a complex metapopulation (Heerwaarden et al., 2012, p. 1). The arrangement of agricultural plots, whereby a single farmer often has several fields located far apart and different farmers have fields in close proximity, also contributes to high rates of gene flow (Bellon & Berthaud, 2005, p. 46).

The impacts of GM foods on human health are contested. It is frequently claimed that GM foods have not been found to cause adverse effects among consumers (Brody, 2018). There is insufficient research to draw conclusions about general patterns with relation to GM foods and health, particularly long-term patterns (de Vendomois et al., 2009), and there is no evidence of any negative health effects due to the process of genetic modification itself. However, some individual GM crops have been linked with health concerns. In the case of maize, two examples include varieties modified for herbicide resistance<sup>3</sup> and StarLink maize<sup>4</sup>.

---

produced by formal breeding, or breeding that is directed by professional crop breeders rather than farmers.

3. The grain of herbicide-resistant transgenic varieties, such as Roundup Ready crops, has been found to contain trace amounts of herbicides (González-Ortega et al, 2017) such as glyphosate, which is categorized by the WHO as a probable carcinogen (Brueck, 2019). Modification for herbicide resistance contributes to heavier use of herbicides that are often more toxic than those used on conventional crops.

4. StarLink maize was modified to contain a Bt toxin considered to be

In some cases, such as herbicide residue in GM maize grain, potential health effects are not a direct result, but rather a byproduct, of the genetic engineering. These scenarios still raise concerns about regulatory processes. In the U.S., government regulation for GM crops is completed on a case-by-case basis but is based heavily on unpublished industry studies conducted by crop developers themselves (Freese & Schubert, 2004). Results of these assessments are extrapolated by the USDA in information provided with transgenic crop exports, even though the USDA does not consider risk for locations outside of the U.S. (Soleri & Cleveland, 2006, p. 27). These assessments are also used by the Mexican regulatory bodies who determine innocuity and equivalency ratings for transgenic foods in Mexico (Amerena, Mayorga, & Pérez Ortega, 2017). While I do not claim that GM crops are inherently or necessarily harmful to human health, I do assert that the health concerns which have been expressed in debates over transgenic maize in Mexico should not be readily discarded, particularly because maize in Mexico is consumed as a much more prominent part of the diet, and in more direct forms, than in the U.S. (González-Ortega et al., 2017).

In light of the role that native maize diversity plays in food security and culture in Mexico, I discuss transgenic contamination as a useful marker – although certainly not the only marker – of the extent to which native maize varieties and the farming communities in which they are cultivated are able to persist under current conditions.

### Transgenic Maize and Transgenic Contamination in Mexico: A Brief Political, Social, and Scientific History

In 2001, a study by Ignacio Chapela and David Quist, published in the journal *Nature*, found transgenic contamination in native maize landraces in the remote *Sierra Norte* region of Oaxaca. This was the first evidence of transgenic contamination in maize landraces. Quist & Chapela used Polymerase Chain Reaction (PCR) to test for the presence of a genetic sequence common to transgenic maize constructs. They found evidence of transgenes in four of the six native maize samples they had collected, as well as in a sample from a local *Diconsa*<sup>5</sup> store. A test using a different procedure (inverse PCR) showed diverse sequences surrounding the transgenic constructs identified in the native maize samples, which Quist & Chapela argued was evidence of transgene introgression. Quist & Chapela's publication, particularly their claims about introgression, were initially highly controversial. But their main conclusion of transgene presence in landraces was eventually widely accepted (Agapito-Tenfen & Wickson, 2017).

Many were alarmed by this finding, as there had been a moratorium on planting transgenic maize in Mexico since 1998. The Mexican government carried out further studies in 2001-2002 (never published in peer-reviewed journals) that confirmed transgenic contamination in several communities in Oaxaca and Puebla and found 37% of maize tested from *Diconsa* to be transgenic (Commission for Environmental Cooperation, 2004, p. 32). Non-segregated maize grain imported from the U.S. was distributed by

a potential allergen. It was not approved for human consumption but was found in food products in the U.S. in 2000 (Federation of American Scientists, 2011).

5. *Diconsa* is a governmental program that operates rural community stores, which offer basic foods and supplies at a reduced price.

*Diconsa* at the time (Dyer et al., 2009, p. 2). Farmers are known to sometimes plant seed from *Diconsa* stores experimentally or in place of their own seed, and this was considered a likely source of contamination (Quist & Chapela, 2001; Dyer et al., 2009; Agapito-Tenfen et al., 2017).

In response to these initial findings of transgenic contamination, indigenous communities and organizations in nine Mexican states conducted a series of studies in 2003 using ELISA (enzyme-linked immunosorbent assay; a method for transgenic protein detection) kits. Results were presented in a press release in October 2003. Transgenes were found in one-quarter of 138 sampled communities, all comprised of farmers who saved their own seed from native landraces. Many samples were found to contain two to four different transgenes, suggesting that contamination had been present for a long time. Samples from all states were found to contain StarLink maize, a variety not approved for human consumption in the U.S. (ETC group, 2003).

In 2002, a group of organizations, communities, and citizens had petitioned the Commission for Environmental Cooperation (implemented by NAFTA) to carry out a comprehensive study of maize diversity and the potential impacts of transgenic maize release in Mexico. The report was published in 2004. It acknowledged that transgene flow had occurred, warned of the possibility of further contamination, and called for further research and precautionary policies – including enforcement of the moratorium and minimization of transgenic maize imports (Commission for Environmental Cooperation, 2004).

A study published by Ortiz-Garcia et al. in 2005 found no transgenes in samples from the same region where Quist & Chapela (2001) had found contamination, despite using similar methods. Ortiz-Garcia et al.'s sampling methods were subsequently criticized (Cleveland et al., 2005), as were their claims that transgenes could have disappeared in the region, which were based on the hypothesis that hybrids between transgenic varieties and landraces could be less fit (Soleri & Cleveland, 2006, p. 29). The Biosafety Law for Genetically Modified Organisms (LBOGM) was also passed in 2005. It states as its objective to “prevent, avoid, and reduce the possible risks” of GM organisms in Mexico (Procuraderia Federal de Protección al Ambiente, 2014) but is commonly known as the “Monsanto Law” by opponents of transgenic maize in Mexico who believe that it was designed to be ambiguous so as to open the door for the continued production and consumption of transgenic products (Amerena et al., 2017).

In 2007, Serratos-Hernandez et al. published a study using ELISA and found recombinant proteins (evidence of transgenes) in two out of 25 communities in the Federal District of Mexico, where maize samples were collected in 2003. Two larger-scale studies were published in 2009. Piñeyro-Nelson et al. (2009) sampled maize from numerous communities in Oaxaca from 2001-2004 for testing using various methods. Transgenes were detected in some of the samples from the area where Quist & Chapela had conducted their study. Dyer et al. (2009) tested maize from eight locations in six states in 2002 using ELISA. They found 1.8% - 3.1% recombinant proteins, which were most abundant in Veracruz but also present in Guanajuato and Oaxaca. This was the first study to include a social survey, and it emphasized the importance of seed movements for potential transgene dispersal (Agapito-Tenfen & Wickson, 2017).

From 2009 to 2013, the Mexican government granted a total of 169 permits on a case-by-case basis for transgenic maize planting in

several states of northern Mexico, and a total of 262 hectares were planted with transgenic maize (EFE, 2017). The LBOGM stipulates that GMO maize cannot be planted in proximity to areas that are centers for maize origin but does not provide a definition for such centers; experimental plantings were limited to the north where native maize densities were considered to be relatively low (Wise, 2014). After requests were filed for commercial planting permits, all transgenic maize plantings were halted in 2013 when a group of activists, scientists, farmers and NGOs initiated a class-action lawsuit to end the granting of permits by the Mexican government. This lawsuit was based on concerns about transgenic maize interbreeding with or outcompeting native maize varieties, as well as the potential for legal action against small farmers in cases of transgenic contamination (Vargas-Parada, 2014). The federal court ordered experimental and commercial planting of transgenic maize suspended until a final verdict was reached. This suspension was confirmed in a 2016 lawsuit (Martinez & Sahores, 2016).

In 2017, Agapito-Tenfen et al. published a paper presenting a comparative study of transgenic contamination in two Oaxacan communities. They tested samples from fields, stores, and markets using real-time PCR, a more sensitive technique. Evidence of transgenes was found and confirmed in six out of 20 samples from one of the communities. The study included a social component, and Agapito-Tenfen et al. emphasized in their results the likely role of seed management practices in varied transgene presence among different communities (Agapito-Tenfen et al., 2017, p. 9468).

Another paper was published in 2017 by a group of scientists from the National Autonomous University of Mexico (UNAM) that showed widespread transgene presence in maize-based food products (González-Ortega et al, 2017). The researchers sampled several hundred maize products in Mexico between 2013-2015 and found transgenes in 82% of all products sampled and 90% of tortillas. Glyphosate, a probable carcinogen (World Health Organization, 2015), was detected in 28% of all samples that tested positive for transgenes. The results of this study were alarming, as official data showed Mexico to be largely self-sufficient in white maize for direct human consumption. Imported yellow maize from the U.S. was thought to be primarily used for processed foods and animal feed (Steve, 2018). González-Ortega et al. (2017) suggest either that transgenic maize grown abroad is entering food manufacturing systems in Mexico, or that domestic seed stocks contain some transgenic maize<sup>6</sup>. They argue for the need to reconsider biosafety guidelines (p. 1159).

The administration of Andrés Manuel López Obrador (2018-2024) has stated an intention to fight against transgenic maize, improve self-sufficiency in food, and decrease dependency on foreign products (Coto, 2018). But current laws leave open the door for transgenic maize in Mexico, as they do not explicitly establish the prohibition of commercial, pilot or experimental maize plantings in Mexico, which remain only suspended (Vélez, 2019). The US-Mexico-Canada agreement (USMCA) – a renegotiated NAFTA – was signed by leaders of the three countries on Nov. 30, 2018 (Office of the U.S. Trade Representative, 2018). Mexico

6. There is no law in Mexico that requires the labelling of foods containing GMOs. A proposed law has been frozen in the Mexican congress since 2016. The LBOGM requires explicit reference to GM contents, but only in cases where they create significant differences compared to conventional products – a qualification that is ambiguous (Amerena et al., 2017).

became the first country to ratify the USMCA on June 19, 2019 (Malkin & Swanson, 2019). The agreement, if ratified by all three countries, would require Mexico to adhere to UPOV 91 (the 1991 Act of the Union for the Protection of New Varieties of Plants) within four years. Mexico currently adheres to UPOV 78, which privileges genetic diversity and traditional seed exchange practices. UPOV 91 would allow for the patenting of genes and varieties, limit exchange of seeds by allowing for the sale only of officially recognized varieties, and legally require the adoption of intellectual property norms in Mexico (Perea, 2019).

National policy around transgenic maize in Mexico has been ambiguous and contradictory, with frequent changes and reversals due to constant pressure from activist movements and agribusiness companies for policy changes in opposite directions. Governmental action has failed to consistently support native maize diversity and small-scale farmers. Recent studies showing widespread transgene presence in foods and continued presence of transgenic contamination in maize landraces make clear that the issue remains urgent.

### Mixture, Contamination, and Gene Flow in Native Maize Landraces

Environmental factors and the selection practices of farmers planting maize landraces foster the maintenance of multiple different varieties amidst significant gene flow, resulting in metapopulations that are highly subdivided (Pressoir & Berthaud, 2003, p. 95). Meanwhile, the regular introduction of new genetic material via pollen and seed flow is a source of new alleles that contributes to diversity within varieties. This is important for their continued ability to adapt to changing local conditions (Rendón-Aguilar et al., 2015, p. 167). Farmers may introduce new seeds into their seed supplies through experimental planting along the edges of fields, leading to pollen flow with their own varieties. Farmers may intentionally hybridize varieties in this manner (Azeez, Adubi, & Durodola, 2018, p. 3). Additionally, farmers may completely or partially replace their seed stock due to loss of seed or intentional replacement.

Several previous studies refer to farmers' practices of regularly replacing varieties that they believe have gotten "tired" in order to maintain productivity (Louette, Charrier, & Berthaud, 1997; Louette & Smale, 2000; Rendón-Aguilar et al., 2015). The introduction of new seeds can counter the loss of vigor that occurs if outside genetic material is not brought into a farmer's seed supply, known as inbreeding depression (Bellon & Berthaud, 2005, p. 47)<sup>7</sup>. Seeds may be introduced either through exchange with other farmers who grow landraces, or through the planting of seeds from outside sources, such as seeds purchased at stores or acquired during travels<sup>8</sup>. The composition of varieties cultivated by farmers thus changes over time, due to the entry of new genetic material from both local and

7. Inbreeding depression is a result of deleterious recessive mutations becoming homozygous.

8. Rendón-Aguilar et al. (2015) describe how farmers in the Sierra Sur region of Oaxaca frequently buy seeds outside of the community, such as in stores for agrochemical products during travels to larger towns or cities (p. 167). Louette et al. (1997) describe in a community in Jalisco how farmers frequently plant seeds from ears acquired as gifts from friends or family outside the zone, or maize cobs bought for food may be planted.

non-local sources (Rendón-Aguilar et al, 2015; Louette & Smale, 2000). Seeds sourced from elsewhere are classified in the same way as local seeds, based on the phenotype of ears. They can thus be incorporated into local seed stocks when they have the same phenotypic characteristics as a local variety (Louette et al., 1997, p. 35). There is no consensus about the point at which seed mixing or gene flow with MVs prevents a local variety from still qualifying as native or belonging to a landrace (Azeez et al., 2018, p. 4).

Although the mixing of landraces and MVs is not new, the issue of transgenic contamination has brought attention to the reality that seeds of local maize landraces are not isolated from non-native varieties. Transgenic contamination is seen to pose a threat because of its ability to infiltrate and spread, due to the open-pollination biology of maize and the flexible nature of native maize landraces. Patterns of gene flow within small-scale maize farming systems and farmers' practices of mixing their seeds with seeds from non-local sources point to the importance of understanding possible implications if transgenes enter such systems, as these characteristics could be conducive to the diffusion of transgenes (Bellon & Berthaud, 2005, 45).

### Genetic Analyses in San Miguel

In January 2017, I collected maize samples grown by 35 families in 41 different fields in San Miguel for genetic investigation. I collected 2-5 ears per field from families in their homes, post-harvest.<sup>9</sup> I conducted this sampling in collaboration with the office of the comisariado (communal land authority) in San Miguel. In summer 2018, I also collected six samples of maize sold in stores in the community. I exported samples to the Harvard Herbaria from the National Institute for Research on Forestry, Agriculture, and Livestock (INIFAP) in Oaxaca<sup>10</sup>.



Figure 2: One sample of maize collected in San Miguel, with ears from a single field.

I completed lab work during the 2018-2019 academic year. I aggregated and ground kernels from each field to create 41 pooled samples and then completed DNA extractions<sup>11</sup>, which I sent to

9. I selected families through consultation with the comisariado's office. Sampling was not completely random, but I collected samples from all major cultivation zones in the community.

10. Samples were shipped with appropriate documentation, including a letter from the comisariado of San Miguel, a letter from the head of the INIFAP, and a permit from the Harvard Herbaria.

11. My goal was to make the study as comprehensive as possible to

Arq Genetics for real-time PCR using two markers (the Cauliflower Mosaic Virus 35S promoter, CaMV P-35S, and the Nopaline Synthase Terminator, T-nos, from *Agrobacterium tumefaciens*)<sup>12</sup>. These markers are found in most transgenic maize varieties (Agapito-Tenfen et al., 2017, p. 9464). Analyses by Arq Genetics did not detect either marker in any of the maize samples I collected<sup>13</sup>.

maximize possibilities of detecting transgenes. I therefore chose to use all of the ears and kernels that I collected rather than using an equal number from each field, even though this limits the conclusions that can be drawn about transgene frequency. I ground each sample using a kitchen blender, which I sterilized thoroughly between each sample preparation by rinsing with water, then soaking in 10% bleach solution for at least an hour, then rinsing again and treating with DNA denaturing solution (LookOut DNA Erase, Sigma-Aldrich). I completed DNA extractions using the Maxwell<sup>®</sup> RSC Instrument after subsampling 0.07 – 0.1 grams of maize flour from each sample.

12. The primers that were used for analysis are presented below:

CaMV 35S. Product length: 100

Primer	Sequence	Template	Length	Tm	GC%
Forward	CTGACGTAAGGGATGACGCA	Plus	20	59.83	55.00
Reverse	TGGTGATTTCAGCGTGTCT	Minus	20	59.60	50.00

T-nos. Product length: 187

Primer	Sequence	Template	Length	Tm	GC%
Forward	TGCCGGTCTTGCATGATTA	Plus	20	59.82	50.00
Reverse	CACCGCGCGATAATT	Minus	18	59.68	55.56

13. The images below (Figures 3 and 4) show the melt curves for all samples along with positive and negative controls (marked as +Control and -Control & NTC respectively). For the positive control, transgenic field corn was used. For the negative controls, water and an unrelated extraction were used.

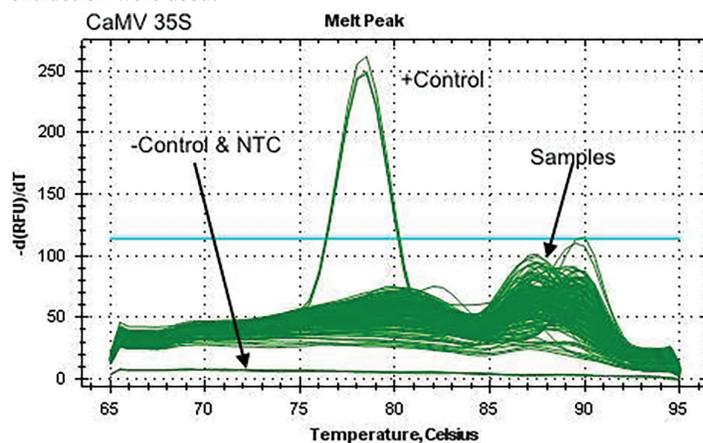


Figure 3: Melt curves for CaMV P-35S

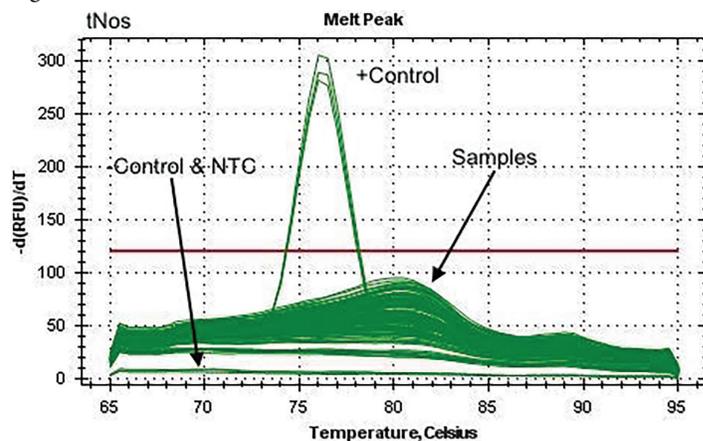


Figure 4: Melt curves for T-nos.

These results should not be interpreted as conclusive evidence of transgene absence in maize grown in San Miguel. They do suggest that if transgenes are present, they are likely found at a very low frequency.

Several factors may have contributed to this lack of detected transgenic contamination. The value that farmers place on knowledge about production and strong forms of communality may contribute to farmers' decisions to plant locally sourced seeds. The community maintains reciprocal exchange systems, which are reflected in many aspects of life including agriculture. San Miguel's semi-autonomous governance, communally owned land, and sense of community may also be influential in farmers' practices. This points to the importance of indigenous governance and social organization in preserving crop diversity and genetic resources

In addition, I did not detect transgenic contamination in maize sampled from stores<sup>14</sup>. Therefore, my genetic results alone do not suggest a lack of pollen flow between maize of MVs sold in the community and native maize varieties. But my ethnographic research suggests that such pollen flow is likely limited, as all farmers who mentioned having experimentally planted maize grain purchased from stores told me that it did not successfully produce ears. In other communities, researchers have documented farmers planting maize grain purchased from local stores, and this is commonly considered a likely source of transgenic contamination (see Agapito-Tenfen et al., 2017; Piñeyro-Nelson et al, 2009; Rendón-Aguilar et al, 2015).

Finally, the difficult agricultural conditions in San Miguel, including frequent droughts and rocky soils, support the continued planting of native maize varieties because other varieties do not successfully produce in the community. Native varieties are the only ones that can produce a fairly reliable harvest. The sort of seed experimentation and mixture that may have led to transgenic contamination in other parts of Oaxaca is not absent in San Miguel, but environmental conditions have likely minimized their impact. Although most respondents' denied that they had planted seeds acquired elsewhere in an initial survey I conducted in 2017, it is in fact very common for farmers in San Miguel to experiment with different types of seeds whenever they have the opportunity to do so. They may experimentally plant seeds in their patio, or on the

Both negative controls showed no amplification. All other samples showed an unrelated product at a very low level; this unrelated binder appeared to bind efficiently to the primers but had a different profile on the melt curve. Due to concerns about the unrelated product, I requested that Arq genetics re-test some of my samples using a different assay. All six samples from stores were re-tested using the same primers utilized by Agapito-Tenfen et al. (2017), based on methods certified by the Joint Research Center. I chose to re-test these samples because I expected the samples from stores to be most likely to test positive for transgenes, and I did not have sufficient funding to re-test all of my samples. In addition, I sent a different set of extractions for the samples from stores to FoodChain testing (Genetic ID), a company that specializes in GMO testing. Both sets of results were negative for constructs indicative of GM maize.

14. It may be significant that the most commonly purchased maize in San Miguel is grown in the state of Puebla rather than other parts of Mexico. Much of the maize that is grown commercially in Mexico and imported into communities like San Miguel comes from northern Mexico, where transgene presence is probably more likely due to the experimental plantings that took place from 2009-2013.

edge of a field. When I showed friends pictures of the maize that my parents grow at my home in Vermont, their first response was almost always reflections about whether those seeds might grow successfully in San Miguel. Many people also encouraged me to take back some of their seeds to try planting at my parents' house. Survey respondents denied planting other seeds simply because these experimental plantings were never, or rarely, successful, so they had not adopted the seeds.

Farmers in San Miguel have not planted non-local varieties on a larger scale because of environmental conditions, particularly the pattern of frequent droughts. This does not mean that there is a complete lack of pollen flow, as farmers do experimentally plant seeds from other sources; even if these plants do not produce ears, they may produce pollen. However, it does suggest that local varieties may experience significantly less gene flow from non-locally sourced varieties than in other communities where more extensive mixing and replacement with foreign varieties has been found to be common (see Rendón-Aguilar et al. 2015; Louette et al. 1997; Agapito-Tenfen et al. 2017). The same difficult conditions that lead many farmers to abandon or decrease agricultural production may be fostering the relative isolation of local varieties, as is supported by the lack of detected transgenes in samples from San Miguel. This study in San Miguel therefore suggests important interactions between social norms and environmental conditions that have not been discussed in previous considerations of transgene spread. If communities with the most difficult agricultural conditions constitute some of the communities where native seed stocks are most isolated from MVs (including transgenic varieties), this could have significant implications that warrant further research and consideration.

### Responses in San Miguel: Communal Maize, Contamination, and Chemicals

In August 2019, I met with Gabriela Linares Sosa and Aldo González of the Union of Organizations of the Sierra Juarez of Oaxaca (UNOSJO), a Zapotec Indigenous organization from the *Sierra Norte* region of Oaxaca. The UNOSJO forms part of the *Espacio Estatal en Defensa del Maíz Nativo de Oaxaca* (State Space in Defense of Oaxaca's Native Maize), a group of organizations in Oaxaca that has played an important role in movements opposing transgenic maize in Mexico. I had met with Gabriela and Aldo in 2017 and contacted them again with the hope that they could lead a discussion in San Miguel to clarify farmers' understanding of transgenic contamination, an idea that I had discussed with members of the *comisariado's* office. Aldo and Gabriela agreed to lead a discussion in San Miguel and encouraged me to invite farmers in San Miguel to attend a two-day state meeting titled "Communal Maize from Oaxaca for the World" being coordinated by the *Espacio Estatal* at the end of September, with the stated objective to "discuss the importance of communal maize in Oaxaca, and denounce the dispossession of seeds to privatize them via patents." This state meeting was organized in part to address the biopiracy of *olotón* maize, an issue that I will discuss later.

In early September, I revisited all of the homes in San Miguel where I had collected maize ears to share the results of my study for transgenic contamination and provide information about the UNOSJO's events. Approximately 50 farmers attended the talk that Aldo gave in San Miguel on September 20th, when he discussed transgenic maize, biopiracy, and the implications for indigenous

communities. I attended the state meeting in the capital city of Oaxaca, along with three farmers from San Miguel, on September 27-28.

Previous studies on transgenic contamination in Mexico have not discussed how or whether results were presented to participating farmers and communities – a significant gap in literature, as farmers' and communities' responses to the issue of transgenic contamination is a significant factor in determining the dynamics of transgene flow in Mexico. My research in San Miguel presents a model for how genetic testing can be used to engage farmers and communities in discussions about their seeds through collaboration with local organizations. Such engagements are the only way to gain a better understanding of how farmers' perspectives affect transgene flow. They are also essential to ensure that communities are being adequately included and fully informed regarding studies about their maize.

Most San Miguel residents with whom I spoke during initial surveys and interviews were not familiar with transgenic contamination. Some had not heard of it at all. Others had heard of transgenic maize but did not know exactly what it was. They generally connected it immediately with chemicals, and perceived it to be unnatural, as one farmer expressed:

Well... I heard that word [transgenic]... And just the other day I had the curiosity to say to my son, "look there in the dictionary" ... more or less what he told me is that when it is planted, it needs a lot of water and a lot of fertilizer. Ay no, I told him, it is not good for us then. No, we eat what we would say is natural. Just a little bit of fertilizer is applied. Some people apply it, some people don't.

Many farmers denied the possibility that San Miguel's maize could be contaminated, even if they did not understand what transgenic contamination was. This denial was often based on claims about contamination coming from chemicals. Transgenes can enter native maize seedstocks only via pollen or seed flow, but there are connections between transgenic maize and chemicals in that transgenic crops require heavy use of chemical inputs. San Miguel residents' responses were shaped by their perceptions of contamination, as most had little to no knowledge about GMOs. Because chemicals are the only element in local agricultural practices that comes from outside, some assumed that this was the only way that contamination could enter. San Miguel residents associate high levels of chemical use with foods that are unknown. Because they know little about transgenic maize, they assume that it is unnatural, and full of chemicals.

Although government distribution of seeds and agricultural supplies is common in rural Mexico, sometimes as part of political campaigns, no one I spoke with in San Miguel reported the government ever having distributed seeds in San Miguel. As one farmer described:

No. The government doesn't gives us anything... If they have improved seeds or something like that, [we don't get] any. It is *criollito* [native] what we have. Yes, that is what we always saving so that... those seeds keep going. So that we don't need anything.... If we stop eating it, there won't be anything to plant. Yes. A little has to be saved for the next year.

Thus, although farmers in San Miguel emphasized that commercially produced foods are grown very differently from their own crops, particularly with regards to chemical use and irrigation, most have had little to no exposure to the seeds used in commercial maize production.

## Transgenic Contamination in Context

Neoliberal economic policies that limit the ability of small-scale Mexican farmers to continue producing maize have also led to the influx of transgenic maize imported from the U.S. Soleri & Cleveland (2006) state: "The biggest threat to maize diversity in Mexico is the synergy between micro level genetic processes and macro level regional and global economic processes, which creates a situation that is more than the sum of its parts" (p. 28). It is necessary to support small-scale farmers in order to preserve native maize landraces (Hartigan, 2017, p. 62).

Fitting (2006) discusses the importance of considering transgenic contamination alongside larger patterns affecting native maize producers. She describes how it is not just transgenic maize imports that threaten maize diversity, but also the increasing struggles and migration of small-scale maize farmers (p. 15). The fact that many Oaxacan families export their labor through migration to the U.S. in order to purchase maize from other sources because they can no longer grow enough of their own maize, despite living in the center of maize origin and diversity, is an irony that should not be overlooked. Decreased subsistence maize production, migration, and transgenic contamination are symptoms of the same problems. In San Miguel, many farmers choose to migrate because they are unable to gain sufficient income through agriculture or other local activities to undertake projects such as building a house or educating their children.

Meanwhile, native maize seeds continue to form an important base for food security. As Brandt (2014) discusses in the context of Zapatista communities in Chiapas, small-scale agriculture using local seeds poses an alternative to commercial production:

The Mother Seeds project participants are working to define and circulate corn in a way that presents what they see as an alternative to the practices of neoliberal economics that brought GM-corn to Mexico... Zapatista corn offers the possibility of material participation in the enactment of a different kind of world... it demonstrates that not all corn is equivalent – either economically or culturally (p. 894).

Native maize varieties have a long history and are part of dynamic, adaptable social and environmental systems. Farmers' perspectives on their seeds fit into larger national debates around native maize in Mexico. These debates have implications for the future of maize diversity and the future of small-scale farming in the context of climate change, neoliberalism, and intellectual property law.

## The Case of Olotón Maize

In August 2018, a paper was published in the journal *PLoS Biology* titled "Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota" (Van Deynze et al., 2018). It was authored by researchers from the University of

California Davis, the University of Wisconsin-Madison, and Mars, Incorporated (a large global conglomerate that specializes in candy and pet food; Pskowski, 2019) and described the results of more than a decade of research on the *olotón* maize landrace from the Mixe region of Oaxaca. This research confirmed *olotón* maize's ability to fix its own nitrogen using aerial roots that secrete a sugar-rich mucus, which hosts bacteria that can pull nitrogen from the air and fix it into a form usable by the maize plant. The mucus, due to its chemical composition, has the ability to recruit these bacteria from the environment; authors found that the maize was capable of producing this mucus and recruiting the same nitrogen-fixing bacteria in environments not limited to its native regions. The mucus drips from the roots, fertilizing the plant. Van Deynze et al. (2018) found that the plant could cover 29 to 82 percent of its nitrogen needs through this process (p. 11), allowing it to grow to heights of 16 to 20 feet in nitrogen poor soil with no fertilizers (Daley, 2018). Mexican scientists had been aware of the *olotón* landrace's unique morphology for many years and suspected it was fixing its own nitrogen, but they had lacked funds and technology for the costly research to confirm it.

Van Deynze et al. (2018) stated that they had worked with a "Sierra Mixe community," the name of which was not specified. They stated that biological materials were accessed under a benefit sharing agreement between the community and BioN2 (a Mars subsidiary), that permission had been granted from the Mexican government, and that an internationally recognized certificate of compliance had been issued under the Nagoya Protocol (an international agreement intended to ensure the equitable sharing of benefits from genetic resources) (p. 11).

Articles soon came out in *Smithsonian* and *The Atlantic*, referring to *olotón* maize as the "corn of the future" (Daley, 2018) and the "wonder plant that could slash fertilizer use" (Yong, 2018). Videos and articles published by UC Davis and Mars, Incorporated emphasized the potential environmental benefits of developing a commercial variety with this characteristic. Nitrogen fertilizer production uses 1-2% of total global energy supply. The use of nitrogen fertilizers contributes significantly to numerous environmental problems, including algal blooms and dead zones (Daley, 2018). It will be many years before a nitrogen-fixing commercial maize variety is developed, if developing such a variety is even feasible. But if developed, it could drastically reduce the amount of fertilizer used in commercial maize production, reducing both costs and environmental impacts. Researchers claimed it could also be of great benefit in developing countries, where access to fertilizers is often limited (Daley, 2018).

However, concerns soon arose about the researchers' intention to develop a patented variety and the fairness by which benefits would be shared with the indigenous peoples who grow *olotón* maize. In addition, it was discovered that the researchers had been exporting maize for at least nine years before receiving permission from the federal government. An article in Spanish on the news site *Animal Político* in November 2018, titled "Two public universities in the U.S. and a transnational company pirate Oaxacan maize" (Martínez, 2018), described how the researchers had failed to comply with federal guidelines.

This case raises complicated questions about intellectual property law and the exploitation of genetic resources maintained by indigenous peoples and small-scale farmers. The researchers made an agreement only with one community in the Mixe – the

town of Totontepec – but maize with this characteristic is grown in several regions of Oaxaca as well as in other parts of Mexico and Guatemala (Pskowski, 2019). Maize varieties such as the *olotón* landrace have been developed by indigenous farmers over the course of thousands of years and are considered in Mexico to be *bienes comunes*, or common goods (Martínez, 2018). Development of a seed patent using genetic material from *olotón* maize raises concerns about equitable access – some community members in Totontepec have expressed fear that they will no longer be able to grow their own seeds if such a patented variety is developed (Pskowski, 2019). Journalist Pskowski states:

Totontepec's maize is a reminder that the policies meant to safeguard the genetic resources of indigenous communities, in Mexico and around the world, are very much a work in progress... fair, long-lasting agreements are rare.

San Miguel's short maize plants and small ears pose a great contrast to *olotón* maize. Yet, the adaptation of maize landraces grown in San Miguel to dry, local conditions is equally extraordinary. Native maize landraces possess a wealth of genetic information; the case of *olotón* maize reminds us that such genetic information remains powerful in contexts not limited to those in which it is planted and maintained.

## Conclusion: Seeds, Community, and Knowledge

Today, just three companies control over half of the global commercial seed market, and 10 companies control 70% (ETC group, 2012). In the discussion he led in San Miguel, Aldo González described the importance of *guelaguetza* (reciprocal exchange) and the threat that patents and transnational companies pose to such ways of living:

This is the way that our communities have lived for a long time, and it doesn't require a credit card, because it is an exchange, it is the solidarity between our communities. That has allowed for our communities to live well for a long time. When those people that just want to do business, well if they make maize with those characteristics they are also going to put their marker on them, no? And if they find that marker in other farmers [maize] they are going to say, you stole my property, no? We say that really it isn't their property. The place for the origin of maize is here. We are the ancestors of the first people that grew maize on this planet, and they are stealing from us all of that information. (Aldo González of UNOSJO; September 20, 2019)

Local seed systems form part of governmental and social systems in communities like San Miguel. Communal land ownership allows virtually all community members to access land for planting, foraging, and collecting firewood. One of the slogans during the state meeting, "*Maíz comunal, tierra comunal*," (communal maize, communal land) reflects this essential connection between seeds and lands that are shared within the community without private ownership. As many emphasized, communality is one of the greatest strengths of Oaxacan communities. The maintenance of native maize varieties that are freely exchanged, sold in small quantities, and mixed is an essential part of this communality.

Efforts to develop a patented variety using genetic information from the *olotón* landrace work in opposition to the practices that developed such a unique biological entity. Protocols in place are insufficient to address the complex issues involved. It is unclear what informed consent means in communities where concepts like intellectual property rights and patents are unfamiliar. Similarly, the presence of transgenic maize in Mexico represents a material and symbolic threat to native maize diversity. Non-segregated maize imports are sometimes justified with the claim that maize sold as “grain” is intended for consumption rather than planting (Dyer et al. 2009), but this goes against how communities understand their maize.

In the context of transgenic contamination, the ability to know the details of how crops were produced and seeds were saved is critical. After Aldo’s discussion in San Miguel about the value of local seed exchange and sharing systems, one farmer asked how to control for potential transgenic contamination when exchanging seeds. Aldo replied:

The only control that we can have is that every farmer knows what it is that s/he has planted. If I am going to give my seed to another person, I have to guarantee, look, this is the seed that my parents, my grandparents planted... and that is why I am confident that it is a good seed. But if I say, look, my parents lost the seed and I bought it but I am giving it to you because I am a good person, well, then no. (Aldo González of UNOSJO; meeting in San Miguel; September, 2019).

Local knowledge and production systems, like those maintained in San Miguel, are the only way to preserve native maize landraces.



Figure 5: Three women stand in their *milpa* in San Miguel.

As I have emphasized, maize diversity is inseparable from the livelihoods of the farmers that maintain it. Climate change and agricultural policies work together to marginalize agricultural production in communities like San Miguel, and this has important implications for the conservation of crop diversity. Landraces represent an invaluable genetic resource for adaptation to climate change and development of future varieties. Further research on maize landraces is essential in enabling farmers to respond to and address the threats that transgenic contamination, climate change, and other factors pose for the maintenance of maize diversity. Such research must be done in collaboration with communities and with their interests at the forefront. My research in San Miguel exhibits

the need for more effective interdisciplinary, collaborative research about native maize diversity. The issue of transgenic contamination reflects the vulnerability of native maize seeds, which become highly charged political objects in the context of international policy.

On the second day of the state meeting in Oaxaca, participants formed a parade that traveled through the center of the city to the Museum of Contemporary Art. Farmers walked and danced carrying *mazorcas*, tortillas, and other products from their *milpas*. Upon arriving at the museum, they built a collective altar. Maize was shared among farmers, symbolizing an alternative to the concentration of genetic resources in the hands of large agro-industrial corporations. An attending farmer from San Miguel left the meeting with the pockets of her apron stuffed with maize and bean seeds of all shapes and colors, grown from farmers from all over the state. Inside her bag, she carried several cups of seeds of *olotón* maize which she had bought from a woman from the municipality of Totontepec. Next year, she will plant some of these seeds in her fields. Perhaps they will fail to mature, like most of the seeds with which San Miguel farmers experiment. Or perhaps they will produce tassels and spread some of their pollen to her maize plants and those on the edges of neighboring fields, adding new genetic information to local maize seeds that have been developing and changing for thousands of years.

## References

- Agapito-Tenfen, Sarah and Wickson, Fern. (2018). “Challenges for Transgene Detection in Landraces and Wild Relatives: Learning from 15 years of Debate over GM Maize in Mexico.” *Biodiversity and Conservation* 27, no. 3, 539-66.
- Agapito-Tenfen, Sarah; Lopez, Flor R.; Mallah, Narmeen; Abou-Slemayne, Gretta; Trtikova, Miluse; Nodari, Rubens O.; and Wickson, Fern. (2017). “Transgene Flow in Mexican Maize Revisited: Socio-Biological Analysis across Two Contrasting Farmer Communities and Seed Management Systems.” *Ecology and Evolution* 7, no. 22, 9461-72.
- Amerena, Rosi; Mayorga, Juan; and Pérez Ortega, Rodrigo. (October 28, 2017). “¿Tus Alimentos Tienen Transgénicos? En México Ninguna Ley Obliga a Que Las Empresas Te Lo Digan.” *Animal Político*, Accessed September 28, 2019. <https://www.animalpolitico.com/2017/10/alimentos-transgenicos-mexico-ley/>.
- Aragón Cuevas, Flavio. (2011). “Maíces Nativos de Oaxaca.” Presentation, Comisión Intersecretarial de Bioseguridad de los Organismos Genéticamente Modificados, México, D.F., September 6, 2011. Accessed October 30, 2019. [https://www.conacyt.gob.mx/cibiogem/images/cibiogem/redes/redmexogm/eventos/foros/Autoridades/5-INIFAP\\_MAICES%20CRIOLLOS%20OAXACA.pdf](https://www.conacyt.gob.mx/cibiogem/images/cibiogem/redes/redmexogm/eventos/foros/Autoridades/5-INIFAP_MAICES%20CRIOLLOS%20OAXACA.pdf)
- Arteaga, María Clara; Moreno-Letelier, Alejandra; Mastretta-Yanes, Alicia; Vázquez-Lobo, Alejandra; Breña-Ochoa, Alejandra; Moreno-Estrada, Andrés; Eguiarte, Luis E; and Piñero, Daniel. (2016). “Genomic Variation in Recently Collected Maize Landraces from Mexico.” *Genomics Data* 7, 38-45.
- Azeez, Musibau A.; Adubi, Amos O.; and Durodola, Felicia A. (2018). “Chapter 1: Landraces and Crop Genetic Improvement.” In *Rediscovery of Landraces as a Resource for the Future*, edited by Oscar Grillo.
- Bellon, M.R. and Berthaud, J. (2005). “Maize Diversity, Gene Flow and Transgenes in Mexico.” In *Issues on gene flow and germplasm management*.
- Brandt, Marisa. (2014). “Zapatista Corn: A Case Study in Biocultural Innovation.” *Social Studies of Science* 44, no. 6, 874-900.
- Brody, Jane E. (April 23, 2018). “Are G.M.O. Foods Safe?” *The New York Times*. Accessed October 30, 2019. <https://www.nytimes.com/2018/04/23/well/eat/are-gmo-foods-safe.html>

- Brueck, Hillary. (June 17, 2019). "The Epa Says a Chemical in Monsanto's Weed-Killer Doesn't Cause Cancer — but There's Compelling Evidence the Agency Is Wrong." *Business Insider*. Accessed October 16, 2019. <https://www.businessinsider.com/glyphosate-cancer-dangers-roundup-epa-2019-5>.
- Camacho Villa, Tania Carolina; Maxted, Nigel; Scholten, Maria; and Ford-Iloyd, Brian. (2005). "Defining and Identifying Crop Landraces." *Plant Genetic Resources: Characterization and Utilization* 3, no. 3, 373-84.
- Cleveland, David; Soleri, Daniela; Aragón Cuevas, Flavio; Crossa, José; and Gepts, Paul. (2005). "Detecting (Trans)Gene Flow to Landraces in Centers of Crop Origin: Lessons from the Case of Maize in Mexico." *Environmental Biosafety Research* 4, no. 4, 197-208.
- Cleveland, David; Soleri, Daniela; and Smith, Steven. (2000). "Un Marco Biológico Para Entender El Fitomejoramiento De Los Agricultores." *Economic Botany* 54, no. 3, 377-94.
- Colectivo Oaxaqueño en Defensa de los Territorios. (2011). "A Todos Los Pueblos, Comunidades, Campesinos, Investigadores, Académicos Y Ciudadanos De Oaxaca Y México." News release. Accessed October 16, 2019. Retrieved from <https://maiznativodeoaxaca.wordpress.com/material-para-descargar/>.
- Commission for Environmental Cooperation. (2004). "Maize & Biodiversity: The Effects of Transgenic Maize in Mexico." Edited by Communications Department of the CEC Secretariat. Canada.
- Coto, Diego. (August 13, 2018). "¿Qué Hará Amlo Con El Maíz Transgénico En México?" *Negocios Inteligentes*. Accessed September 28, 2019. <https://negocios-inteligentes.mx/que-hara-amlo-con-el-maiz-transgenico-en-mexico/>.
- Daley, Jason. (August 10, 2018). "The Corn of the Future Is Hundreds of Years Old and Makes Its Own Mucus." *Smithsonian*. Accessed October 16, 2019. <https://www.smithsonianmag.com/science-nature/corn-future-hundreds-years-old-and-makes-its-own-mucus-180969972/>.
- de Vendômois, Joël Spiroux; Roullier, François; Cellier, Dominique; and Séralini, Gilles-Eric. (2009). "A Comparison of the Effects of Three Gm Corn Varieties on Mammalian Health." *International Journal of Biological Sciences*, 706-26.
- Dyer, George A; Serratos-Hernández, J. Antonio; Perales, Hugo R; Gepts, Paul; Piñeyro-Nelson, Alma; Chávez, Angeles; Salinas-Arreortua, Noé; et al. (2009). "Dispersal of Transgenes through Maize Seed Systems in Mexico (Maize Transgenes in Mexico)." *PLoS ONE* 4, no. 5, 5734.
- EFE. (November 25, 2017). "Tribunal Mantiene Suspensión Para Siembra De Maíz Transgénico En México." EFE. Accessed September 28, 2019. <https://www.efc.com/efe/america/mexico/tribunal-mantiene-suspension-para-siembra-de-maiz-transgenico-en-mexico/50000545-3449197>.
- ETC Group. (October 10, 2003). "Contaminación transgénica en México: mucho más grave." *Boletín de prensa colectivo de comunidades indígenas y campesinas de Oaxaca, Puebla, Chihuahua, Veracruz, CECCAM, CENAMI, Grupo ETC, CASIFOP, UNOSJO, AJAGI*. Accessed October 30, 2019. <https://www.etcgroup.org/es/content/contaminacion-transgenica-en-mexico-mucho-mas-grave>
- ETC Group. (June 25, 2012). "Just 3 companies control more than half (53%) of the global commercial market for seed." ETC Group. Accessed October 30, 2019. <http://www.etcgroup.org/content/just-3-companies-control-more-half-53-global-commercial-market-seed>
- Federation of American Scientists (FAS). (2011). "Starlink Maize: A Cautionary Tale." *Case Studies in Agricultural Biosecurity*. Accessed October 30, 2019. <https://fas.org/biosecurity/education/dualuse-agriculture/2.-agricultural-biotechnology/starlink-corn.html>
- Fitting, Elizabeth M. (2011). *The Struggle for Maize : Campesinos, Workers, and Transgenic Corn in the Mexican Countryside*. Durham [N.C.]: Duke University Press.
- Food and Agriculture Organization (FAO). (2019). "Part I: Legal and Policy Concepts Relating to the Protection of Plant Varieties and Plant Breeders' Rights." Accessed October 21, 2019. <http://www.fao.org/3/y5714e/y5714e02.htm>.
- Freese, William, and Schubert, David. (2004). "Safety Testing and Regulation of Genetically Engineered Foods." *Biotechnology & genetic engineering reviews* 21, 299.
- González-Ortega, E; Piñeyro-Nelson, A; Gómez-Hernández, E; Monterrubio-Vázquez, E; Arleo, M; Dávila-Velderrain, J; Martínez-Debat, C; and Álvarez-Buylla, E.R. (2017). "Pervasive Presence of Transgenes and Glyphosate in Maize-Derived Food in Mexico." *Agroecology and Sustainable Food Systems* 41, no. 9-10, 1146-61.
- Hartigan, John. (2017). *Care of the Species : Races of Corn and the Science of Plant Biodiversity*. Minneapolis: University of Minnesota Press.
- Heerwaarden, Joost van; Ortega Del Vecchio, Diego; Alvarez-Buylla, Elena R; and Bellon, Mauricio R. (2012). "New Genes in Traditional Seed Systems: Diffusion, Detectability and Persistence of Transgenes in a Maize Metapopulation (New Genes in Traditional Seed Systems)." 7, no. 10, 46123.
- Heerwaarden, Joost van. (2007). "Population Genetics of Traditionally Managed Maize : Farming Practice as a Determinant of Genetic Structure and Identity of Maize Landraces in Mexico." Dissertation, Wageningen University.
- Linares Sosa, Gabriela and Barmeyer, Niels. (2014). "El Capisayo: Conocer Para Defender." *Guelatao de Juárez, Oaxaca: UNOSJO S.C.*
- Linares Sosa, Gabriela and González, Aldo. (2017, 2019). Private meetings. UNOSJO, Guelatao de Juárez, Oaxaca.
- Louette, Dominique; Charrier, André; and Berthaud, Julien. (1997). "Conservacion in Situ De Maiz En Mexico: Diversidad Genetica Y Manejo De Las Semillas En Una Comunidad Tradicional." *Economic Botany* 51, no. 1, 20-38.
- Louette, D., and Smale, M. (2000). "Farmers' Seed Selection Practices and Traditional Maize Varieties in Cuizalapa, Mexico." *Euphytica* 113, no. 1, 25-41.
- Malkin, Elisabeth & Swanson, Ana. (June 19, 2019). "Mexico Ratifies Trade Deal with the U.S. And Canada." *The New York Times*. Accessed September 28, 2019. <https://www.nytimes.com/2019/06/19/world/americas/mexico-nafta-usa-canada.html>.
- Martínez, Mercedes López and Sahores, Ercilia. (2016). "Court Ruling a Victory for Mexico Farmers and Anti-Gmo Activists." *Regeneration International*. <https://regenerationinternational.org/2016/03/17/court-ruling-a-victory-for-mexico-farmers-and-anti-gmo-activists/>.
- Martínez, Paris. (November 5, 2018). "Dos Universidades Públicas De Eu Y Una Trasnacional Piratean Maíz Oaxaqueño." *Animal Político*. Accessed September 28, 2019. <https://www.animalpolitico.com/2018/11/dos-universidades-publicas-de-eu-y-una-trasnacional-piratean-maiz-oaxaqueño/>.
- Office of the United States Trade Representative. (2018). "United States-Mexico-Canada Agreement." Accessed October 21, 2019. <https://ustr.gov/trade-agreements/free-trade-agreements/united-states-mexico-canada-agreement>.
- Ortiz-Garcia, S; Ezcurra, E; Schoel, B; Acevedo, F; Soberon, J; and Snow, AA. (2005). "Absence of Detectable Transgenes in Local Landraces of Maize in Oaxaca, Mexico (2003-2004)." *Proceedings of the National Academy of Sciences of the United States of America* 102, no. 35, 12338-43.
- Perea, Ernesto. (June 12, 2019). "Firma De Tmec Abriría La Puerta a Patentar Genes Y Cobro De Regalías a Agricultores De México Por Parte De Transnacionales." *Imagen Agropecuaria*. Accessed October 16, 2019. <http://imagenagropecuaria.com/2019/06/12/firma-de-tmec-abriria-la-puerta-a-patentar-genes-y-cobro-de-regalias-a-agricultores-de-mexico-por-parte-de-trasnacionales/>.

- Piñeyro-Nelson, A.; Van Heerwaarden, J.; Perales, H. R.; Serratos-Hernández, J. A.; Rangel, A.; Hufford, M. B.; Gepts, P.; et al. (2009). "Transgenes in Mexican Maize: Molecular Evidence and Methodological Considerations for GMO Detection in Landrace Populations." *Molecular Ecology* 18, no. 4, 750-61.
- Pressoir, G., and Berthaud, J. (2003). "Population Structure and Strong Divergent Selection Shape Phenotypic Diversification in Maize Landraces." *Heredity* 92, no. 2, 95.
- Procuraduría Federal de Protección al Ambiente. (September 30, 2014). "Ley De Bioseguridad De Organismos Genéticamente Modificados." Gobierno de México. Accessed October 21, 2019. <https://www.gob.mx/profepa/documentos/ley-de-bioseguridad-de-organismos-geneticamente-modificados>.
- Pskowski, Martha. (July 16, 2019). "Indigenous Maize: Who Owns the Rights to Mexico's 'Wonder' Plant?" *Yale Environment* 360. Accessed September 28, 2019. <https://e360.yale.edu/features/indigenous-maize-who-owns-the-rights-to-mexicos-wonder-plant>.
- Quinton, Amy. (August 7, 2018). "Can We Grow One of the World's Largest Food Crops without Fertilizer?" *UC Davis Food and Agriculture*. Accessed October 16, 2019. <https://www.ucdavis.edu/food/news/grow-food-crops-without-fertilizer/>.
- Quist, David and Chapela, Ignacio H. (2001). "Transgenic DNA Introgressed into Traditional Maize Landraces in Oaxaca, Mexico." *Nature* 414, no. 6863, 541.
- Rendón Aguilar, Beatriz ; Aguilar Rojas, Verónica ; Aragón Martínez, María Del Consuelo ; Ávila Castañeda, José Francisco ; Bernal Ramírez, Luis Alberto ; Bravo Avilez, David ; Carrillo Galván, Guadalupe; et al. (2015). "Diversidad De Maíz En La Sierra Sur De Oaxaca, México: Conocimiento Y Manejo Tradicional." *Polibotánica*, no. 39, 151-74.
- Serratos - Hernández, José Antonio; Gómez Olivares, José Luis; Arreortua, Noé; Rodríguez, Enrique B.; Gutiérrez, Fabián I.; de Ita, Ana. (2007). "Transgenic Proteins in Maize in the Soil Conservation Area of Federal District, Mexico." *Frontiers in Ecology and the Environment* 5, no. 5, 247-52.
- Soleri, Daniela and Cleveland, David. (2006). "Transgenic Maize and Mexican Maize Diversity: Risky Synergy?". *Agriculture and Human Values* 23, no. 1, 27-31.
- Soleri, Daniela; Cleveland, David A.; and Aragón Cuevas, Flavio. (2006). "Transgenic Crops and Crop Varietal Diversity: The Case of Maize in Mexico." *BioScience* 56, no. 6, 503-13.
- Stephen, Lynn. (2007). *Transborder Lives: Indigenous Oaxacans in Mexico, California, and Oregon*. Durham: Duke University Press.
- Steve, Oscar. (June 16, 2018). "El Maíz Transgénico Ya Está En México, Y El Verdadero Problema Es Que No Sabemos En Que Productos Por Falta De Leyes." *Xataka México*. Accessed September 28, 2019. <https://www.xataka.com.mx/investigacion/asi-como-maiz-transgenico-termino-90-ciento-tortillas-mexico-pese-que-esta-prohibido>.
- Unión de Científicos Comprometidos con la Sociedad (UCCS). (October 11, 2017). "Estudio Científico: Presencia Masiva De Transgenes Y Del Herbicida Glifosato En Alimentos Derivados De Maíz En México." *Asociación de Consumidores Orgánicos*. Accessed September 28, 2019. <https://consumidoresorganicos.org/2017/10/11/estudio-cientificopresencia-masiva-transgenes-del-herbicida-glifosato-en-alimentos-derivados-maiz-en-mexico/>.
- Van Deynze, Allen; Zamora, Pablo; Delaux, Pierre-Marc; Heitmann, Cristobal; Jayaraman, Dhileepkumar; Rajasekar, Shanmugam; Graham, Danielle; et al. (2018). "Nitrogen Fixation in a Landrace of Maize Is Supported by a Mucilage-Associated Diazotrophic Microbiota." *PLoS Biology* 16, no. 8, 2006352.
- Vargas-Parada, Laura. (July 1, 2014). "Gm Maize Splits Mexico." *Nature*. Accessed October 16, 2019. <https://www.nature.com/news/gm-maize-splits-mexico-1.15493>.
- Vélez, Octavio. (October 11, 2019). "Iniciativa permitiría maíz transgénico." *NVI Noticias*. Accessed October 30, 2019. <https://www.nvinoticias.com/nota/128066/iniciativa-permitiria-maiz-transgenico>
- Wise, Timothy A. (2014). "Monsanto Meets Its Match in the Birthplace of Maize." *TripleCrisis*. Accessed October 16, 2019. <http://triplecrisis.com/monsanto-meets-its-match-in-the-birthplace-of-maize/>.
- Wohlgemuth, Neusa Hidalgo-Monroy. (2014). "Migration and Indigenous Communities in the Southern States of Oaxaca and Chiapas, Mexico." *Perspectives on Global Development and Technology* 13, no. 3, 379-400.
- World Health Organization. (March 20, 2015). "IARC Monographs Volume 112: evaluation of five organophosphate insecticides and herbicides." *International Agency for Research on Cancer, Lyon, France*. <https://www.iarc.fr/wp-content/uploads/2018/07/MonographVolume112-1.pdf>
- Yong, Ed. (August 9, 2018). "The Wonder Plant That Could Slash Fertilizer Use." *The Atlantic*. Accessed October 16, 2019. <https://www.theatlantic.com/science/archive/2018/08/amaizeballs/567140/>

# Regulation of Transcription and Chromatin Structure by Spt6 and Elf1 in Yeast

Ann Yang  
Harvard College '22

Eukaryotic transcription is a complex process that requires the precise and orchestrated recruitment of many initiation, elongation, and termination factors. Many of these transcription factors are not structurally or functionally well understood. In particular, the elongation factor Spt6 has broad and diverse roles in regulating transcription which have been studied to varying degrees of detail. While many of the functions of Spt6 have been elucidated, many of the finer mechanisms of these functions remain unknown, making Spt6 a particularly key protein of interest for transcription studies. This review summarizes recent studies of the many roles of Spt6 in regulating transcription with an emphasis on the control of chromatin structure as a mechanism of transcriptional regulation. Additionally, interactions between Spt6 and several key proteins are discussed in the context of transcriptional regulation. The relationship between Spt6 and the relatively unexplored elongation factor Elf1 is highlighted and structurally analyzed for possible direct interaction. Structural analysis approximately reconstitutes the *in vivo* spatial relationship between Spt6 and Elf1, thus providing insight on the likelihood of a physical interaction between these proteins. As part of examining the Spt6-Elf1 relationship, this review also covers the characterization of Elf1 and potential roles for Elf1 independent of Spt6. Our current knowledge of Spt6 is extensive, but future experiments are necessary to establish the connections between Spt6 and less-studied proteins such as Elf1, particularly for analyzing indirect interactions which may occur through multiprotein pathways.

## Introduction

The budding yeast *Saccharomyces cerevisiae* is the leading model organism for studying gene expression. *S. cerevisiae* is a single-celled eukaryotic organism, able to divide rapidly under simple growth conditions. However, the true power of yeast as a model system is in the ease with which its genes and gene expression can be mutated and controlled either by plasmids or the yeast chromosomes (Duina et al., 2014). As a result, yeast is a powerful and easily manipulatable model system for investigating transcription. Furthermore, given the high degree of conservation among eukaryotes, yeast is an excellent system for understanding transcription in higher eukaryotes as well.

Regulation of transcription at the genetic level is crucial for proper gene expression and cell maintenance. Transcription in eukaryotic cells is a complex process that requires the recruitment of many transcription factors. RNA polymerase II (RNAPII), aided by these factors, transcribes DNA into RNA. This process can be divided into three distinct phases: initiation, elongation, and termination (Venkatesh and Workman, 2015). During initiation, RNAPII recognizes and binds to promoter sequences with the help of general transcription factors (GTFs). These GTFs unwind double-stranded DNA at the transcription start, thus forming a transcription bubble and initiating RNAPII activity. After initiation, these factors are replaced with elongation factors which promote RNA synthesis during the elongation phase. As the RNAPII elongation complex moves along the template strand, DNA is unwound to allow for transcription of the pre-mRNA. However, as the complex passes, the pre-transcription chromatin structure is re-established (Jonkers and Lis, 2015). Elongation is followed by termination when RNA is released from RNAPII and RNAPII is released from the DNA template (Venkatesh and Workman, 2015). Regulation of this process is necessary for ensuring proper cell function and viability and may be accomplished by a variety of methods including activity of regulatory factors, DNA modifications, and control of chromatin structure (Jonkers and Lis, 2015; Venkatesh and Workman, 2015).

The yeast genome is packaged as chromatin. In eukaryotic cells, DNA is wound ~1.7 times around an octamer of histone proteins to form nucleosomes. The core structure consists of two copies of each histone: H3, H4, H2A and H2B. Nucleosomes in turn coil and stack to form chromatin fibers which loop and fold to form chromosomes (Luger et al., 1997; Venkatesh and Workman, 2015). Typical haploid *S. cerevisiae* cells contain ~12,000 kb of genomic DNA organized this way into 16 chromosomes (Duina et al., 2014).

Chromatin is a dynamic structure. In addition to efficiently packaging the genome into the nucleus, chromatin structure plays key roles in controlling multiple cellular processes such as transcription, recombination, and DNA replication by regulating the accessibility of DNA to the machinery involved in each of these processes. Both biochemical and genetic studies have advanced our understanding of how chromatin structure regulates transcription. For example, *in vitro* experiments revealed the barrier that nucleosomes pose to transcription initiation and elongation. *In vivo*, genetic methods identified roles for nucleosomes and histones in regulating transcription. Yeast studies employing both approaches have been instrumental in advancing our knowledge of chromatin, transcription, and their relationship (Rando and Winston, 2012).

Proper regulation of transcription elongation involves the recruitment of many regulatory factors. During elongation, RNAPII forms a complex with multiple regulatory factors such as the PAF complex, Dst1, Spt4/5, Spt6, Spn1, Elf1, and FACT (Schier and Taatjes, 2020). Several of these protein factors have roles in processing nascent RNA, activating RNAPII, modifying chromatin, and controlling chromatin structure (Buratowski, 2009; Joo et al., 2019). Advancements in structural biology along with mutagenesis and functional assays have increased the extent to which the RNAPII elongation complex has been characterized. However, many of the dynamics of elongation and the factors involved in regulating this process still remain unclear.

The class of factors that regulate transcription through control of

chromatin structure operate through a diverse set of pathways. For example, the chromatin remodeler Swi/Snf promotes transcription by altering histone-DNA interactions to remove nucleosome barriers to transcription. The chromatin modifying complex SAGA is involved in histone H3 acetylation and histone H2B ubiquitylation during elongation. Histone chaperones FACT and Spt6 interact directly with nucleosomes to alter chromatin structure. FACT is a complex composed of two proteins, Spt16 and Pob3, that functions in nucleosome reassembly and disassembly. Spt6 is a large protein with many domains and interactions that exhibits broad and varied effects on chromatin structure (Rando and Winston, 2012).

This paper reviews studies covering major findings on the roles of Spt6 and a related factor, Elf1, in regulating transcription with an emphasis on these factors' control of chromatin structure. In particular, the role of Spt6 in regulating transcriptional elongation through nucleosome dynamics is highlighted. While Spt6 is known to regulate nucleosome dynamics, many of the mechanisms of this regulation are not yet known. It is the goal of this review to organize the current mechanistic models of Spt6 regulation of nucleosome dynamics. The majority of the studies reviewed use yeast as a model system. While studies employing other model systems have been crucial to informing our current understanding of Spt6 and Elf1, many of the key discoveries discussed in this paper come from yeast studies. However, given the high degree of conservation among eukaryotes, studies of larger eukaryotes are included when appropriate.

## The Many Roles of Spt6

Spt6 is a multifunctional transcriptional regulator. Spt6-mediated chromatin effects have consequences for transcription. One possible way that Spt6 regulates transcription is by controlling chromatin structure, thereby affecting accessibility of DNA to elongating RNAPII complexes and subsequently increasing or decreasing levels of transcription. Both *in vitro* and *in vivo* experiments have shown Spt6 to affect nucleosome occupancy and nucleosome dynamics. Furthermore, Spt6 interactions with histones, nucleosomes, RNAPII, the elongation factor Spn1, and casein kinase II (CKII) likely mediate these changes in chromatin structure. However, many of the mechanisms operating behind Spt6-dependent changes in chromatin structure remain to be elucidated. Additionally, while not the focus of this review, Spt6 may also regulate transcription directly. It should be noted that Spt6 regulation of chromatin structure and transcription are not mutually exclusive. Spt6 is a key regulator of elongation with central roles in mediating both chromatin structure and transcription.

### Interaction with RNAPII

Spt6 may directly regulate transcription through interactions with RNAPII. While the role of this interaction and its significance for transcription is unclear, Spt6 is well-established as an elongation factor that travels with elongating RNAPII. Studies on the mammalian and *Drosophila* orthologues of Spt6 characterize it specifically as a positive regulator of transcription elongation (Andrulis et al., 2000; Ardehali et al., 2009; Endoh et al., 2004; Kaplan et al., 2000). Furthermore, these studies also identified direct interactions between Spt6 and RNAPII.

The interaction between Spt6 and RNAPII is mediated by multiple domains, modifications, and factors. C-terminal tandem

Src homology 2 (tSH2) domains in yeast Spt6 are crucial for this interaction (Close et al., 2011; Diebold et al., 2010; Yoh et al., 2007). Additionally, phosphorylation of key residues in the C-terminal domain (CTD) of RNAPII promotes recruitment of Spt6 to transcribed genes (Brázda et al., 2020; Burugula et al., 2014; Yoh et al., 2007). Furthermore, the Spt6-RNAPII interaction may be partially mediated by the histone deacetylases Rpd3 and Hos2 (Burugula et al., 2014). Recently the linker region of the Rpb1 subunit of RNAPII was found to bind the tSH2 domains of Spt6 while the C-terminal residues were dispensable for binding Spt6. Phosphorylation of residues S1493, T1471, and Y1473 in this linker region promotes Spt6 binding to Rpb1 (Sdano et al., 2017). However, these findings are not necessarily in contradiction to the previous studies establishing the interaction between Spt6 and the CTD of RNAPII. While the linker region may serve as the primary binding site, the tSH2 domains of Spt6 also bind the RNAPII C-terminal domain *in vitro*. This Spt6-CTD interaction may be important for stabilizing recruitment of Spt6 or retaining Spt6 at transcribed genes, which is consistent with the Rpb1 linker recruiting Spt6 (Brázda et al., 2020; Sdano et al., 2017). The different interactions between Spt6 and RNAPII may regulate different functions necessary for recruitment of Spt6 to RNAPII.

The Spt6-RNAPII interaction plays roles in regulating chromatin structure. While Spt6 may regulate elongation directly through interacting with RNAPII, this interaction also has important consequences for chromatin structure. Recruitment of Spt6 by Ser2 in the CTD of RNAPII has been proposed to regulate histone occupancy at the 5' end of coding regions, and facilitation of this recruitment by histone deacetylases is consistent with a model in which Spt6 reassembles histones displaced by RNAPII elongation (Burugula et al., 2014). Interaction between Spt6 and the Rpb1 linker also affects chromatin structure. Mutation of Rpb1 S1493 is associated with a phenotype indicative of an active promoter that is normally repressed by the local chromatin structure. This defect in chromatin structure suggests a role for the Spt6-Rpb1 interaction in maintaining repressive chromatin structures during transcription (Sdano et al., 2017). These findings are consistent with a role for Spt6 in reassembling nucleosomes after passage of an elongating RNAPII molecule. Whether this interaction regulates chromatin structure directly or indirectly is uncertain. However, there is evidence to suggest that the Spt6-RNAPII interaction facilitates recruitment of hIws1, the human analog of the factor Spn1, a conserved transcription factor implicated in recruitment of chromatin-remodeling factors (Yoh et al., 2007; Zhang et al., 2008). Thus, there are multiple mechanisms by which the Spt6-RNAPII interaction may control chromatin structure, either directly in the wake of elongation or through recruitment of an additional factor.

### Effects of Spt6 on Nucleosome Occupancy and Dynamics

Spt6 affects nucleosome occupancy. Loss of Spt6 in *S. cerevisiae* results in decreased nucleosome occupancy over coding regions, preferentially over highly transcribed genes (Doris et al., 2018; Ivanovska et al., 2011). Furthermore, experiments done using an spt6 mutant allele in the closely related fission yeast, *Schizosaccharomyces pombe*, also found disrupted nucleosome positioning and occupancy over highly transcribed regions, including a general loss of the +1 nucleosome. However, nucleosome loss was not found to correlate with changes in levels of mRNA transcripts of these genes, suggesting a non-regulatory function for Spt6 over transcribed regions

(DeGennaro et al., 2013). Conversely, analysis of the regulatory region of *CHAI*, a gene repressed by Spt6 activity, shows a shift in nucleosome positioning and de-repression of the gene under rich growth conditions, suggesting a role for Spt6 in remodeling the +1 nucleosomes at regulatory regions of coding sequences (Ivanovska et al., 2011). In addition, genome-wide mapping indicates a role for Spt6 in maintaining 5' and 3' nucleosome-depleted regions (NDRs) and maintaining nucleosomes in the regions flanking these NDRs (Perales et al., 2013). These effects on nucleosome occupancy indicate a transcription-dependent remodeling of nucleosomes by Spt6.

One possible explanation for decreased nucleosome occupancy over transcribed genes in *spt6* mutants is a role for Spt6 in mediating nucleosome reassembly and disassembly. Current evidence supports a model in which Spt6 functions in nucleosome reassembly in the wake of transcription. In this model, over regions of low or moderate transcription, nucleosomes should have sufficient time to reassemble before passage of the next RNAPII molecule, thereby maintaining nucleosome levels. However, at highly transcribed genes, nucleosomes do not have sufficient time to reassemble nucleosomes before disassembly upon passage of the next RNAPII molecule, resulting in reduced nucleosome occupancy at these genes. Reduced nucleosome occupancy seen in *spt6* mutants and slowed nucleosome reassembly rates are consistent with this model (Adkins and Tyler, 2006; Kaplan et al., 2003). Furthermore, Spt6-mediated nucleosome dynamics have consequences for transcriptional regulation. Spt6 plays roles in maintaining chromatin structure during elongation, thus repressing initiation of cryptic transcription from within coding regions (DeGennaro et al., 2013; Kaplan et al., 2003). One way Spt6 may repress cryptic transcription is by preventing accumulation of histone variant H2A.Z from gene bodies, as this accumulation can contribute to cryptic transcription (Jeronimo et al., 2015). Nucleosome reassembly at promoters was also found to require Spt6 and function in repression of transcription of the corresponding genes (Ivanovska et al., 2011; Perales et al., 2013). Thus Spt6 likely reassembles nucleosomes, either directly or indirectly, in the wake of transcription elongation.

### Spt6 Interaction with Histones

Spt6 may mediate nucleosome assembly through interaction with histones. Spt6 is classically characterized as an H3-H4 histone chaperone. An *spt6* mutation was found to confer the same alterations to chromatin structure as a deletion of one pair of the genes encoding histones H2A-H2B, suggesting the possibility of an interaction between Spt6 and histones. *In vitro*, Spt6 binds to H3-H4 and H2A-H2B, indicating that Spt6 can interact directly with each histone. Furthermore, overexpression of H3-H4 and H3 alone, but not overexpression of H4 alone, suppresses *spt6* phenotypes. These results are consistent with the strong direct interaction between Spt6 and H3 detected *in vitro*; the weaker *in vitro* interaction between Spt6 and H4 is suggestive of a weak *in vivo* interaction (Bortvin and Winston, 1996). Mutations in histones H2A and H2B are also able to suppress phenotypes conferred by an *spt6-F249K* mutation (McCullough et al., 2015). Thus, Spt6 interacts with H3-H4 and H2A-H2B *in vivo*. Given the necessity of histones for nucleosome formation, Spt6 interaction with histones is likely to function in assembling nucleosomes.

The histone-Spt6 interaction may function in nucleosome assembly. Spt6 is able to assemble nucleosomes *in vitro* in the presence of histones, suggesting a role for the histone-Spt6

interaction for nucleosome assembly *in vivo* (Bortvin and Winston, 1996). Mutations of residues in the globular domain of histone H3 that interact with Spt6 are associated with reduction of nucleosome occupancy at highly transcribed regions (Hainer and Martens, 2011, 2016), and slowed nucleosome dynamics (Hainer and Martens, 2016). Additionally, H3 mutants fail to suppress mutant *spt6* phenotypes, and co-immunoprecipitation experiments indicate a reduced interaction between Spt6 and H3 in H3 mutants (Bortvin and Winston, 1996; Hainer and Martens, 2016). Thus, this reduced interaction is associated with defects in nucleosome occupancy, reassembly, and disassembly, which supports a role for the Spt6-H3 interaction in regulating these processes in wild-type cells. One mechanism that has been proposed is Spt6 interacting with H3 to alter histone-DNA interactions, thus regulating chromatin structure. However, alternatively, the reduced Spt6-H3 interaction may be the result of changes in nucleosome dynamics in the H3 mutants (Hainer and Martens, 2016). Future experiments will be necessary to distinguish the reduced Spt6-H3 interaction as the cause or effect of altered nucleosome dynamics in H3 mutants. Furthermore, while H2A-H2B interacts with Spt6, the effects of this interaction on nucleosome dynamics have not been elucidated (McCullough et al., 2015). Thus, whether Spt6 mediates nucleosome assembly through an interaction with H2A-H2B is unknown.

Altogether, these findings suggest a role for the interaction between histones and Spt6 in nucleosome assembly. The interaction between Spt6 and H3 is associated with defects in nucleosome occupancy and dynamics. However, the mechanistic role of this interaction in promoting nucleosome assembly is unclear. Furthermore, an interaction between Spt6 and H2A-H2B may present another pathway through which Spt6 mediates nucleosome assembly, although this interaction has not been extensively studied in the context of chromatin structure. Ultimately, the defects in nucleosome occupancy and assembly seen in *spt6* and histone mutants is consistent with a role for histone-Spt6 interactions in maintaining normal chromatin structure. Future experiments aimed at determining the mechanistic basis for this assembly of nucleosomes will be necessary to fully understand how histones affect the ability of Spt6 to assemble nucleosomes.

### Spt6 Interaction with Spn1

The Spt6-Spn1 interaction is implicated in regulating chromatin structure. Structural analysis suggests that nucleosomes and Spn1 compete for binding to Spt6 *in vitro*. Therefore, the Spt6-Spn1 interaction may act to regulate the interaction of Spt6 with nucleosomes, suggesting important consequences for maintaining chromatin structure (McDonald et al., 2010). Interestingly, H2A and H2B mutations at the dimer interface that destabilize the nucleosome are able to suppress phenotypes seen in an *spt6* mutant that has reduced binding to Spn1. These results support a model in which the destabilized nucleosome activates another system of chromatin maintenance that bypasses the need for the Spt6-Spn1 interaction (McCullough et al., 2015). Furthermore, Spn1 regulates recruitment of Spt6 during transcription. Analysis of Spt6-Spn1 dynamics at the inducible *CYC1* gene show defects in Spt6 recruitment when Spn1 occupancy is decreased. Spt6 is only recruited upon induction of high transcription levels, and Spt6 is recruited before the chromatin-remodeling complex Swi/Snf. In the absence of Spn1, Swi/Snf is constitutively recruited. Thus, Spn1 may inhibit recruitment of Swi/Snf, an inhibition that is

itself abolished by binding of Spt6 to Spn1 (Zhang et al., 2008). Altogether, the interaction between Spt6 and Spn1 likely has roles in regulating chromatin structure, either directly, through activation of alternative pathways, or through regulating recruitment of other factors implicated in controlling chromatin structure.

### Spt6 Interaction with CKII

Spt6 interacts with casein kinase II (CKII), an essential protein kinase involved in many cellular processes. CKII has roles in modulating chromatin structure through regulation of histone H3 and key transcription factors, such as Spt2, the PAF complex, and the FACT complex in addition to Spt6. For example, phosphorylation of Spt2 by CKII disrupts the interaction between Spt2 and Spt6, thereby promoting the association of Spt2 with coding regions and repressing spurious transcription (Gouot et al., 2018). CKII interacts with and phosphorylates the N terminus of Spt6 both *in vivo* and *in vitro*. This interaction has consequences for chromatin structure and transcription (Dronamraju et al., 2018; Gouot et al., 2018)

The Spt6-CKII interaction has roles for regulating chromatin structure and transcription. Strains expressing *spt6* mutations defective for phosphorylation by CKII show defects in maintaining nucleosome occupancy (Dronamraju et al., 2018). Furthermore, analyses using the reporter system *pGALI-FLO8-HIS3* (Gouot et al., 2018) and the well-characterized *SRGI-SER3* system (Dronamraju et al., 2018) show defects in chromatin structure in cells expressing *spt6* mutations. These cells also show defects in Spt6 protein stability and cellular Spt6 protein levels, indicating the importance of CKII-mediated phosphorylation of Spt6 for proper Spt6 function (Dronamraju et al., 2018; Gouot et al., 2018). However, the exact nature of this phosphorylation's role in maintaining proper Spt6 function and proper chromatin structure is not clear. Consistent with effects on chromatin structure, phosphorylation of Spt6 by CKII also has consequences for transcription. RNA-seq experiments using the same *spt6* mutants showed increased levels of antisense and cryptic transcripts compared to wild-type strains, suggesting a role for this phosphorylation in repressing antisense and cryptic transcription (Dronamraju et al., 2018; Gouot et al., 2018).

CKII-dependent phosphorylation of Spt6 may have a role in regulating Spt6's interactions with other proteins. Depletion of CKII was associated with a decrease in phosphorylation of the RNAPII CTD residue Serine 2 (Gouot et al., 2018), a residue known to interact with the tSH2 domains of Spt6 (Burugula et al., 2014; Yoh et al., 2007). However, the consequences of this CKII depletion on the interaction between Spt6 and RNAPII were not elucidated in this study. Future experiments will be necessary to determine the nature of these effects, if any. Furthermore, phosphorylation of Spt6 by CKII presents a mechanism by which the Spt6-Spn1 interaction may be regulated. In an *spt6* mutant without CKII phosphorylation sites, Spn1 association with Spt6 was significantly decreased compared to wild-type, suggesting a role for CKII-mediated phosphorylation of Spt6 in maintaining the Spn1-Spt6 interaction (Dronamraju et al., 2018). Thus, CKII phosphorylation of Spt6 may be able to promote normal chromatin structure by promoting normal interaction of Spt6 with other proteins including Spn1.

### Overall multifunctionality of Spt6

The histone chaperone Spt6, a highly conserved transcription factor, is a multifunctional protein able to regulate transcription through many pathways. One model for how Spt6 regulates

transcription is by controlling chromatin structure. Multiple studies have established that changes in chromatin structure such as nucleosome occupancy and nucleosome assembly occur when Spt6 is mutated. Alternatively, Spt6 may regulate transcription directly by interacting with RNAPII. Furthermore, Spt6's interactions with histones, nucleosomes, Spn1, and CKII are crucial to its ability to regulate chromatin structure and transcription.

### Connections between Spt6 and the Mysterious Protein Elf1

In addition to its interactions with RNAPII, Spn1, and CKII, Spt6 likely also interacts with unidentified or less well-characterized factors. One factor that genetically interacts with Spt6 is Elf1 (*elongation factor 1*). While Elf1 has been characterized as a transcription elongation factor and shown to make several genetic interactions, its role in transcription and the role of these genetic interactions is largely unknown. Identification of an interaction between these two proteins could indicate another pathway Spt6 is involved in and serve to better characterize Elf1 as a transcription factor.

### Characterization of Elf1

While its exact roles are unclear, Elf1 has been established as an elongation factor. Elf1 was initially identified through a genetic screen for mutations in genes that cause lethality in combination with mutations in the genes encoding the known elongation factors TFIIIS (*dst1Δ*) and Spt6 (*spt6-14*). Sensitivity to mycophenolic acid (MPA) and 6-azauracil (6AU), chemicals known to inhibit transcription elongation, in *elf1* mutation strains suggested Elf1 as an elongation factor. Furthermore, *elf1Δ* genetically interacts with mutations in genes encoding elongation factors. When combined with a deletion mutation in the gene encoding the elongation factor TFIIIS (*dst1Δ*), *elf1Δdst1Δ* cells show increased sensitivity to 6AU and MPA compared to either single mutation as well as inability to grow on galactose, indicating a genetic interaction between *elf1Δ* and *dst1Δ*. In addition to *dst1Δ*, tetrad and synthetic genetic array analyses showed *elf1Δ* to genetically interact with *spt4Δ*, several *spt5* and *spt6* missense mutations, and deletion mutations in genes encoding subunits of the Paf1 complex. These interactions with mutations in genes encoding elongation factors suggest a role for Elf1 in transcription elongation (Prather et al., 2005).

### Relationship between Spt6 and Elf1

Elf1 preferentially localizes to actively transcribed regions in a manner partially dependent on Spt4 and Spt6. ChIP experiments show high levels of Elf1 localization at the coding regions of transcribed genes and reduced localization over the promoter and activator sequences of these genes. However, the recruitment of Elf1 to transcribed regions was reduced in certain *spt4* and *spt6* mutant strains, suggesting a role for Spt4 and Spt6 in recruiting Elf1 to coding regions (Prather et al., 2005).

The role of Elf1 in transcription elongation may be related to that of Spt6. Genetic interactions between *elf1Δ* and *spt6* mutations and reduced recruitment of Elf1 to transcribed regions in an *spt6* mutant suggest a role for Elf1 related to Spt6 function. Given the role for Spt6 in controlling chromatin structure over transcribed regions, it is possible that Elf1 also affects chromatin structure. In an assay for initiation of cryptic transcription, *elf1Δ* cells initiated

cryptic transcription to a greater extent than wild-type cells under high transcription conditions. Increased levels of cryptic initiation indicate a defect in maintaining the nucleosomal barrier to transcription in *elf1Δ* cells and suggest a role for Elf1 in maintaining proper chromatin structure during transcription (Prather et al., 2005). These results parallel Spt6's function in maintaining chromatin structure during elongation. However, whether or not Elf1's role is dependent on Spt6 function is unknown.

### Interaction of Elf1 with Other Proteins

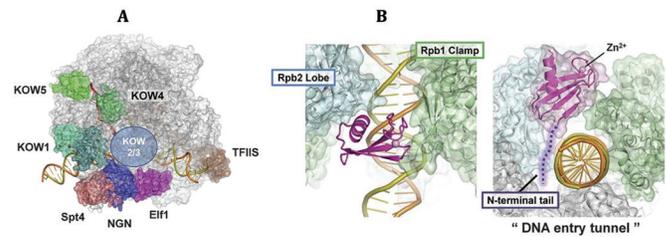
Understanding the interaction of Elf1 with other cellular proteins is crucial to understanding the functions of Elf1 and whether there are consequences for the Spt6-Elf1 relationship. One such interaction is between Elf1 and CKII. Copurification experiments show that Elf1 associates with both the catalytic and regulatory subunits of CKII. This physical association suggests that CKII-mediated phosphorylation of Elf1 is important for Elf1 function (Prather et al., 2005). Consistent with this idea, Elf1 is phosphorylated by monomeric and tetrameric forms of CKII *in vitro*. Furthermore, Elf1 contains several putative CKII sites with the most likely *in vitro* phosphorylation sites identified by mass spectrometry as Ser95 and Ser117 (Kubinski et al., 2006; Prather et al., 2005). However, the significance and role of this interaction *in vivo* remains unclear.

Elf1 also copurifies with RNAPII and Spn1. While proteomics approaches (Gavin et al., 2002; Krogan et al., 2002) and early copurification experiments with Elf1 did not identify interactions between Elf1 and other proteins, a genome-wide profiling of RNAPII transcription factors showed similar profiles for Elf1 and Spn1 (Mayer et al., 2010). Spn1 copurifies with RNAPII and Elf1 but does not interact directly with Elf1. This result is consistent with an indirect interaction between Elf1 and Spn1 within the RNAPII complex (Mayer et al., 2010). Furthermore, Elf1 does not copurify with other elongation factors. One explanation for this lack of direct interactions may be a requirement for Elf1 association with chromatin in order to physically associate with these proteins, which standard purification methods cannot identify (Prather et al., 2005).

### Elf1 Structure in the RNAPII Elongation Complex

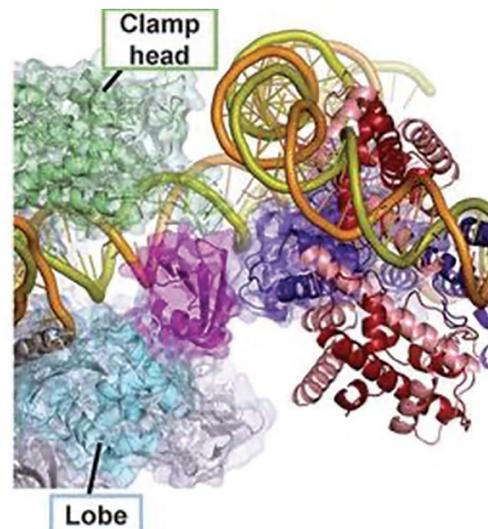
Structural studies have also provided a way to investigate the role of Elf1 and its spatial connections to Spt6. Within the elongation complex, Elf1 bridges the RNAPII central cleft. Recent structural studies have employed cryo-EM and X-ray crystallography approaches to solve the structure of the RNAPII elongation complex bound to Elf1 and the elongation factor Spt4/5 from the yeast *Komagataella pastoris* (Ehara and Sekine, 2018; Ehara et al., 2017, 2019). In addition to locating Elf1 between the lobe and clamp domains of the RNAPII elongation complex, these studies also showed Elf1 to be oriented with its C-terminal  $\alpha$  helix interacting with the Rpb2 lobe and the opposite side contacting the Rpb1 clamp (Ehara et al., 2017, 2019). In this position, Elf1 fills the gap over the RNAPII central cleft, thus closing the "DNA entry tunnel" for passage of downstream DNA during elongation (Figure 1). Furthermore, the disordered N-terminal tail of Elf1 may interact with downstream DNA. This interaction is consistent with a role for Elf1 in preventing DNA dissociation from the EC, thus stabilizing the RNAPII elongation complex (Ehara et al., 2017). In this case, the interaction between Elf1 and RNAPII may not be detected in

the absence of chromatin and thus cannot be identified by standard purification approaches. However, *in vitro* experiments suggest that Elf1 slows the rate of elongation, an effect that is diminished when its RNAPII-interacting residues or DNA-interacting N-terminal tail are mutated, supporting a role for Elf1 in preventing DNA dissociation (Ehara and Sekine, 2018; Ehara et al., 2017).



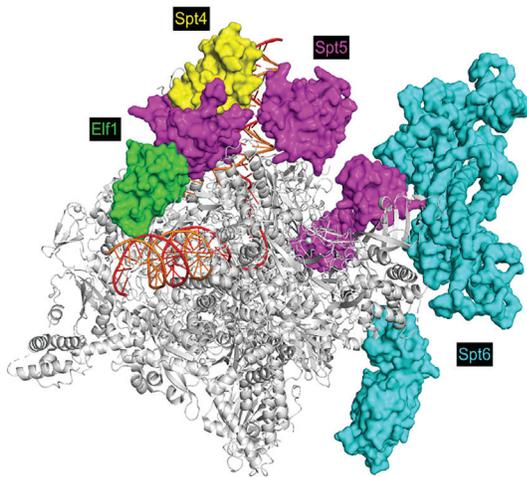
**Figure 1: The structural position of Elf1.** A) Structure of the RNAPII elongation complex bound to Elf1 and Spt4/5. B) Elf1 bridges the RNAPII central cleft between the Rpb2 lobe and Rpb1 clamp. See Ehara et al., 2017, Figures 1E, 3B.

Elf1 has been proposed to prevent DNA dissociation by altering histone-DNA interactions. Recently, cryo-EM structures of transcribing RNAPII elongation complexes show that Elf1 cooperates with Spt4/5 to separate downstream DNA from the nucleosome, thus preventing DNA reassociation to histones and DNA dissociation from the elongation complex (Ehara et al., 2019). Additionally, the N-terminal tail of Elf1 may compete with histones H3-H4 for interactions with DNA, thus promoting dissociation of DNA from histones. Thus, Elf1 may cooperate with Spt4/5 to lower the nucleosomal barrier to transcription elongation (Ehara and Sekine, 2018). Moreover, in the absence of Elf1 and Spt4/5, the nucleosome is trapped in the central cleft between the Rpb2 lobe and Rpb1 clamp that Elf1 normally occupies during elongation (Figure 2). By occupying this position, Elf1 reduces the RNAPII-nucleosome interaction and prevents the elongation complex from becoming trapped (Ehara et al., 2019).



**Figure 2: The EC-nucleosome interface at SHL(-1).** Elf1 occupies the gap between the Rpb2 lobe and Rpb1 clamp head. In the absence of Elf1 (magenta), the nucleosome becomes trapped in the central cleft between the Rpb2 lobe and Rpb1 clamp head.

The structural relationship(s) between Elf1 and other elongation factors remains an area of potential investigation. Copurification experiments suggest that Elf1 and Spn1 interact indirectly within an RNAPII complex (Mayer et al., 2010). Given the interaction between Spn1 and Spt6, Elf1 may also affect Spt6 through the elongation complex. Alternatively, Elf1 may indirectly interact with Spt6 via Spn1. However, based on previous copurification experiments and the putative structural position of Spt6 relative to Elf1, a direct interaction is unlikely (Figure 3; Prather et al., 2005). Interestingly, both Elf1 and Spt6 contact domains of the highly conserved core transcription factor Spt5 in the RNAPII elongation complex. Thus, Spt5 may also mediate an indirect interaction between Elf1 and Spt6.



**Figure 3.** RNAPII elongation complex with elongation factors. Elf1 (green) and Spt6 (cyan) are unlikely to interact directly within the elongation complex. However, both Elf1 and Spt6 make contact with domains in Spt5 (magenta). *K. pastoris* RNAPII elongation complex bound to Spt4/5 was overlaid with mammalian Spt6 and *K. pastoris* Elf1 in PyMOL. Adapted from PDB 5XON, 5XOG, and 6GMH (Ehara et al., 2017; Vos et al., 2018)

### Conservation of Elf1 and implications

Orthologues of Elf1 are highly conserved and multifunctional. Multiple orthologues of Elf1 have been identified by sequence similarity (Daniels et al., 2009; Prather et al., 2005). The initial characterization of Elf1 in yeast has implications for understanding the potential roles of its orthologues. In Archaea, only some of the genomes containing an Elf1 orthologue also coded for histones, suggesting a histone-independent function for this orthologue of Elf1. Additionally, both Archaea and eukaryotes are able to regulate transcription at the chromatin level; the conservation of Elf1 suggests that this mechanism of regulating transcription is related rather than independently-evolved (Daniels et al., 2009). Mammalian Elf1, Elof1, is also implicated in embryonic development and post-transcriptional regulation of gene expression. *Elof1* mutants exhibit clear morphological defects and fail to initiate gastrulation. This observation, in combination with results from an alternative splicing system, suggests that Elof1 functions in regulating alternative splicing (Tellier et al., 2019). While these morphological defects cannot be observed in single-celled yeast, Elf1 may be implicated in regulating alternative splicing. Although not a transcriptional role, future experiments investigating this topic may determine if such a function is dependent on Spt6 and thus advance our understanding of both proteins beyond their involvement in eukaryotic transcription.

## Conclusion

Yeast studies have been crucial for advancing our understanding of transcription and key transcription factors. The relationship between chromatin structure and transcription has become increasingly apparent and significant. Proper regulation of transcription requires recruitment of many regulatory factors, many of which have roles in controlling chromatin structure. The elongation factor Spt6 falls into this class of proteins. Spt6-mediated chromatin effects have extensive and diverse consequences for transcription. Genetic studies have shown that defects in Spt6 are associated with changes in nucleosome occupancy and nucleosome dynamics. Furthermore, the control Spt6 exerts over chromatin structure and transcription may be influenced by its interactions with other proteins such as histones, RNAPII, Spn1, and CKII. Genetic interactions between Spt6 and the comparatively less-investigated elongation factor Elf1 have been important for elucidating the role of Elf1 in regulating transcription. Recent structural insights suggest that Elf1 prevents DNA dissociation from the RNAPII elongation complex. However, this insight remains to be confirmed *in vivo*.

### Future directions

The implication of Elf1 in transcription elongation, coupled with the relatively small amount of information known about it, makes Elf1 an especially exciting and interesting target for future investigations. Particularly, the connection to Spt6 may be key to understanding the role of Elf1 in regulating chromatin structure and elongation. One approach that future studies may take to investigate this topic is identifying *elf1* mutations that suppress defects in chromatin structure caused by an *spt6* allele, analogous to the approach taken by McCullough et al. (2015). Structural insight on a yeast RNAPII elongation complex bound to Elf1 and Spt6 may also further elucidate the relationship between the two factors as well as the role of Elf1 in transcription. Finally, computational approaches aimed at uncovering the pathways Elf1 is implicated in have the potential to reveal any connections between Spt6 and Elf1.

## References

- Adkins, M.W., and Tyler, J.K. (2006). Transcriptional activators are dispensable for transcription in the absence of Spt6-mediated chromatin reassembly of promoter regions. *Mol. Cell* 21, 405–416.
- Andrulis, E.D., Guzmán, E., Döring, P., Werner, J., and Lis, J.T. (2000). High-resolution localization of *Drosophila* Spt5 and Spt6 at heat shock genes *in vivo*: Roles in promoter proximal pausing and transcription elongation. *Genes Dev.* 14, 2635–2649.
- Ardehali, M.B., Yao, J., Adelman, K., Fuda, N.J., Petesch, S.J., Webb, W.W., and Lis, J.T. (2009). Spt6 enhances the elongation rate of RNA polymerase II *in vivo*. *EMBO J.* 28, 1067–1077.
- Bortvin, A., and Winston, F. (1996). Evidence that Spt6p controls chromatin structure by a direct interaction with histones. *Science* (80-. ). 272, 1473–1476.
- Brázda, P., Krejčíková, M., Kasiliauskaite, A., Šmiřáková, E., Klumpler, T., Vácha, R., Kubiček, K., and Štefl, R. (2020). Yeast Spt6 Reads Multiple Phosphorylation Patterns of RNA Polymerase II C-Terminal Domain *In Vitro*. *J. Mol. Biol.* 4092–4107.
- Buratoski, S. (2009). Progression through the RNA Polymerase II CTD Cycle. *Mol. Cell* 36, 541–546.

- Burugula, B.B., Jeronimo, C., Pathak, R., Jones, J.W., Robert, F., and Govind, C.K. (2014). Histone Deacetylases and Phosphorylated Polymerase II C-Terminal Domain Recruit Spt6 for Cotranscriptional Histone Reassembly. *Mol. Cell. Biol.* 34, 4115–4129.
- Close, D., Johnson, S.J., Sdano, M.A., McDonald, S.M., Robinson, H., Formosa, T., and Hill, C.P. (2011). Crystal structures of the *S. cerevisiae* Spt6 core and C-terminal tandem SH2 domain. *J. Mol. Biol.* 408, 697–713.
- Daniels, J.P., Kelly, S., Wickstead, B., and Gull, K. (2009). Identification of a crenarchaeal orthologue of Elf1: Implications for chromatin and transcription in Archaea. *Biol. Direct* 4, 1–5.
- DeGennaro, C.M., Alver, B.H., Marguerat, S., Stepanova, E., Davis, C.P., Bahler, J., Park, P.J., and Winston, F. (2013). Spt6 Regulates Intragenic and Antisense Transcription, Nucleosome Positioning, and Histone Modifications Genome-Wide in Fission Yeast. *Mol. Cell. Biol.* 33, 4779–4792.
- Diebold, M.L., Koch, M., Loeliger, E., Cura, V., Winston, F., Cavarelli, J., and Romier, C. (2010). The structure of an Iws1/Spt6 complex reveals an interaction domain conserved in TFIIS, Elongin A and Med26. *EMBO J.* 29, 3979–3991.
- Doris, S.M., Chuang, J., Viktorovskaya, O., Murawska, M., Spatt, D., Churchman, L.S., and Winston, F. (2018). Spt6 Is Required for the Fidelity of Promoter Selection. *Mol. Cell* 72, 687–699.e6.
- Dronamraju, R., Kerschner, J.L., Peck, S.A., Hepperla, A.J., Adams, A.T., Hughes, K.D., Aslam, S., Yoblinski, A.R., Davis, I.J., Mosley, A.L., et al. (2018). Casein Kinase II Phosphorylation of Spt6 Enforces Transcriptional Fidelity by Maintaining Spn1-Spt6 Interaction. *Cell Rep.* 25, 3476–3489.e5.
- Duina, A.A., Miller, M.E., and Keeney, J.B. (2014). Budding yeast for budding geneticists: A primer on the *Saccharomyces cerevisiae* model system. *Genetics* 197, 33–48.
- Ehara, H., and Sekine, S. (2018). Architecture of the RNA polymerase II elongation complex: new insights into Spt4/5 and Elf1. *Transcription* 9, 286–291.
- Ehara, H., Yokoyama, T., Shigematsu, H., Yokoyama, S., Shirouzu, M., and Sekine, S.I. (2017). Structure of the complete elongation complex of RNA polymerase II with basal factors. *Science* (80- ). 357, 921–924.
- Ehara, H., Kujirai, T., Fujino, Y., Shirouzu, M., Kurumizaka, H., and Sekine, S. (2019). Structural insight into nucleosome transcription by RNA polymerase II with elongation factors. *Science* (80- ). 363, 744–747.
- Endoh, M., Zhu, W., Hasegawa, J., Watanabe, H., Kim, D.-K., Aida, M., Inukai, N., Narita, T., Yamada, T., Furuya, A., et al. (2004). Human Spt6 Stimulates Transcription Elongation by RNA Polymerase II In Vitro. *Mol. Cell. Biol.* 24, 3324–3336.
- Gavin, A.C., Bösch, M., Krause, R., Grandi, P., Marzioch, M., Bauer, A., Schultz, J., Rick, J.M., Michon, A.M., Cruciat, C.M., et al. (2002). Functional organization of the yeast proteome by systematic analysis of protein complexes. *Nature* 415, 141–147.
- Gouot, E., Bhat, W., Rufiange, A., Fournier, E., Paquet, E., and Nourani, A. (2018). Casein kinase 2 mediated phosphorylation of Spt6 modulates histone dynamics and regulates spurious transcription. *Nucleic Acids Res.* 46, 7612–7630.
- Hainer, S.J., and Martens, J.A. (2011). Identification of Histone Mutants That Are Defective for Transcription-Coupled Nucleosome Occupancy. *Mol. Cell. Biol.* 31, 3557–3568.
- Hainer, S.J., and Martens, J.A. (2016). Regulation of chaperone binding and nucleosome dynamics by key residues within the globular domain of histone H3. *Epigenetics and Chromatin* 9, 1–14.
- Ivanovska, I., Jacques, P.-E., Rando, O.J., Robert, F., and Winston, F. (2011). Control of Chromatin Structure by Spt6: Different Consequences in Coding and Regulatory Regions. *Mol. Cell. Biol.* 31, 531–541.
- Jeronimo, C., Watanabe, S., Kaplan, C.D., Peterson, C.L., and Robert, F. (2015). The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. *Mol. Cell* 58, 1113–1123.
- Jonkers, I., and Lis, J.T. (2015). Getting up to speed with transcription elongation by RNA polymerase II. *Nat. Rev. Mol. Cell Biol.* 16, 167–177.
- Joo, Y.J., Ficarro, S.B., Chun, Y., Marto, J.A., and Buratowski, S. (2019). In vitro analysis of rna polymerase II elongation complex dynamics. *Genes Dev.* 33, 578–589.
- Kaplan, C.D., Morris, J.R., Wu, C.T., and Winston, F. (2000). Spt5 and Spt6 are associated with active transcription and have characteristics of general elongation factors in *D. melanogaster*. *Genes Dev.* 14, 2623–2634.
- Kaplan, C.D., Laprade, L., and Winston, F. (2003). Transcription elongation factors repress transcription initiation from cryptic sites. *Science* (80- ). 301, 1096–1099.
- Krogan, N.J., Kim, M., Ahn, S.H., Zhong, G., Kobor, M.S., Cagney, G., Emili, A., Shilatifard, A., Buratowski, S., and Greenblatt, J.F. (2002). RNA Polymerase II Elongation Factors of *Saccharomyces cerevisiae*: a Targeted Proteomics Approach. *Mol. Cell. Biol.* 22, 6979–6992.
- Kubinski, K., Zielinski, R., Hellman, U., Mazur, E., and Szyszka, R. (2006). Yeast elf1 factor is phosphorylated and interacts with protein kinase CK2. *J. Biochem. Mol. Biol.* 39, 311–318.
- Luger, K., Mäder, A.W., Richmond, R.K., Sargent, D.F., and Richmond, T.J. (1997). Crystal structure of the nucleosome core particle at 2.8 Å resolution. *Nature* 389, 251–260.
- Mayer, A., Lidschreiber, M., Siebert, M., Leike, K., Söding, J., and Cramer, P. (2010). Uniform transitions of the general RNA polymerase II transcription complex. *Nat. Struct. Mol. Biol.* 17, 1272–1278.
- McCullough, L., Connell, Z., Petersen, C., and Formosa, T. (2015). The abundant histone chaperones Spt6 and FACT collaborate to assemble, inspect, and maintain chromatin structure in *saccharomyces cerevisiae*. *Genetics* 201, 1030–1045.
- McDonald, S.M., Close, D., Xin, H., Formosa, T., and Hill, C.P. (2010). Structure and Biological Importance of the Spn1-Spt6 Interaction, and Its Regulatory Role in Nucleosome Binding. *Mol. Cell* 40, 725–735.
- Perales, R., Erickson, B., Zhang, L., Kim, H., Valiquett, E., and Bentley, D. (2013). Gene promoters dictate histone occupancy within genes. *EMBO J.* 32, 2645–2656.
- Prather, D., Krogan, N.J., Emili, A., Greenblatt, J.F., and Winston, F. (2005). Identification and Characterization of Elf1, a Conserved Transcription Elongation Factor in *Saccharomyces cerevisiae*. *Mol. Cell. Biol.* 25, 10122–10135.
- Rando, O.J., and Winston, F. (2012). Chromatin and transcription in yeast. *Genetics* 190, 351–387.
- Schier, A.C., and Taatjes, D.J. (2020). Structure and mechanism of the RNA polymerase II transcription machinery. *Genes Dev.* 34, 465–488.
- Sdano, M.A., Fulcher, J.M., Palani, S., Chandrasekharan, M.B., Parnell, T.J., Whitby, F.G., Formosa, T., and Hill, C.P. (2017). A novel SH2 recognition mechanism recruits Spt6 to the doubly phosphorylated RNA polymerase II linker at sites of transcription. *Elife* 6, 1–24.
- Tellier, A.P., Archambault, D., Tremblay, K.D., and Mager, J. (2019). The elongation factor Elof1 is required for mammalian gastrulation. *PLoS One* 14, 1–11.
- Venkatesh, S., and Workman, J.L. (2015). Histone exchange, chromatin structure and the regulation of transcription. *Nat. Rev. Mol. Cell Biol.* 16, 178–189.
- Vos, S.M., Farnung, L., Boehning, M., Wigge, C., Linden, A., Urlaub, H., and Cramer, P. (2018). Structure of activated transcription complex Pol II–DSIF–PAF–SPT6. *Nature* 560, 607–612.
- Yoh, S.M., Cho, H., Pickle, L., Evans, R.M., and Jones, K.A. (2007). The Spt6 SH2 domain binds Ser2-P RNAPII to direct Iws1-dependent mRNA splicing and export. *Genes Dev.* 21, 160–174.

Zhang, L., Fletcher, A.G.L., Cheung, V., Winston, F., and Stargell, L.A. (2008). Spn1 Regulates the Recruitment of Spt6 and the Swi/Snf Complex during Transcriptional Activation by RNA Polymerase II. *Mol. Cell. Biol.* 28, 1393–1403.

# Features



## Serena Zhao '24

The ocean has played vital roles in maintaining a healthy, functional planet since the beginnings of Earth's existence. Universally recognized as one of the most important - and most endangered - parts of Earth's hydrosphere, the ocean covers more than 70% of Earth's surface and is home to an incredibly diverse array of marine organisms, some of which are found nowhere else on the planet. Plankton and other photosynthetic organisms in the ocean produce over half of the world's oxygen, and the ocean itself plays an important role in climate regulation and carbon dioxide storage. Humans have long exploited the ocean's vast resources and reaped the benefits: in the United States, approximately \$282 billion in goods and services are produced from the ocean and 76% of all U.S. trade involves some form of marine transportation. In our daily lives, biodiversity in the ocean has been used for everything from food to recreational whale-watching to medicine for cancer and Alzheimer's disease (NOAA, 2017).

In recent decades, oceanic health is threatened by a new intruder: plastic. Plastic is silently invading every corner of the ocean and choking our wildlife, and while we are fully responsible for introducing this new "invasive

species", we have yet to find reliable ways to remove plastic from our oceans - or to even accurately detect these microscopic plastic particles. Scientists are racing against the clock to develop new technology to quantify and remove oceanic plastic, while governments and organizations worldwide are uniting to combat oceanic plastic pollution. All of these efforts, however, have not been simple: challenges have arisen in every direction.

### Plastics and the Ocean

Today, plastic bottles and bottle caps, bags, and straws are a ubiquitous sight on beaches. Though plastic pollution in the ocean was first reported by scientists in the 1970s, global plastic production has increased exponentially since 1950, reaching an astounding 311 million metric tons in 2014 - an over 500% increase from less than 50 million metric tons in the 1970's (Law, 2016). It is projected that, by 2050, approximately 850 million metric tons of plastic will be produced annually. Moreover, over a third of plastics produced are used as disposable plastic packaging, which is discarded within one year of production (Lebreton 2012).

This rapid growth in plastic production and intense consumption of plastics owes itself to the convenience and versatility of plastics in daily life, but simultaneously

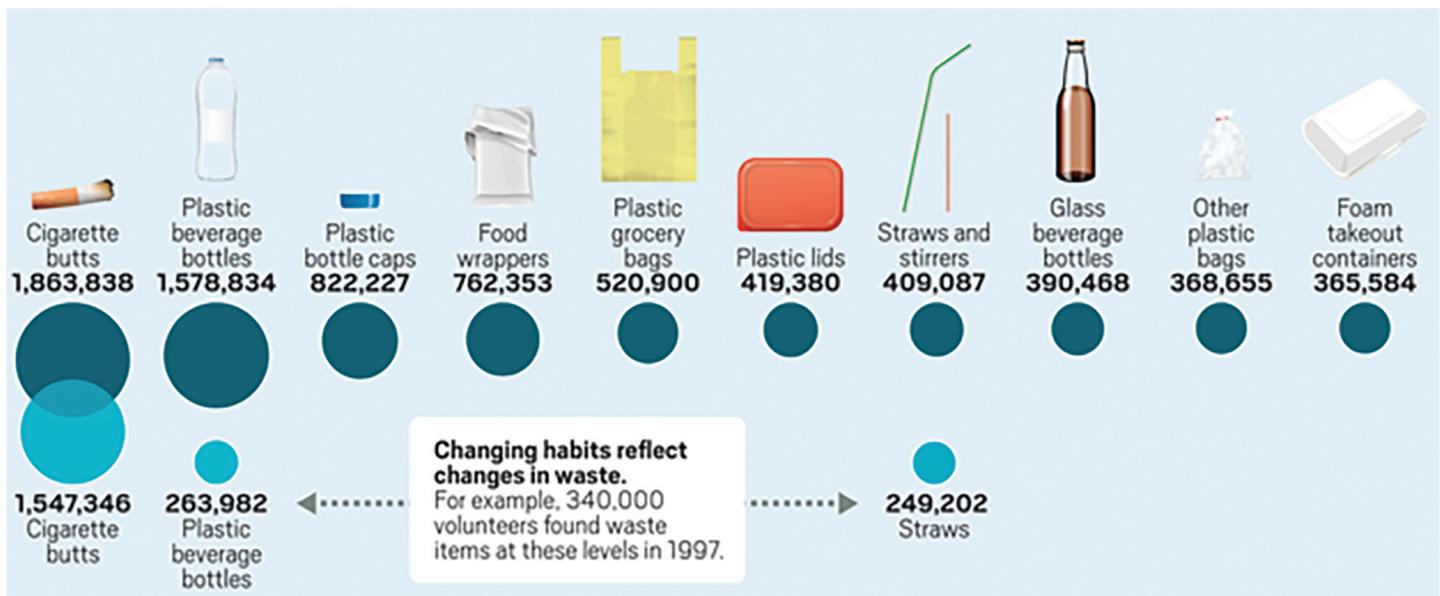


Figure 1. The most common items collected by 500,000-plus volunteers worldwide in the 2017 International Coastal Cleanup. (Source: Graphic from Chemical and Engineering News (Tullo 2018); Data from International Coastal Cleanup.)

presents a significant environmental challenge. While anthropogenic consumption of plastics has become more prevalent, plastic-recycling infrastructure and technology have not: in Europe, only 30% of postconsumer plastics were recycled in 2014, and in the United States, this number drops to 8.8% (Lebreton, 2012). This difference between European and American countries’ recycling rates is due to cultural, political and scientific factors, including stricter environmental laws in European countries, better recycling technology and different recycling methods. In addition, Americans tend to consume more plastic than other countries, while placing less emphasis on environmental recycling practices and eco-consciousness. National differences aside, a general insufficiency in recycling efforts around the world leads to an abundance of plastic accumulation in the oceans. Currently, an estimated 60-80% of all marine debris is plastic, and plastic outnumbers plankton by a ratio of over 6:1 (Law, 2016).

Current environmental efforts are focused on the detection, removal, and replacement of plastics, all of which face challenges. When macroplastics - the scientific term for relatively large particles of plastic, typically able to be seen by the naked eye - enter the ocean, they are subject to solar radiation and wave action, resulting in their breakdown into smaller pieces. However, because plastics are designed to be durable, macroplastics will simply continue to break down over time into tiny microplastics and nanoplastics instead of naturally degrading and disappearing. The microplastics and

nanoplastics generated are not only difficult to detect, but as they simultaneously persist and fragment, they become more widespread and difficult to remove with passing time (Cozar, 2014). Marine plastics pose serious threats to environmental, human, and organismal health as a result of interactions such as entanglement, ingestion, obstruction, chemical leaching, and toxic bioaccumulation (Law, 2016).

### The Circular Problem of “Seeing” Plastics

For the past several decades, scientists have been searching for a way to accurately, efficiently, and cheaply detect the presence and concentrations of plastic in both freshwater and marine bodies. Because plastics are synthetic polymers, typical advanced detection techniques used for DNA extraction or antibody isolation do not work, as chemicals cannot be detected as easily as life-related structures. As the sizes of microplastics decrease, naked-eye observations become impractical and simple filtering and sorting techniques are both inefficient and prone to inaccuracy (Allen 2020). In short, it is difficult to both detect and remove plastics from water: these particles are essentially “invisible” to us.

Many labs have turned towards lasers, spectrophotometry, and chemical analyses to develop methods and sensors for oceanic plastic detection. One such method, Raman spectroscopy, is a technique used to study molecular states of a system and is capable of deducing chemical compositions of materials. Recently,

## "Many labs have turned towards lasers, spectrophotometry, and chemical analyses to develop methods and sensors for oceanic plastic detection."

a new technology known as Raman Tweezers (RTs), which is an inverted microscope coupled to a Raman spectrometer, has been introduced. Although the method is able to accurately optically trap and chemically identify sub-20 micrometer to 50 nanometer diameter plastics, RT setup is incredibly complicated, involving several laser sources, diodes, notch filters, and imaging cameras. The method is far too complex and technical to be operable by non-experts and too expensive to be widely accessible (Gillibert et al. 2019). To address these issues, prototypes of portable sensors have been built and developed to detect microplastics. These prototypes rely on optical methods - measuring both laser light reflection and transmission from transparent plastic particles - to screen the type, size, and nonplanarity of microplastics (Asamoah et al., 2019). However, the accuracy of these prototypes are below those of intricate spectroscopic methods, and the switch between the two involves, in essence, a trade-off between accuracy and convenience.

As modern computational technology advances, some research groups have taken a non-engineering approach to addressing the inconvenience of physical detection methods while maintaining their accuracy. Instead of directly measuring plastic concentrations in water, new computational methods seek to model the dispersal and breakdown of plastics in water to predict plastic distribution in the ocean over time. Numerical modeling, which is the modeling of Earth's physical movements using math, represents plastic transport with the General Advection Equation, which is a partial differential equation (PDE) that computes tracer - in this case, plastic - concentration at various locations and times, subject to initial and boundary conditions. By incorporating different factors - plastic characteristics, vertical movement through water columns, fragmentation, and others - into the PDEs, the models can be fitted to virtually any plastic-dispersing scenario, increasing the scope and convenience of these numerical models. After the PDEs are solved for specific locations and times, the results of the models can be visually represented as colorful,

informative diagrams, thereby increasing the accessibility of the data to non-scientists (Kulkarni and Lermusiaux, 2019). When done right and done accurately, numerical modeling of plastic distribution is a powerful tool: it gives scientists the ability to both forecast the future and backcast the past - in other words, scientists can predict where plastic will disperse over time while analyzing its originating locations, thereby concluding concentrations of plastics at different locations at different points in time. However, despite the advantages of numerical models, it is difficult for scientists to gauge their true accuracy unless field data is available for comparison. In addition, many models require calibration using true data values to complete computations: even though computers are incredible at solving expensive problems inexpensively, they still need baseline information to solve those problems, and some of that information - namely, real measurements of plastic concentration in the ocean for baseline use - is unavailable.

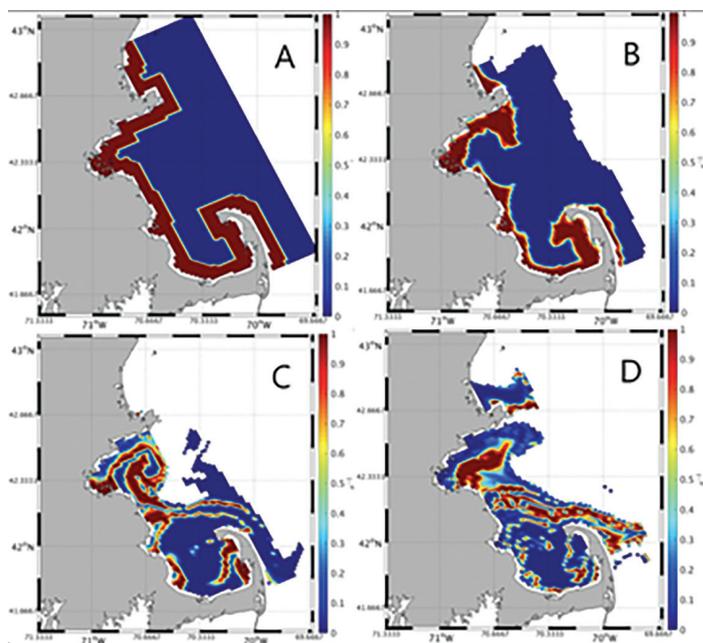


Figure 2. Sample diagrams depicting a hypothetical oceanic plastic dispersal scenario in Massachusetts Bay, where plastics originate at the coastline in uniform concentration. As shown by the gradient to the right of each subdiagram, dark red represents high plastic concentrations and dark blue represents no plastic. Subdiagram A shows initial conditions, B shows distribution at time  $t = 1$  day, C shows distribution at time  $t = 7$  days, and D shows distribution at time  $t = 20$  days. Changes in plastic distribution and concentration is visualized by the changes in color distribution on the subdiagrams. (Source: Graphic produced by author; model and data sourced from Kulkarni and Lermusiaux (2019).) (Tullo 2018); Data from International Coastal Cleanup.)

This presents a circular problem. Because physical detection methods are either expensive and inaccessible or inaccurate and unusable, no “real-life” field data of oceanic plastic concentrations is available to scientists. This problem of a high price tag, however, can be solved by cheap computational methods that eliminate the need for complex machinery and expensive materials, but these methods are not widely publicized due to the need for field data as bases for verification and calibration: as explained above, no such data is available.

### Expectation Versus Reality

While researchers are developing scientific methods to detect oceanic plastic pollution and understand the problem, governments around the world have begun to recognize the severity of plastic pollution and are implementing new policies to combat it. In June of 2019, the Prime Minister of Canada, Justin Trudeau, announced that the Canadian government will be banning single-use plastics by 2021, following the lead of more than 60 nations including India and member nations of the European Union. The Canadian federal government will be working with provinces and territories to introduce standards and targets for plastics manufacturers and retailers to increase plastic waste responsibility while supporting efforts by Canada’s minister of environment to create a nationwide strategy for zero plastic waste. In January of 2019, Peru banned single-use plastics in Peru’s 76 natural and cultural protected areas with the goal of replacing single-use plastics with “reusable, biodegradable plastic or others whose degradation does not generate contamination by microplastics or dangerous substances.” In December of 2018, Peru’s Congress had also passed a law to decrease single-use plastic bags across the country over the next three years, another effort to eliminate plastic waste in the environment. In the United States, cities from San Diego to Washington D.C. have banned the use of styrofoam containers, which are notoriously difficult to recycle, and plastic straws in favor of reusable, washable, or biodegradable products. Aquariums in 17 different states in the United States have also banded together to promote “No Straw November”, a creative campaign pushing for the elimination of single-use plastics that has already influenced large businesses such as United Airlines and regional governments. International initiatives such as the International Coastal Cleanup - started by the Ocean Conservancy - and the New Plastics Economy Global Commitment - in which two hundred and fifty organizations responsible for 20%

of the plastic packaging produced around the world have committed to reducing waste and pollution - have brought together citizens, cities, companies, and organizations in pursuit of a common goal of eliminating plastic waste (Howard, 2019).

### "Governments around the world have begun to recognize the severity of plastic pollution and are implementing new policies to combat it."

This seemingly united front of nations and businesses raises optimistic hopes but paints a false picture of reality. Though many are onboard to truly decrease plastic use, many governments and businesses are still unwilling to implement new environmentally-friendly policies or change their business operations in “green” ways. The United States has been notoriously terrible at encouraging true environmental change: congressional lobbyists for big businesses pose roadblocks to greener policymaking and local businesses complain of the increased costs of sustainable, plastic-free business operations. In addition, the promises of greener policies made by many countries are not enforceable and serve mainly as statements of what they hope to achieve. As a result, times of instability and economic difficulty - such as the current COVID-19 pandemic - can significantly offset environmental progress and actually undo change, as there is no international organization with the power to strictly enforce global environmental policies. More subtly, the scientific front on the issue of plastic pollution is also not unified. Because labs around the world are developing so many unique ways to study, detect, and quantify plastics, it is incredibly challenging, if not downright impossible, to compare data between different labs and different regions. Attempts to standardize microplastic detection and quantification by organizations have resulted in the publication of various methods and protocols, including NOAA’s “Laboratory Methods for the Analysis of Microplastics in the Marine Environment” and JPI-Oceans’ “Standardized Protocol for Monitoring Microplastics in Sediments”, that further complicate scientific efforts (Allen, 2020). In short, a global scientific consensus must be reached on the issue of environmental plastic detection and data reporting for the problem to be understood on a global scale and for progress to be made.

## An Outlook of the Future

As with all other environmental issues, change starts with us. Environmental and industry experts predict that by 2050, the oceans could have more plastic than fish, with a projection of at least 937 million tons of plastic but only 895 million tons of fish (Harrington, 2017). Scientific progress is promising, but even so, it is up to every citizen of this world to put their personal efforts into reducing plastic consumption, encouraging STEM education, and promoting environmentalism across society. With still 30 years until 2050, the world may never have to see a day where plastic outnumbers fish in the ocean.

## References

Allen, Liz. "This is Why Microplastics Are So Hard To Detect In The Ocean." *Forbes*, 26 February 2020, <https://www.forbes.com/sites/allenelizabeth/2020/02/26/this-is-why-microplastics-are-so-hard-to-detect-in-the-ocean/#603d6d273dff>.

Asamoah, Benjamin O., et al. "A prototype of a portable optical sensor for the detection of transparent and translucent microplastics in freshwater." *Chemosphere*, vol. 231, pp. 161-167. Published 17 May 2019.

Cozar, Andres, et al. "Plastic debris in the open ocean." *PNAS*, vol. 111 (28), pp. 10239-10244. Published 15 July 2014.

Gillibert, Raymond, et al. "Raman Tweezers for Small Microplastics and Nanoplastics Identification in Seawater." *Environmental Science and Technology*, vol. 53 (15), pp. 9003-9013. Published 1 July 2019.

Harrington, Rebecca. "By 2050, the oceans could have more plastic than fish." *Business Insider*, 26 January 2017, <https://www.businessinsider.com/plastic-in-ocean-outweighs-fish-evidence-report-2017-1>.

Howard, Brian Clark, et al. "A running list of action on plastic pollution." *National Geographic*, 10 June 2019, <https://www.nationalgeographic.com/environment/2018/07/ocean-plastic-pollution-solutions/#close>.

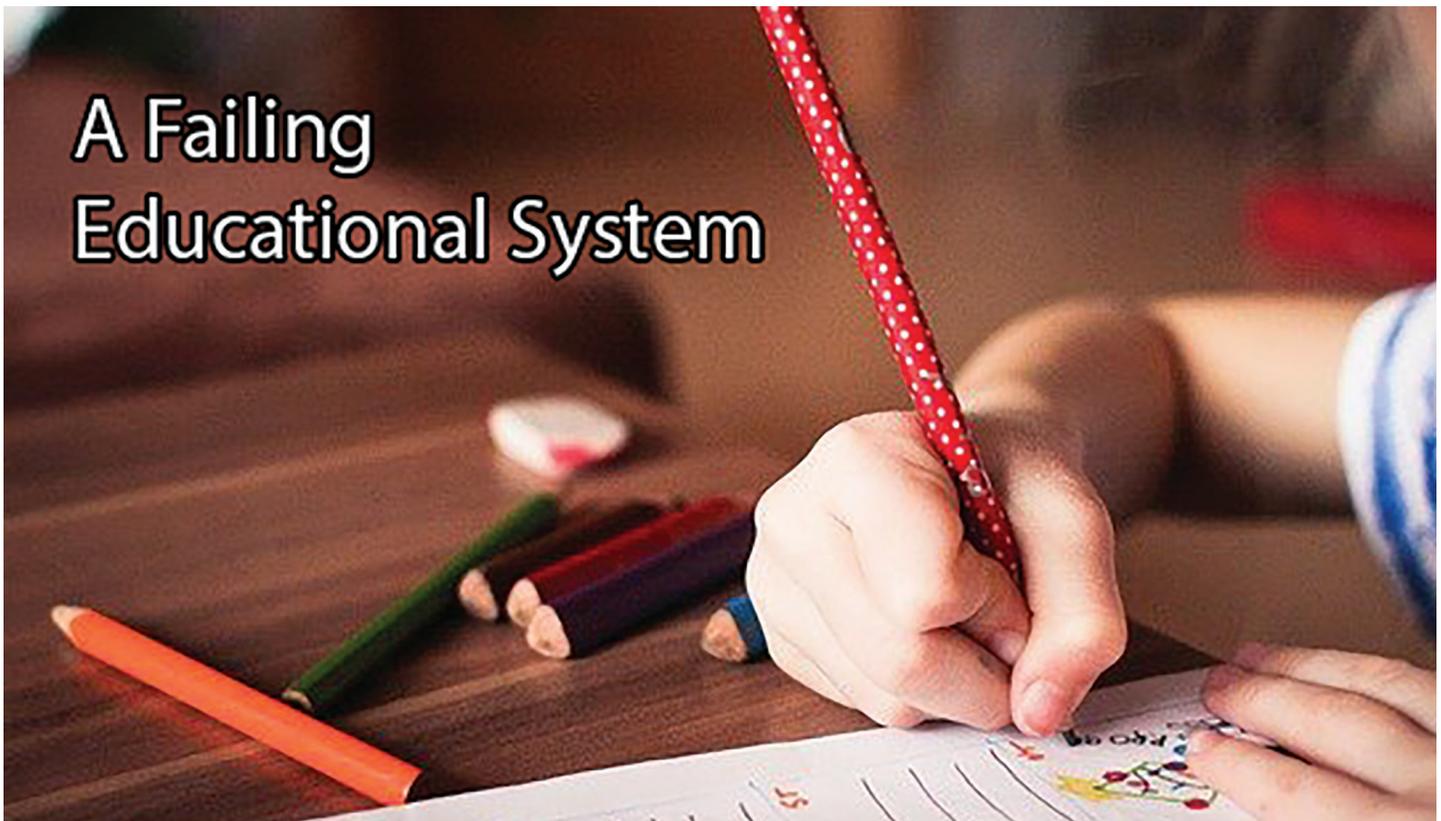
Kulkarni, Chinmay S. and Lermusiaux, Pierre F.J. "Advection without compounding errors through flow map composition." *Journal of Computational Physics*, vol. 398. Published 1 December 2019.

Law, Kara L. "Plastics in the Marine Environment." *Annual Review of Marine Science*, vol. 9, pp. 205-229. Published 7 September 2016.

Lebreton, L.C.-M., et al. "Numerical modelling of floating debris in the world's oceans." *Marine Pollution Bulletin*, vol 64 (3), pp. 653-661. Published 20 January 2012.

NOAA. "Why should we care about the ocean?" *National Ocean Service*, 24 May 2017, <https://oceanservice.noaa.gov/facts/why-care-about-ocean.html>.

Tullo, Alexander H. "Fighting Ocean Plastics at the Source." *Chemical and Engineering News, American Chemical Society (ACS)*, 16 Apr. 2018, [cen.acs.org/materials/polymers/Fighting-ocean-plastics-source/96/i16](https://cen.acs.org/materials/polymers/Fighting-ocean-plastics-source/96/i16).



# A Failing Educational System

Ramon Rivera '24

## Deficiencies of the Current System

The public K-12 education system in the United States is subject to a wide array of criticism from both sides of the political spectrum. From calls for more funding to problems with its bureaucratic structure, no one seems to be content with the current system. The most recent poll from Gallup reflects that only forty-one percent of the population has “a great deal” or quite a lot” of confidence in public schools. This figure has actually been positively impacted by the ongoing pandemic and is significantly higher than the average mark of recent years that fluctuated between the high twenties and low thirties. Despite this recent improvement, the confidence in public schools still falls short of other key institutions such as the military, small businesses, police, and medical system (Brenan, 2020). This lack of widespread and overwhelming support for the public school system supports the idea that new reforms to the education system would be welcomed. Furthermore, even as the nature of the criticisms of the public school system varies according to political beliefs, there are many reasons to believe that reform is needed. The reality is that the current results by American students fall short of what would be expected of a country with the economic

might and global position of the U.S.

The Programme for International Student Assessment (PISA) is an international assessment that is given to fifteen-year-old students in a variety of countries every three years. This test measures students' proficiency in science, reading, and mathematics. In the two most recent administrations of this test (2015 & 2018), the U.S. was behind the United Kingdom, Finland, Germany, and other countries in all three subjects (DeSilver, 2020). The U.S. only managed to finish in the top ten in any of the subjects in 2018 when it ranked eight in reading in 2018. This makes evident that students in the U.S. are not learning at the level that would be desired.

In an even more disappointing sign, the U.S. is showing a wide gap between those who perform in the top levels and the rest of the students. The results of students in the U.S. are showing that instead of having test scores with a low deviation among themselves, students are

**"The reality is that the current results by American students fall short of what would be expected of a country with the economic might and global position of the U.S."**

scoring on opposite levels either doing extremely well or extremely bad. An even more worrying statistic is that this gap seems to be more pronounced among different socioeconomic classes “with 27% of top performers registering as wealthier, advantaged students and only 4% as poorer, disadvantaged students” (Camera, 2019). This is a clear sign of a system that is leaving the most vulnerable students and those that need the most resources and help behind.

The underperformance in assessments like PISA is not the only reason why the public school system is in need of reform. A more widespread problem in the education system is the way in which poorer students are left behind. This is highly pronounced in the difference in the performances of students in rich and suburban communities versus those students in poor rural and urban communities. There is almost a twenty percent difference in the graduation rates of suburban and urban schools, with urban schools barely hitting a fifty percent graduation rate (Irizarry, 2015). This is in addition to the overcrowding and lack of resources that are common in urban and poorer schools. The tragic reality is that due to the choiceless nature of much of the public educational system, these students are obliged to study their whole lives at these schools that simply do not meet their needs.

### Where is the Problem?

An argument can be made that instead of widespread reform, the public education system just needs greater funding and certainly there is some truth to this. For example, a recent study by The Century Foundation found that “the United States is underfunding its K-12 public schools by nearly \$150 billion annually, robbing more than 30 million school children of the resources they need to succeed in the classroom” (The Century Foundation, 2020). Therefore, it is evident that greater funding targeted at struggling schools may help improve the quality of education in these places. However, there is evidence that says that greater funding alone is not enough to bring up the school system to great levels. For example, the U.S. spends about \$720 billion each year on public K-12 schooling (Knight, 2020). This comes down to an approximate \$11,762 per student (e.Republic, 2020). However, the two states with the greatest per-pupil spending (New York and Washington D.C.) are not in the top ten in the public school ranking (McCann, 2020). Meanwhile, the top public school system (Massachusetts) spends almost seven thousand dollars less per student than New York. Something that provides greater support

for the theory that greater spending alone can not solve the public schools’ problems is the fact that Virginia ranks eight places ahead of New York and more than thirty-five places ahead of Washington D.C. but spends approximately half of what these states spend on a per-pupil basis (e.Republic, 2020). With this in mind, we can say that a different kind of reform is needed to get the U.S. public schools to a top-level worldwide.

**"The main idea with these and all school choice programs is that parents are given a choice and are not forced to move to a new community or leave their kid in a school that they do not like."**

### A Different Approach

In recent years, a new approach to public education that presents an alternative and possible solution to the problems that plague the public school system has gained momentum in the national conversation. This new approach is known as school choice and it basically “allows public education funds to follow students to the schools or services that best fit their needs” (EdChoice, 2020). What this means is that the public funds that would be destined to the public school where a kid would go would be redirected and given to the parents so that they can choose whichever school or program they think is better for their kid. There are different types of school choice. Three of the most popular types of school choice are education savings accounts, school vouchers, and charter schools. Education savings accounts (ESA’s) are basically accounts where the parents of a child receive public funds that are used to cover the child’s educational expenses. On the other hand, School Vouchers give parents the opportunity to choose a private school for their child through a voucher given by the government that is used to cover all or part of the private school’s tuition. Finally, charter schools are public schools that are run independently from the school district. In the case of charter schools, if the number of students that desire to study there exceeds the number of available spots then normally a lottery is carried out (EdChoice, 2020). The main idea with these and all school choice programs is that parents are given a choice and are not forced to move to a new community or leave their kid in a school that they do not like.

## Results

In the past decade, such programs have begun to expand and are now available in more states with 6,900 charter schools in 43 states and D.C. and school voucher programs in 15 states plus D.C. There is now a good amount of research that has been done on the efficacy of these school choice programs. For example, a 2016 meta-analysis study of 19 voucher programs around the world found that students that participate in these programs experience higher reading and math scores (Danish et al., 2016). It is worth noting that they found this positive effect to be greater in other parts of the world than in the U.S. which means that there is still space for improvement. Other studies found increases in graduation rates among participants and higher levels of civic engagement, and an improvement in racial integration, among other positive effects. All of this while only two studies, out of more than twenty, showed a negative effect in test scores among participants; these two studies that showed negative effects were on a Louisiana Voucher Program that was a victim of special circumstances that scared away most

**"The evidence clearly shows that the implementation of school choice programs improves the education of participant students and also of those who remain in traditional public schools."**

eligible private schools (DeAngelis and Erickson 2018).

Furthermore, a 2013 review found that twenty out of twenty-one studies indicate that competition from school choice programs actually increases the test scores of students that remain in traditional public schools (Egalite, 2013). This would be supported by the logic that, as the monopolistic power of public schools decreases due to the competition created by school choice programs, public schools are forced to improve to keep their students and funding. The evidence clearly shows that the implementation of school choice programs improves the education of participant students and also of those who remain in traditional public schools. Some of the criticism surrounding these programs stems from the injustice of the lottery nature of some of them and also from the lack of transparency these schools have, among other things (Strauss, 2019). These criticisms can easily be addressed

by sensible policy-making that takes into consideration these problems. In end, the evidence indicates that school choice programs are beneficial to students and are a way of giving students and their parents the tools they need to be academically successful.

## Conclusion

It is evident that the current public school system in the U.S. is in need of some reform. All of the evidence makes it clear that there is a need for more investment and a different approach to the way that public education is carried out in the U.S. The current system leaves poor kids behind while providing inconsistent results at best for the rest of the population. There must be comprehensive policy changes so that the three main failures of the current system are addressed. The three failures that ought to be addressed in order to build a successful system are the underperformance of students when compared to other countries, the lack of a choice for parents who feel their kids are not getting a decent education and the lack of widespread and overwhelming confidence in the system. As I have demonstrated throughout the essay, the most effective and practical solution to this is introducing a school choice program on a national scale where every parent who wants can benefit from it.

The introduction of a national school choice program would be beneficial for the success of students for a variety of reasons. Firstly, most research indicates that school choice and voucher programs have a positive effect on the test scores of participating students with only a small proportion of studies showing a negative effect. Furthermore, most studies show that participants in school choice programs enjoy greater long-term academic attainment, with no single study finding negative effects. This is something that research indicates would translate to better employment opportunities and a generally improved life outlook (EdChoice, 2020). Additionally, school choice programs mean that parents actually have a choice on where to send their kids to school. This alone is a significant change from where the system stands today and one that allows parents to feel better about their kids' opportunities and future, all while providing a more level playing field for poor and underprivileged kids. This is reflected in all the studies that show that school choice programs increase parents' satisfaction with their children's education. All of these reasons make it clear that a school choice program would be a tool of improvement for our educational system. Of course, there are risks and potential downfalls that must be addressed

and require that the government be involved in how these programs are implemented. Without the correct implementation and oversight, these programs would be at the risk of falling victim to the same problems as our current system. School choice programs are aimed at giving more opportunities and a level playing field to underprivileged students, that must be guaranteed and looked after in these programs. With this in mind, school choice programs, such as vouchers, scholarships, tax programs, and even charter schools, are a great way to improve the current public school system in the U.S.

## References

- Brenan, Megan. "Amid Pandemic, Confidence in Key U.S. Institutions Surges," November 3, 2020, <https://news.gallup.com/poll/317135/amid-pandemic-confidence-key-institutions-surges.aspx>.
- Camera, Lauren. "U.S. Students Show No Improvement in Math, Reading, Science on International Exam," U.S. News & World Report (U.S. News & World Report, December 3, 2019), <https://www.usnews.com/news/education-news/articles/2019-12-03/us-students-show-no-improvement-in-math-reading-science-on-international-exam>.
- DeAngelis, Corey and Erickson, Heidi Holmes. "What Leads to Successful School Choice Programs? A Review of the Theories and Evidence," *Cato Journal* 38 (November 2018): pp. 247-263, <https://www.cato.org/sites/cato.org/files/serials/files/cato-journal/2018/2/cato-journal-v38n1-chapter-13.pdf>.
- DeSilver, Drew. "U.S. Academic Achievement Lags That of Many Other Countries," Pew Research Center (Pew Research Center, August 21, 2020), <https://www.pewresearch.org/fact-tank/2017/02/15/u-s-students-internationally-math-science/>.
- EdChoice. "The 123s of School Choice: What the Research Says about Private School Choice Programs in America" EdChoice, 2020 edition, <https://www.edchoice.org/wp-content/uploads/2020/04/123s-of-School-Choice-2020.pdf>.
- EdChoice. "Types of School Choice," EdChoice, November 4, 2020, <https://www.edchoice.org/school-choice/types-of-school-choice/>.
- EdChoice. "What Is School Choice?," EdChoice, January 18, 2019, <https://www.edchoice.org/school-choice/what-is-school-choice/>.
- "Education Spending Per Student by State," Education Spending Per Student by State, June 1, 2018, <https://www.governing.com/gov-data/education-data/state-education-spending-per-pupil-data.html>.
- Egalite, A. J. (2013) "Measuring Competitive Effects from School Voucher Programs: A Systematic Review." *Journal of School Choice* 7 (4): 443–64.
- e.Republic, "Education Spending Per Student by State," Education Spending Per Student by State, June 1, 2018, <https://www.governing.com/gov-data/education-data/state-education-spending-per-pupil-data.html>.
- Irizarry, Darryl. "Urban Educational Inequalities: Why the Growing Concern?," American Bar Association, July 2, 2015, <https://www.americanbar.org/groups/litigation/committees/childrens-rights/articles/2015/urban-educational-inequalities-why-growing-concern/>.
- Knight, David. "Federal Spending Covers Only 8% of Public School Budgets," *The Conversation*, July 14, 2020, <https://theconversation.com/federal-spending-covers-only-8-of-public-school-budgets-142348>.
- McCann, Adam. "States with the Best & Worst School Systems," *WalletHub*, July 27, 2020, <https://wallethub.com/edu/e/states-with-the-best-schools/5335>.
- Shakeel, M. Danish and Anderson, Kaitlin and Wolf, Patrick, *The Participant Effects of Private School Vouchers Across the Globe: A Meta-Analytic and Systematic Review* (May 10, 2016). EDRE Working Paper No. 2016-07.
- Strauss, Valerie. "Analysis | What 'School Choice' Means in the Era of Trump and DeVos," *The Washington Post*, April 18, 2019, <https://www.washingtonpost.com/news/answer-sheet/wp/2017/05/22/what-school-choice-means-in-the-era-of-trump-and-devos/>.
- The Century Foundation, "TCF Study Finds U.S. Schools Underfunded by Nearly \$150 Billion Annually," The Century Foundation, July 22, 2020, <https://tcf.org/content/about-tcf/tcf-study-finds-u-s-schools-underfunded-nearly-150-billion-annually/?session=1>.

## Utilizing Linguistics to Develop Novel Retrosynthesis Pathways for Drug Development



### Dianelis Lopez '22

The field of retrosynthesis allows us to identify important functional groups or motifs that are information rich in order to determine the reactive properties of a compound. In 1828, Friedrich Wöhler synthesized urea in the laboratory, which was the first organic molecule. The techniques of organic synthesis have developed and advanced through time, allowing them to become revolutionary in chemical research (De Souza, 2017). The methods used in retrosynthesis involve “deconstructing” into more simplified starting materials, and then these pieces are used to develop the best synthetic route. The framework of retrosynthesis was coined by Elias James Corey, and previous methods involved trial and error approaches in order to combine available molecules. However, retrosynthesis emphasizes working in reverse and using the target molecule at the starting material, which reveals multiple synthetic routes (De Souza, 2017). These routes are compared by production cost and feasibility through different reagents. Then, the most efficient route is chosen in order to start synthesis in an industrial level. This knowledge can also become very useful in the development of therapeutic drugs and when determining how certain drugs will behave inside the body.

In medicine, there are various natural compounds that

can be used to treat and possibly cure diseases. Since these molecules are often found in animals or plants, then the synthetic synthesis of the compounds is important for the creation of medical drugs that are readily accessible. Retrosynthesis allows for the understanding of these products and proposes possible routes to achieve synthesis for commercial purposes. Additionally, understanding the different pathways that lead to the creation of a molecules allows for the selection of the most environmentally friendly path. For example, retrosynthesis has allowed for the production of medications such as paclitaxel, which is a chemotherapy medication used to treat various types of cancers (Werk, 2008). Initially, the production of Paclitaxel required using trees called *Taxus brevifolia*, which limited the supply of the drug and made the process slow. However, scientists are now able to synthesize the drug at the laboratory through retrosynthetic approaches and diminish the environmental impact. The synthesis of Paclitaxel was first done at Florida State University and was known as the Holton Taxol total synthesis. For

**"retrosynthesis has allowed for the production of medications such as paclitaxel, which is a chemotherapy medication used to treat various types of cancers"**

this process, the “Patchoulene oxide” was determined to be the starting material and a multi-step approach was utilized to synthesize the entire compound (Werk, 2008). Now, there are many more routes utilized to synthesize this compound, and contribute towards the preservation of natural products.

## "The field of disease research should consider incorporating more humanistic approaches in order to understand diseases."

In an effort to elucidate the reactivity of a molecule, it could be useful to look into the methods utilized in linguistics when analyzing sentence structure (Cadeddu, 2014). The field of computational linguistics has developed methods in order to scan texts for maximum common strings (MCS) of letter or words and ranking these MCSs with a frequency score. In order to apply this principle of quantitative analysis, it is important to determine how this ranking will be conducted for molecules (Cadeddu, 2014). Studies suggest that using functional groups as MCSs deviate from the curve observe in the English language. However, when our programming searches for fragments, then the curve seems to follow the same curve as word frequency in the English language (Figure 1).

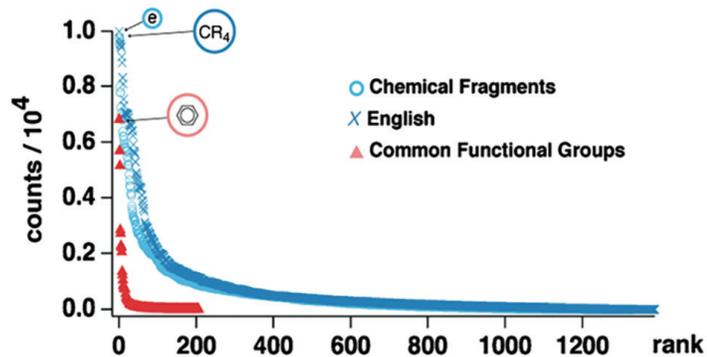


Figure 1. The Dark blue crosses represent the rank-frequency distribution of maximum common substrings in English sentences. The light blue circles represent the distribution of common molecular sub-fragments. In contrast, the red triangles represent the rank-distribution of common functional groups and are significantly different. In a set of sentences or molecules, the frequency is the normalized frequency of occurrence of substrings, fragments, or groups.

Additionally, this software utilizes a score called tf-idf scoring (term frequency–inverse document frequency). This is a numerical statistic that determines how relevant, information-rich, a certain word is. For example, the word “the” is usually present multiple times across a text; therefore, it is not an information rich word. However,

words such as “foundation” are a little less present and tend to convey more information (Cadeddu, 2014). Therefore, this word will be assigned a higher tf-idf score. Similarly, molecule fragments are given a score according to how much information that fragment contains. Then, the information score is assumed to be representative of the importance of this section in determining reactivity (Cadeddu, 2014). In Figure 2, we can see that the size of the words and of the specific fragments is altered according to the score assigned. The bigger words and molecules are assumed to carry more information. When looking at molecules, the software will focus on identifying the largest common structural fragments (Figures 3 and 4).

Implementing research techniques from the field of linguistics into organic chemistry research could aid in bridging the disconnect between the humanities and basic science research. Humanities research is often discredited and treated as less credible given that it is not data-driven; however, it is necessary to move towards accepting research techniques in the humanities as credible and recognized that their translation into the basic science field could tremendously advance our current understanding. The field of disease research should consider incorporating

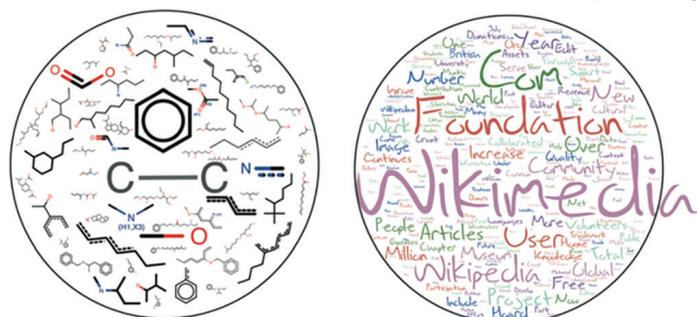


Figure 2. In the “word cloud”, the word’s size expresses this word’s relative relevance and is proportional to its tf-idf score. In the left panel, there is a “cloud” of organic chemistry structural motifs instead of words. In the right panel, there is a word cloud for the Wikimedia Foundation’s 2009–2010 annual report.

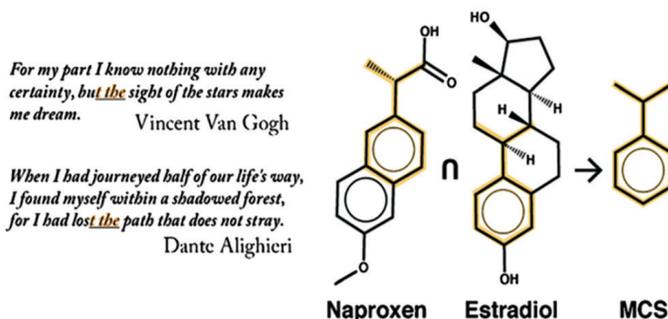


Figure 3. Shows two English sentences and an example of a maximal substring (highlighted).

Figure 4. Shows the maximal subfragment of two organic molecules

more humanistic approaches in order to understand diseases. Diseases are not just affecting the biology of a person, but they lead to different illness experiences which are valid and should be recognized in the research process. Additionally, incorporating more novel research methods could lead to the discovery of new synthesis routes that might be more feasible, environmentally friendly, and cost effective.

## References

Cadeddu, Andrea, Wylie, Elizabeth K, Jurczak, Janusz, Wampler-Doty, Matthew, & Grzybowski, Bartosz A. (2014). Organic Chemistry as a Language and the Implications of Chemical Linguistics for Structural and Retrosynthetic Analyses. *Angewandte Chemie (International Ed.)*, 53(31), 8108-8112.

De Souza, Rodrigo O. M. A, Miranda, Leandro S. M, & Bornscheuer, Uwe T. (2017). A Retrosynthesis Approach for Biocatalysis in Organic Synthesis. *Chemistry : A European Journal*, 23(50), 12040-12063.

Werk, Michael, Langner, Soenke, Reinkensmeier, Bianka, Boettcher, Hans-Frank, Tepe, Gunnar, Dietz, Ulrich, . . . Ricke, Jens. (2008). Inhibition of restenosis in femoropopliteal arteries: Paclitaxel-coated versus uncoated balloon: Femoral paclitaxel randomized pilot trial. *Circulation (New York, N.Y.)*, 118(13), 1358-1365.



# Challenges of Coronavirus Epidemiological Modeling

Andrea Rivera '22

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) outbreak has become a major public health emergency since it was first detected in December 2019. Since then, 217 countries and territories around the world have reported a total of 54.8 million confirmed cases of COVID-19 with a dead toll surpassing 1.3 million deaths. As such, artificial intelligence based on machine learning and mathematical models are currently being developed to estimate the spread of the virus across different countries and provide important information for public health officials and policy makers seeking to slow down its spread. Many different models are currently being tested in order to forecast future infections. However, accurately modeling the spread of COVID-19 remains a challenge due to various factors unique to this virus which make it extremely difficult to predict such as a long incubation period, tracking of individuals, data accuracy, asymptomatic carriers, and underlying genetic differences.

## Infectious Disease Modeling

In order to accurately predict the progression and spread of an infectious disease, it is vital to understand the underlying mechanisms of transmission. These diseases

typically spread because of exposure to an infection, which results in the formation of an infected host. When an infected host contacts more people, the disease continues to spread. In the case of COVID-19, the virus is an acquired pathogen that is spread through a pathogenic agent. One of the simplest models for the transmission of infectious diseases is called the epidemiologic triad, which consists of an external agent, a susceptible host, and an environment that brings the host and agent together (Shinde et al 2020). Figure 1 depicts the interaction between the host, environment, and agent of such a triad, a simple relationship that can be used to model COVID-19 transmission.

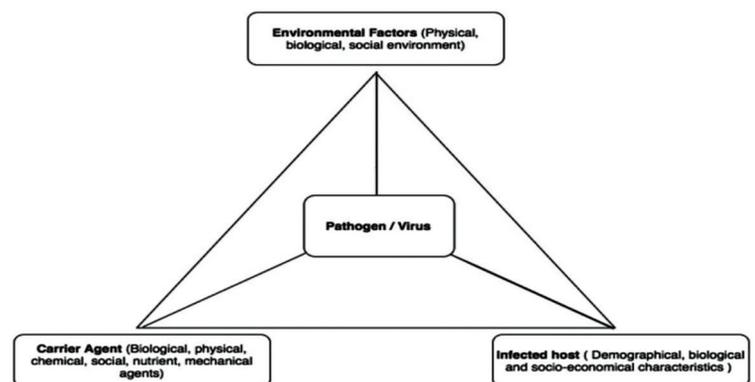


Figure 1: Epidemiologic Triad Source: Shinde et al, (2020)

There are three basic regional-scale models that can be used for forecasting and assessing the course of infectious disease transmission: exponential growth, a self-exciting branching process, and compartmental models. These seemingly simple models can help predict the progression of the pandemic with some accuracy at different stages. In the case of COVID-19, there is an exponential growth phase during the first 15 to 20 days from the outbreak if no public health interventions are implemented (Bertozzi et al.2020). A self-exciting branching process or compartmental model can also be used to model the spread of COVID-19 as proposed by Bertozzi et al, as these models can be adapted to predict the long-term evolution of the pandemic by incorporating factors that can account for dynamic changes that results from deaths, decrease in susceptible individuals, and public health interventions. These three basic models and how closely they predict collected COVID-19 data will be further explored in this section.

**"artificial intelligence based on machine learning and mathematical models are currently being developed to estimate the spread of the virus"**

The COVID-19 epidemic exhibits exponential behavior during its early stages, when the number of infected individuals is substantial but recovered and dead individuals are negligible.

As such, an exponential growth model is suited for the first 15 to 20 days from the start of the outbreak, an estimate calculated using data from the Wuhan outbreak (Bertozzi et al.2020). This model predicts that if at a given time ( $t$ ) there are  $I(t)$  infected individuals and these individuals infect others at  $\alpha$  transmission rate then in the early stage of the pandemic:  $I(t) = I_0 e^{\alpha t}$ . This simple model allows you to estimate the number of infected individuals at any given time given the number of initial infected individuals ( $I_0$ ) and the rate at which COVID-19 is transmitted ( $\alpha$ ), which can be estimated using previous transmission data. A recent study applied this exponential model to the cumulative infections and deaths data from South Korea, Italy, France, Germany, Spain, United Kingdom, and the United States and the data closely fits the model's predicted results for the pandemic's earliest stage, making this model a good predictor for early transmission without any public health interventions (Bertozzi et al.2020). Both the cumulative

infections and cumulative deaths as predicted by this model for the countries previously mentioned can be seen in figure 2.

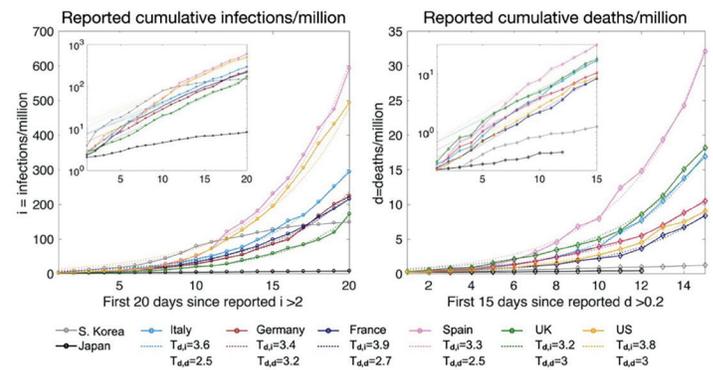


Figure 2: Exponential Growth Model Applied to Cumulative Infection and Deaths for Several Countries Source: Bertozzi et al, (2020)

The exponential growth model has very limited applications given that it is only able to predict the initial stages of infection and assumes that no public health interventions are put in place. A more useful model would be a branching point process model, which allows parametric or nonparametric estimation of the reproduction number and transmission timescale and can also help estimate the probability of extinction early in the pandemic (Bertozzi et al.2020). A branching point model is commonly used to help surveil infectious diseases. Using this type of model, the intensity rate of the infection can be modeled as:

$$\lambda(t) = \mu + \sum_{t_i < t} \mathfrak{R}(t_i) w(t - t_i)$$

Equation 1

where  $t$  is the present time and  $t_i$  is the time of previous infections (Bertozzi et al.2020). An important feature of this model is that the reproduction (transmission) rate,  $\mathfrak{R}(t)$  evolves over time, which means that it can take into consideration public health interventions such as social distancing, lockdown, isolation, etc. More importantly, this model can also predict the long term behavior of the disease by incorporating a prefactor that can account for the increase or decrease in the susceptible population. Equation 2 incorporates this prefactor, where  $I_c(t)$  is the number of infections up to time  $t$  and  $N$  refers to the entire population number.

$$\lambda^h(t) = (1 - I_c(t)/N) (\mu + \sum_{t_i < t} \mathfrak{R}(t_i) w(t - t_i))$$

Equation 2

## "This model can help predict the rate of change of the susceptible, exposed, infected, and recovered individuals over time"

Finally, a compartmental model could also be used to describe the long-term transmission of COVID-19. These compartmental models are very commonly used in epidemiological infectious disease modeling because they simplify the mathematical modeling as the population is divided into different groups. The most simple model is called an SIR model, which estimates the number of people infected with an infectious disease in a closed population over time where S represents the susceptible population, I represents the infected population, and R represents the recovered population. However, this model would be too simple to predict the spread of a disease like COVID-19. A related model called SEIR (susceptible–exposed–infected–recovered) would be more appropriate as it includes an “exposed” compartment that incorporates the delay between the person being exposed and infected, a period that can take up to two weeks with COVID-19 (Bertozzi et al.2020). Given these compartments, the SEIR model equations are:

$$\begin{aligned}\frac{dS}{dt} &= -\beta \frac{IS}{N} \\ \frac{dE}{dt} &= \beta \frac{IS}{N} - aE \\ \frac{dI}{dt} &= aE - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

Where  $\beta$  is the transmission rate,  $\gamma$  is the recovery rate, and  $a$  is the inverse  $\gamma$  of the average incubation time. The first differential equation represents the rate of change of the susceptible population over time, which is dependent on the transmission rate for the disease and negatively affected by the number of infected people. This negative relationship occurs because the only way for the susceptible people to leave this compartment is to go into the infected compartment. The rate of change of the recovered individuals over time is positively affected by the infected population and the recovery rate, as the only way for the infected individuals to leave this compartment is to move to the recovered compartment. The remaining differential equations follow a similar logic and calculate the rate of change of each compartment by an individual's ability to move from one compartment to another and their corresponding rates. This model can help predict

the rate of change of the susceptible, exposed, infected, and recovered individuals over time using estimated transmission rate, recovery rate, and incubation time given COVID-19 reported data

## Proposed COVID-19 Model

The previously described regional-scale and compartmental models presented are used for forecasting and assessing the transmission of many infectious diseases. However, there are many different features of COVID-19 that make it harder to predict using these models compared to other infectious diseases. To take these factors into account, Ivore et al., developed a new  $\theta$ -SEIHRD model which incorporates the known special characteristics of this disease, particularly the undetected infections. Previous models have not been able to incorporate this feature, which is one of the main challenges of coronavirus modeling. Additionally, this model takes into account the different sanitary and infectiousness conditions of hospitalized people and the fraction  $\theta$  of total detected cases over the real total infected cases (Ivorra, B. et al. 2020). Overall, what makes this model so useful is that it is simple enough to allow for calculations and estimation of its parameters while at the same time capturing the most important aspects of the disease.

## "the biggest challenges of COVID-19 modeling is accurately reporting data and tracking infected people and people with whom they came into contact"

This model divides the total population into many more compartments than the standard SIR model. In fact, this model assumes that everybody in the population is in one of nine compartments: susceptible (S), exposed (E), infectious (I), infectious but undetected ( $I_u$ ), hospitalized or in quarantine at home that will recover ( $H_r$ ), hospitalized that will die ( $H_d$ ), dead (D), recovered after being previously detected as infectious ( $R_D$ ), and recovered after being previously infectious but undetected ( $R_u$ ). Figure 3 summarizes these compartments and shows the relationship between them. For example, the people in the exposed compartment move on to the infectious department after the incubation period with a rate of  $\gamma_E$ . Similarly, the people from the infectious compartment will move on to one of three compartments: hospitalized

or in quarantine at home that will recover, hospitalized that will die or infectious but undetected with different rates. The model parameters were all estimated using the data from Chinese Mainland, Macao, Hong-Kong and Taiwan as reported by the World Health Organization. The model parameters and their estimations are described in table 1.

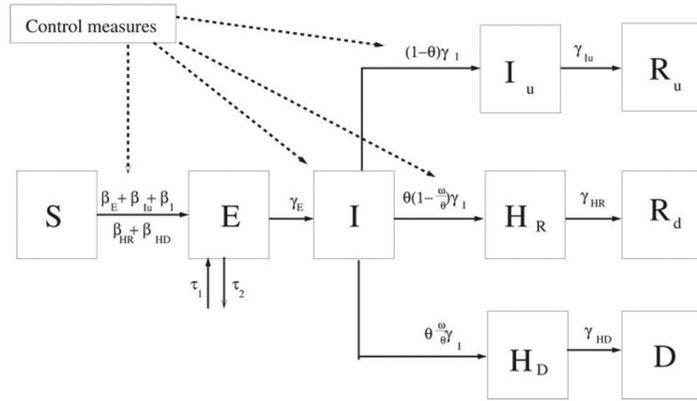


Figure 3:  $\theta$  -SEIHRD Model for COVID-19 Transmission  
Source: (Ivorra, B. et al. 2020)

Notation	Value	Description
$\gamma_E$	0.1818	Transmission rate from exposed to infected ( $day^{-1}$ )
$\gamma_I(t)$	[0.1493, 1.486]	Transition rate from infected individuals to other compartments at time $t$ ( $day^{-1}$ )
$\gamma_{H_R}(t)$	[0.0752, 0.1370]	Transition rate from $H_R$ to $R_D$ at time $t$ ( $day^{-1}$ )
$\gamma_{I_u}(t)$	[0.0752, 0.1370]	Transition rate from $I_u$ to $R_u$ at time $t$ ( $day^{-1}$ )
$C_o$	14	Convalescence period (day)

Table 1:  $\theta$  -SEIHRD Model Parameters Source: (Ivorra, B. et al. 2020)

With these compartments and using the same logic as for the SEIR model explained above, the  $\theta$  -SEIHRD model equations are:

$$\begin{aligned} \frac{dI}{dt}(t) &= \gamma_E E(t) - \gamma_I(t) I(t), \\ \frac{dI_u}{dt}(t) &= (1 - \theta(t)) \gamma_I(t) I(t) - \gamma_{I_u}(t) I_u(t), \\ \frac{dH_R}{dt}(t) &= \theta(t) \left(1 - \frac{\omega(t)}{\theta(t)}\right) \gamma_I(t) I(t) - \gamma_{H_R}(t) H_R(t), \\ \frac{dH_D}{dt}(t) &= \omega(t) \gamma_I(t) I(t) - \gamma_{H_D}(t) H_D(t), \\ \frac{dR_d}{dt}(t) &= \gamma_{H_R}(t) H_R(t), \\ \frac{dR_u}{dt}(t) &= \gamma_{I_u}(t) I_u(t), \\ \frac{dD}{dt}(t) &= \gamma_{H_D}(t) H_D(t). \end{aligned}$$

The model parameters and outputs are described more carefully by Ivorra, B et al. Some possible outputs given this system of differential equations could be cumulative number of COVID-19 cases and deaths (in country  $i$ ) at day  $t$ , the basic reproduction number and the effective reproduction number of COVID-19 (for country  $i$ ), the number of people in the hospital (in country  $i$ ), the maximum number of hospitalized people at the same time (in territory  $i$ ) during the time interval  $[t_0, T]$ , etc. However, it is important to note that some of the  $t_0$  parameters had to be estimated using assumptions due to lack of empirical data regarding COVID-19. As such, this model can help not only calculate the number of COVID-19 cases and deaths, but also determine the maximum number of people that can be hospitalized at a certain time. This latter information is critical to plan and avoid over-saturation of a country's healthcare system.

### Challenges

Although the proposed model for COVID-19 transmission does seem to yield predicted transmission rates that are similar to the reported global data, many questions still remain unanswered. There is still much that remains unknown regarding the underlying molecular mechanisms of this disease and how it varies with environmental and genetic factors. For example, many studies have tried to identify trends regarding climatic factors and genetic differences and how these impact COVID transmission. Fully understanding these differences would strengthen our current models and introduce new assumptions to existing ones. There are also challenges to coronavirus modeling that have nothing to do with our understanding of the disease itself. A model's prediction is only as accurate as the data that is given and one of the biggest challenges of COVID-19 modeling is accurately reporting data and tracking infected people and people with whom they came into contact with in order to accurately estimate model parameters. Finally, the long average incubation period for COVID-19 makes it extremely difficult to identify patients beforehand, especially those that are asymptomatic. This also poses a problem when trying to predict the long term behavior of the pandemic as it is very difficult for a model to take every single one of these factors into account and yield accurate results.

## Future Directions

Although the proposed models might differ in their methodology and implementation, the conclusions drawn remain the same. All of the models highlight the importance of sustained social distancing measures during early stages of transmission in order to slow down the speed of transmission (Shinde et al 2020). By slowing down transmission, it is possible to avoid or reduce the over-saturation of health care systems and have enough room to effectively treat infected individuals. As such, these models can serve as tools to implement informed public health measures and help reduce the spread of COVID-19 in different countries. Epidemic modeling must be used in order to inform public health decisions and these models need to be constantly revised as the pandemic progresses to ensure that healthcare systems can prepare for what is to come.

## References

- Shinde, G. R., Kalamkar, A. B., Mahalle, P. N., Dey, N., Chaki, J., & Hassanien, A. E. (2020). Forecasting Models for Coronavirus Disease (COVID-19): A Survey of the State-of-the-Art. *SN Computer Science* , 1 (4), 197. <https://doi.org/10.1007/s42979-020-00209-9>
- Bertozi, Andrea L., et al. "The Challenges of Modeling and Forecasting the Spread of COVID-19." *PNAS* , National Academy of Sciences, 21 July 2020, [www.pnas.org/content/117/29/16732](http://www.pnas.org/content/117/29/16732) .
- Ivorra, B., Ferrández, M. R., Vela-Pérez, M., & Ramos, A. M. (2020). Mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19) taking into account the undetected infections. The case of China. *Communications in nonlinear science & numerical simulation* , 88 , 105303. <https://doi.org/10.1016/j.cnsns.2020.105303>

