

Project Summary

Overview How does the genetic architecture of quantitative traits change as a result of demography and selection during the maize domestication bottleneck and the further bottleneck that some maize populations underwent from Central America to South America?

If we compare maize and teosinte (which are locally adapted in their respective pops), do we see evidence of:

- many genes of small effect or few genes of large effect underlying important traits?
- do these differences match our predictions based on their differing demographic histories?

Broadly relevant because these results could inform on maintaining diversity in crops for the future in ways that may have much larger long term impacts in the maintenance of diversity as well as fitness/adaptation in the face of climate change and future adaptation to changing environmental conditions.

Intellectual Merit

Broader Impacts

Project Description

A. Introduction

A critical goal of evolutionary biology today is to understand how organisms are able to adapt to new or changing conditions. This is especially relevant in the face of global climate change and other increasingly common anthropogenic changes to the environment (cite climate change papers). Understanding the process and the outcomes of adaptation can also further inform crucial goals such as improving crop yields.

The demographic history of populations or species plays a major role in the strength of selection on traits and organisms (cite), and thus has the ability to leave lasting changes or signatures in the genome (cite). A large body of work aims to infer the past demographic history of a population based on these genomic signatures (cite). However, inferring demographic history is a difficult task, as there are many possible histories that may have occurred, and they have the potential to leave similar, or even identical, signals in some species (cite).

The complexity of demographic history is increased manyfold when considering the various architectures that species' genomes comprise. Many ecological traits important for local adaptation have a complex, quantitative genetic basis, and much heterogeneity has been found among these traits both within and among species (cite Orr 2001, Slate 2005). Whether this genetic architecture consists of many loci of small effect or few of large effect can therefore play a role in the impact of demography and selection, as well as mutation, on the genome.

My proposed research aims to investigate these important factors (demographic history, selection, and genetic architecture) and their effects and interactions in terms of shaping the genome. I will address these questions using the maize/teosinte system. Maize (*Zea mays*, ssp. *mays*) is the domesticated species commonly known as corn, an annual plant. It is known to have been domesticated from its ancestor, the wild teosinte, approximately 9,000 years ago in southwestern Mexico. In particular, subspecies *Zea mays parviglumis* is the direct progenitor of maize. While two other subspecies of wild teosinte, *mexicana* and *huehuetenangensis*, exist and are found at higher elevations on the Mexican Central Plateau and in western Guatemala, respectively (cite Hufford 2012). Maize and teosinte are extensively studied and serve as ideal models for this research. Demographic history of the species is well documented: supported by both archaeological and other human records of its use and domestication in the Americas (cite). Extensive genetic and genomic data is also available, allowing the known demographic history of the species to be assessed in terms of genomic signatures of domestication (cite?), as well as specifically parameterized in terms of important values such as effective population sizes (cite Beissinger in prep).

Some such quantitative phenotypes include yield, plant height, and flowering time, which are of critical importance to agriculture.

Quantitative phenotypes such as yield, plant height, and flowering time are of critical importance to agriculture. Deleterious alleles likely play a large role in many of these phenotypes: crop plants have undergone dramatic demographic shifts, usually involving a domestication bottleneck followed by expansion as cultivation spread, and some authors even argue that selection on domestication traits has inadvertently increased the frequency of alleles deleterious for other phenotypes (cite gunther2010). Consistent with this hypothesis, my lab has recently shown that genes associated with a number of quantitative traits in maize are enriched for deleterious alleles compared to randomly chosen genes (cite mezmouk2014). However, while we know that demography impacts the frequency of individual deleterious variants, we have a poor understanding of the interaction of demography and selection on phenotypic variation. In particular, we know little about how these two forces interact to determine the genetic architecture – the number of genes and their effect –

e.g. stationary pop growth looks same as range expansion unless you look at different parameters

of a trait. Such information is crucial for understanding variation in phenotype, designing breeding strategies, utilizing diversity from wild relatives, or even engineering new traits using biotechnology.

then go into how we expect the combination of demog and seln to interact and change genetic architecture in different ways

we can look at this in maize as it makes a great system to compare two closely related species before and after different demog processes. it also has vast amounts of genomic data available allowing us to investigate the genetic architecture of these pops

it is thought, and shown in some human pops, that demog. history such as expansion leads to an increase in deleterious alleles, and of larger effects - b/c of continued inferred expansions and bottlenecks. is there any evidence of this in maize?

genetic architecture underlying traits affects how easy/hard and quick/slow local adaptation can occur. important for breeding, conservation, predicting response to climate change, etc. useful info for crops/domesticated species (and also things like disease in humans?)

selection interacts with demography. $N_e s > 1$ for selection to win. as demography changes, $N_e s$ changes. so demography is known to directly affect the strength of selection, but what is less studied is how this may restructure the genome in terms of how evolution proceeds for adaptation to new or changing conditions.

Different demographic histories such as bottlenecks, repeated founder effects during expansion, or rapid population growth can have effects that interact with selection. Small population sizes can lead to purging (recessives become homozygous and removed in smaller pops), but also increase in deleterious alleles (surfing phenomenon due to random genetic drift). mutations that affect a trait related to fitness will then be impacted by demography x selection interaction. in annual plants, nearly ALL traits related to fitness we thus predict that genetic architecture (number and size of mutations) should be impacted by demographic change. this is not understood well in any system. controversial in humans (lohmueller vs. pritchard etc.). in plants, summaries are on gross overall N_e (small vs. big) and ignore recent demographic change.

B. Research Objectives, Methods & Significance

Objective I: Investigate the genetic architecture of important traits in teosinte

This first objective aims to estimate the distribution of fitness effects (DFE) in teosinte (*genus spp*).

Objective II: Simulate the demographic history of maize domestication from teosinte

Maize was domesticated in...

Objective III: Estimate and compare the genetic architecture underlying traits in maize post-domestication from simulations and genomic data

rationale and significance

Maize was domesticated ≈ 9000 years ago in SW Mexico which bottlenecked populations to a small size, but was subsequently followed by a large population expansion more recently. This demographic event can be detected genetically, as shown by Beissinger in prep (github repo), where populations were bottlenecked to 5% of their previous size followed by spread across central and southern America and into highland and lowland environments. Populations of maize have since recovered to much larger effective population sizes than even before the domestication bottleneck (humongous growth to at least 300K but maybe as much as 1E9, citation).

Being a crop species that is incredibly useful to humans (lots of citations and examples of usage), there is also a wealth of knowledge on quantitative traits. will need to explain rare alleles pops and experiment some (PGRP15 grant)

This system thus serves as a great resource to compare the effects of this history on the genome in maize versus its extant, wild ancestor teosinte, particularly to investigate how the genetic architecture of these important traits may have evolved differently as a result of this combination of demography and selection.

0.1 Obj 1 - Estimate the Distribution of Fitness Effects (DFE)

using teosinte genomes

- from polymorphism/divergence data. use HapMap2 or current teosinte genomes (I think I'd vote for latter) <http://goo.gl/CLmsmX> and <http://www.genetics.org/content/177/4/2251.short>) can either use estimated demographic model or use noncoding sites to normalize SFS

Methods: estimate the DFE using Eyre-Walker's DoFE http://www.lifesci.susx.ac.uk/home/Adam_Eyre-Walker/Website/Software.html

can validate by comparing to GERP distribution partitioning variance components, e.g. <http://www.ncbi.nlm.nih.gov/pubmed/25439723> GREML software

useful because the distribution of mutation effect sizes is not generally known, and is especially difficult for small effect mutations. objective 1 will inform perhaps what the DFE may look like in any organism with a history similar to teosinte? and just in general add to the body of literature on genetic architecture, mutation effects

0.2 Obj 2 - Simulate scenarios of different traits.

from objective 1 we now know the DFE of teosinte we already know the demographic history of maize since its split from teosinte (citations)

use the DFE results to parameterize a model that will simulate the evolution of maize and its genetic architecture through time during and since its domestication we can simulate maize that expanded into S America separately since it has a different demography and then compare any differences the regions may show in the end simulate traits w/ varying correlation with fitness new mutation effects on fitness determined by DFE, effect on trait by correlation between trait and fitness

Methods: fwdpy (python version of fwdpop, cite <http://www.genetics.org/content/198/1/157.abstract>), allows simultaneous generation of complex demography, natural selection, and quantitative phenotypes, including deleterious mutations and their effect on phenotype

evaluate: how many loci contribute to important traits? how strong are these effects? how do details of demography impact outcome? test against theory e.g <http://arxiv.org/abs/1312.3028>

standing questions: does the DFE significantly change in a meaningful way or a certain direction? mean value the same but narrower or wider distribution? skewed more one way or the other? might expect this to be a different answer for maize in S America vs Central since S America has had a second bottleneck, so more founder effects and more chance for drift

(could also do some broader simulated examples just to stand alone and see if other various outcomes may occur - just don't plan on comparing these to any real data)

0.3 Obj 3 - compare simulation results to modern maize genomes, known to have undergone the same demographies simulated in objective 2

compare to GWAS for maize/teo. do we recapitulate observations? several traits are genotyped/phenotyped in maize/teosinte If the estimated demographic model and DFE are reasonable, the genetic ar-

note to self, update the data description

this part prob not in proposal:

yes, once we can show we can recapitulate real data, i think this is useful

chitecture of simulated phenotypes should closely mimic that of real data. are there differences between central and southern American pops?

Methods: same DoFE approach in C American maize pops for direct comparison in S American pops, can do comparison on subset, e.g. GERP, which we would have from Obj 1 if we compare to other approaches for the sort of validation of the DFE (definitely worth doing if b/c of 2nd bottleneck more deleterious stuff rose in frequency and was then eliminated)

If the real data differ from simulation, we can explore the sensitivity of genetic architecture to changes to the demography or DFE; understanding this sensitivity will then lead to improved estimation of these important parameters.

C. Training Objectives

Hmmm, seems somewhat related to D, need to differentiate and write more about training here, may lead to changes in D.

D. Career Development & Future Research

My career goal is to become an independent, academic researcher who is able to push the boundaries of population genetics and evolutionary biology. As I have in my dissertation research, I aim to study population genetic and genomic processes both empirically from real work data and theoretically through simulations. I believe one of the strongest ways to advance our knowledge is through such comparisons of situations where every parameter, current and historical, is known, as well as the evolutionary outcome (simulations) to natural situations where processes or effects that are poorly understood or still unknown to us can diverge from theoretical expectations and provide the basis for further study and investigation into these processes.

The skills I will develop during this fellowship will benefit my career and put me on the cutting edge for analyses of the newest genomic data and the most recent computational approaches for biological simulations. First, I will gain many skills related to genomic data analysis throughout the course of this research. I have minimal exposure and experience directly working with such data from my dissertation, thus making this a vital opportunity. Genomic technology and data are growing at an incredibly fast pace, and working directly with such data will teach me the most up to date, accurate, and efficient approaches. I will also improve my skills of computational biology through the proposed simulations and be able to learn a new and useful programming language used widely in evolutionary biology, Python. Drs. Ross-Ibarra and Thornton are both at the forefront of a popular movement for open science, making all stages of the research process transparent to any interested parties, and providing products such as data and code immediately and publicly. This is a work ethic I strongly agree with and hope to contribute to as an independent researcher. Our work together will better equip me with the tools and experience that make open science easy, efficient, and profitable for all. Interacting with Drs. Ross-Ibarra and Thornton, as well as other researchers at UC Davis, on a regular basis will be both intellectually stimulating and rewarding experiences that will help me accomplish my career goals.

E. Sponsoring Scientists and Host Institution

The University of California Davis (UCD) is the ideal place to conduct the proposed research. UCD has a world-renowned program in evolutionary biology and faculty in population genetics who are at the top of the field. Jeff Ross-Ibarra is an expert on teosinte, maize, its domestication, and the associated population genetics and genomics of the system. Kevin Thornton is an accomplished

we have no GWAS data for S.Amer. pops, but do have genomes and GERP. we could get freq. etc. of del. mutations from sims and compare to GERP

think of better word?

Jeff, feel free to make that sound better

Likewise Kevin, feel free to modify

don't forget to fill in

quantitative geneticist and computational biologist who will also contribute greatly to this research. They will both serve as effective and capable mentors for my post-doctoral research. In particular, Jeff has been studying the maize/teosinte system for XXyears with a great network of collaborators providing vast resources of data. His work has contributed largely to our knowledge of this system, and more generally on domestication and adaptation as evolutionary processes. Kevin is also the developer and maintainer of fwdpy, the python package proposed for completing the simulations in Objective 2. He will thus serve as a great resource in terms of knowing the exact capabilities of the simulation method and any assumptions of its model that must be taken into account. Furthermore, the Department of Ecology and Evolution, the Department of Plant Biology, and the Department of Plant Sciences at UCD have many exceptional faculty doing research relevant to my interests, providing many research groups to interact with on a daily basis for potential collaborations or feedback on this research. For example, I look forward to interacting with scientists interested in population genetics, such as Graham Coop, and in adaptation, such as Johanna Schmitt. UCD has the necessary computing resources for our proposed work, and as described, vast sources of knowledge and experience on the topics I plan to investigate, ensuring the success of this work. I am excited to join and contribute to UCD's active and vibrant scientific community.

F. Milestones & Timeline

want to do the DFE of maize and teosinte at the same time? no reason we can't right, and then do the simulations. Though if it takes time, teosinte should be prioritized so the sims can be parameterized and started while the maize DFE is estimated

Year 1	accomplish this
Year 2	Finish stuff
Year 3	I don't think there is a year 3?

G. Broader Impacts

The proposed research will have wide-ranging impacts for both the public and the scientific community.

References Cited

- K. J. Gilbert and M. C. Whitlock. Evaluating methods for estimating local effective population size with and without migration. *Evolution*, 69(8):2154–2166, July 2015.

Biographical Sketch — Kimberly Julie Gilbert

A. Professional Preparation

Institution, Location	Major	Degree	Year
University of Virginia, USA	Biology	B.Sc.	2010
University of British Columbia, Canada	Zoology	Ph.D.	2016 (expected)

B. Publications

Five Publications Most Closely Related to the Proposed Project

1. **Gilbert KJ**, MC Whitlock (2015) Evaluating methods for estimating local effective population size with and without migration. *Evolution*, 68(8), 2154-2166.
2. **Gilbert KJ**, MC Whitlock (2015) Q_{ST} - F_{ST} comparisons with unbalanced half-sib designs. *Molecular Ecology Resources*, 15(2), 262-267.
3. Caplins SA, **KJ Gilbert**, C Ciotir, J Roland, SF Matter, N Keyghobadi (2014) Landscape structure and the genetic effects of a population collapse. *Proceedings of the Royal Society B*. 281: 20141798; doi: 10.1098/rspb.2014.1798
4. Keller SR, **KJ Gilbert**, PD Fields, DR Taylor (2012) Bayesian inference of a complex invasion history revealed by nuclear and chloroplast genetic diversity in the colonizing plant, *Silene latifolia*. *Molecular Ecology*, 21(19), 4721-4734.
5. Whitlock MC, **KJ Gilbert** (2012) Q_{ST} in a hierarchically structured population. *Molecular Ecology Resources*, 12(3), 481-483.

Four Other Significant Publications

1. Santiso X, L Lopez, **KJ Gilbert**, R Barreiro, MC Whitlock, R Retuerto (2015) Patterns of genetic variation within and among populations in *Arbutus unedo* and its relation with selection and evolvability. *Perspectives in Plant Ecology, Evolution and Systematics*, 17(3), 185-192.
2. Vines TH, RL Andrew, DG Bock, MT Franklin, **KJ Gilbert**, NC Kane, EJ Kleynhans, J-S Moore, BT Moyers, S Renaut, DJ Rennison, T Veen, S Yeaman (2013) Mandated archiving greatly improves access to research data. *FASEB Journal*, 27(4), 1304-1308.
3. **Gilbert KJ**, RL Andrew, DG Bock, MT Franklin, NC Kane, J-S Moore, BT Moyers, S Renaut, DJ Rennison, T Veen, TH Vines (2012) Recommendations for utilizing and reporting population genetic analyses: The reproducibility of genetic clustering using the program STRUCTURE. *Molecular Ecology*, 21(20), 4925-4930.
4. Vines TH, AYK Albert, RL Andrew, F Débarre, DG Bock, MT Franklin, **KJ Gilbert**, J-S Moore, S Renaut, DJ Rennison (2014) The availability of research data declines rapidly with age. *Current Biology*, 24, 94-97.

C. Select Conference Presentations (chosen from 11 presentations)

- 2015 Validating SNP loci underlying local adaptation in lodgepole pine; KJ Gilbert, S Yeaman, KE Lotterhos, KA Hodgins, H Suren, JA Holliday, S Nadeau, SN Aitken, MC Whitlock *Poster, 15th ESEB Congress, Lausanne, Switzerland*
- 2014 Evaluating methods for estimating effective population size in the presence of migration; KJ Gilbert & MC Whitlock *Oral presentation, Evolution, Raleigh, USA*
- 2012 Range expansion and adaptation across heterogeneous environments; KJ Gilbert & MC Whitlock *Poster, Evo-WIBO Conference (Evolutionary Biology in the Pacific Northwest), Port Townsend, USA*
- 2011 Inferred invasion history of *Silene latifolia* into North America utilizing population genetic data and approximate Bayesian computation; KJ Gilbert, SR Keller, PD Fields, DR Taylor *Poster, 13th Congress of the European Society for Evolutionary Biology, Tuebingen, Germany*

D. Grants and Awards

Cordula and Gunter Paetzold Fellowship UBC \$18,000CAD 2015 – 2016

maybe still want to change around which pubs go in 5 most important?

<i>Declined</i> ; Zoology Graduate Fellowship UBC \$11,000CAD	2015 – 2016
Ann and William Messenger Graduate Fellowship UBC \$700CAD	2015
Zoology Graduate Fellowship UBC \$11,000CAD	2014 – 2015
Frieda Granot Graduate Scholarship in Interdisciplinary Research UBC \$200CAD	2013 – 2014
Theodore E Arnold Fellowship UBC \$7,750CAD	2013 – 2014
Patrick David Campbell Graduate Fellowship UBC \$8,050CAD	2013 – 2014
<i>Declined</i> ; Zoology Graduate Fellowship UBC \$10,000CAD	2013 – 2014
BRITE Fellowship UBC \$10,500CAD <i>per annum</i>	2011 – 2013

E. Synergistic Activities

1. **Working Groups:** Participated in the NESCent Reproducible Science Hackathon (2014), a 21-member working group aimed at developing a curriculum and workflow for teaching reproducible science to researchers of any background. Participated in the SimBank NESCent Catalysis Meeting (2014) which was a 25-member working group to create a collection of openly available simulation results to facilitate testing of statistical population genetic and phylogeographic methods.
2. **Teaching:** Teaching assistant for Fundamentals of Evolutionary Biology (Fall 2012-Spring 2013) where I taught three sections per term of 45 students each and lead discussion-based tutorials. Teaching assistant for Fundamentals of Biostatistics (Fall 2013, 2014, 2015). Taught two sections of 70 students total in 2013, and in 2014 and 2015 served as the lab coordinator for 254 and 276 students enrolled in the course, respectively, while teaching one section of 36 and 35 students respectively.
3. **Service:** Served as a Graduate Student Council Member for the American Society of Naturalists (2013-2016, chair 2015-2016). Served as the graduate student representative on the 2014 evolutionary biology CRC2 job search for the Department of Zoology, University of British Columbia. Organize the Biodiversity Research Centre's weekly evolution discussion group (2014-2016), for students, post-docs, and faculty from the departments of Zoology, Botany, Forestry, and Fisheries to discuss current papers in evolutionary biology. Reviewer for *Molecular Ecology Resources*, *Ecology and Evolution*, *Tree Genetics & Genomes*.
4. **Outreach:** Volunteer mist-netting and bird banding with local Vancouver non-profit organization Wild Research (2013-2015) where I participated in winter, spring migration, and fall migration bird monitoring at Iona Island Bird Observatory, taught volunteers proper bird handling, aging, data collection, and mist net extraction techniques, and assisted in educating public visitors to the station about the species conservation and monitoring, and the general tasks of running a banding station.

F. Collaborators (Total: 25)

U Alberta Jens Roland; *U Basel* Peter Fields; *U British Columbia* Dan Bock, Diana Rennison; *U Calgary* Sam Yeaman; *UC Davis* Serena Caplins; *U Cincinnati* Stephen Matter; *CIRB Paris* Florence Débarre; *Colorado State* Brook Moyers; *U Colorado* Nolan Kane; *U Coruna* Rodolfo Barreiro, Lúa López; *Kwantlen Polytechnic U* Michelle Franklin; *U Laval* Jean-Sébastien Moore; *Mol. Ecol. Managing Editor* Timothy Vines; *U Montreal* Sébastien Renaut; *U New England (Australia)* Rose Andrew; *UT Austin* Thor Veen; *Trent U* Claudia Ciotir; *U Santiago de Compostela* Rubén Retuerto Franco; *Xabier Santiso*; *U Vermont* Stephen Keller; *U Virginia* Douglas Taylor; *Western U* Nusha Keyghobadi; *Women's Health Research Institute* Arianne Albert

Graduate Advisor (Total: 1) *University of British Columbia* Michael C. Whitlock

Biographical Sketch — Jeffrey Ross-Ibarra

1 Professional Preparation

Institution	Area	Degree / Training	Dates
University of California Riverside	Botany	BA, MS	1998, 2000
University of Georgia	Genetics	PhD	2006
University of California Irvine	Genetics	Postdoctoral Research	2008

2 Professional Appointments

Position	Institution	Dates
Associate Professor	University of California Davis	2012-present
Assistant Professor	University of California Davis	2009-2012
Profesor de Asignatura	Universidad Nacional Autónoma de México	2001

3 Products

Most Relevant to the Proposed Research

- Mezouk S, **Ross-Ibarra J** (2014) The pattern and distribution of deleterious mutations in maize. (2014) *G3* 4:163-171
- Hufford MB, Xun X, van Heerwaarden J, Pyhäjärvi T, Chia J-M, Cartwright RA, Elshire RJ, Glaubitz JC, Guill KE, Kaeppler S, Lai J, Morrell PL, Shannon LM, Song C, Springer NM, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Ware D, Buckler ES, Yang S, **Ross-Ibarra J** (2012) Comparative population genomics of maize domestication and improvement. *NATURE GENETICS* 44:808-811
- Cook JP, McMullen MD, Holland JB, Tian F, Bradbury P, **Ross-Ibarra J**, Buckler ES, Flint-Garcia SA (2012) Genetic architecture of maize kernel composition in the Nested Association Mapping and Inbred Association panels. *PLANT PHYSIOLOGY* 158: 824-834
- van Heerwaarden J, Doebley J, Briggs WH, Glaubitz JC, Goodman MM, Sánchez González JJ, **Ross-Ibarra J** (2011) Genetic signals of origin, spread and introgression in a large sample of maize landraces. *PNAS* 108: 1088-1092
- **Ross-Ibarra J**, Tenaillon M, Gaut BS (2009) Historical divergence and gene flow in the genus *Zea*. *GENETICS* 181: 1399-1413.

Additional Products

- Gerke JP, Edwards JW, Guill KE, **Ross-Ibarra J**, McMullen MD (2015) The genomic impacts of drift and selection for hybrid performance in maize. *GENETICS In Press*
- Takuno S, Ralph P, Swarts K, Elshire RJ, Glaubitz JC, Buckler ES, Hufford MB, and **Ross-Ibarra J** (2015) Independent molecular basis of convergent highland adaptation in maize. *GENETICS* 200:1297-1312
- Wills DM, Whipple C, Takuno S, Kursel LE, Shannon LM, **Ross-Ibarra J**, Doebley JF (2013) From many, one: genetic control of prolificacy during maize domestication. *PLOS GENETICS* 9(6): e1003604.
- Studer A, Zhao Q, **Ross-Ibarra J**, Doebley J (2011) Identification of a functional transposon insertion in the maize domestication gene *tb1*. *NATURE GENETICS* 43:1160-1163.

- Gore MA, Chia JM, Elshire RJ, Sun Q, Ersoz ES, Hurwitz BL, Peiffer JA, McMullen MD, Grills GS, **Ross-Ibarra J**, Ware DH, Buckler ES (2009) A first-generation haplotype map of maize. *SCIENCE* 326: 1115-1117.

4 Synergistic Activities

- Faculty Development Award in recognition of university service, 2015
- Editor, G3, PeerJ, Axios Reviews
- DuPont Young Professor 2012-2014 and faculty advisor DuPont Pioneer graduate student symposium in plant breeding 2012-present
- Functional Genetics of Maize Centromeres US-Mexico exchange program, 2011-present
- Presidential Early Career Award for Scientists and Engineers 2009

5 Collaborators and Other Affiliations

Collaborators and Co-editors (Total: 56)

Cornell U Peter Bradbury, Jeffrey Glaubitz, Susan McCouch, Qi Sun, Feng Tian, Sharon Mitchell; *USDA-ARS* Edward Buckler, Sarah Hake, James Holland, Sherry Flint-Garcia, Mike McMullen, Doreen Ware, Jode Edwards; *U Southern California* Peter Ralph; *UC Davis* Alan Bennet, Daniel Runcie, Ed Taylor, Graham Coop, Keith Bradnam, Ian Korf, David Neale, Amélie Gaudin; *UC Irvine* Kevin Thornton; *Carnegie Institute* Davide Sosso; *Stanford* Wolf Frommer; *LANGEBO* Ruairidh Sawers; *U Georgia* Kelly Dawe; *Arizona State* Reed Cartwright; *U Missouri* James Birchler, Katherine Guill, David Wills; *Beijing Genomics Institute* Song Chi, Xun Xu; *U Wisconsin* John Doebley, Jiming Jiang, Shawn Kaeppler; *Syngenta* William Briggs; *Monsanto* Lisa Kanizay; *Dupont Pioneer* Andy Baumgarten, Justin Gerke, Oscar Smith, Tabare Abadie; *U Minnesota* Roman Briskine, Peter Morrell, Chad Myers, Nathan Springer, Peter Tiffin; *MIT* Mary Gehring; *NC State* Major Goodman; *INRA* Clementine Vitte, Maud Tenaillon; *Brigham Young* Clinton Whipple; *Danforth Center* Anthony Studer; *Universidad de Guadalajara* Jesus Sánchez González; *Iowa State* Carolyn Lawrence; *U Hawaii* Gernot Presting; *UC Riverside* Mitchell Provance

Graduate Advisors and Postdoctoral Sponsors (Total: 3)

UC Riverside Norman Ellstrand; *U Georgia* James Hamrick; *UC Irvine* Brandon Gaut

Thesis Advisor and Postgraduate Sponsor (Total: 14)

Postdoctoral: *Iowa State* Matthew Hufford; *Graduate U Advanced Studies* Shohei Takuno; *U Oulu* Tanja Pyhäjärvi, *KWS* Sofiane Mezmouk; *Wageningen* Joost van Heerwaarden; *USDA* Tim Beissinger; *UC Davis* Kate Crosby, Sayuri Tsukahara, Simon Renny-Byfield, Jinliang Yang **Graduate:** Dianne Velasco, Paul Bilinski, Anna O'Brien, Michelle Stitzer

Biographical Sketch — Kevin Richard Thornton

6 Professional Preparation

Institution	Area	Degree / Training	Dates
University of Puget Sound	Botany	BA	1997, 2000
University of Chicago	Genetics	PhD	2003
Cornell University	Genetics	Postdoctoral Research	2007

7 Professional Appointments

Position	Institution	Dates
Associate Professor	University of California Irvine	2012-present
Assistant Professor	University of California Irvine	2007-2012

8 Products

Most Relevant to the Proposed Research

- **Thornton, K. R.** (2014) A C++ template library for efficient forward-time population genetic simulation of large populations. *Genetics* 98:157-166 PMID: 24950894
- **Thornton, K.** (2003) libsequence, a C++ class library for evolutionary genetic analysis. *Bioinformatics* 19(17): 2325-2327 PMID 14630667
- **Thornton, K. R., A. J. Foran, and A. D. Long** (2013) Properties and modeling of GWAS when complex disease risk is due to non-complementing, deleterious mutations in genes of large effect. *PLoS Genetics* 9: e1003258. PMID 23437004

Additional Products

- Cridland, J. M., **K. R. Thornton** and A. D. Long (2015) Gene expression variation in *Drosophila melanogaster* due to rare transposable element insertion alleles of large effect. *Genetics* 199: 85-93.
- Baldwin-Brown, J., A. D. Long, and **K. R. Thornton** (2014) The Power to Detect Quantitative Trait Loci Using Resequenced, Experimentally Evolved Populations of Diploid, Sexual Organisms. *Molecular Biology and Evolution* 31: 1040-1055. PMID 24441104
- Open-source software: <http://molpopgen.github.io/fwdpp/>
- Open-source software: <http://molpopgen.github.io/libsequence/>

9 Synergistic Activities

- Open-source software: <http://molpopgen.github.io/fwdpy/> This software is unpublished, and will be a key resource for this proposal.
- Editor, G3

10 Collaborators and Other Affiliations

Collaborators and Co-editors (Total: 7)

- *Cornell University* Andrew G. Clark
- *North Carolina State University* Trudy Mackay
- *Princeton University* Peter Andolfatto
- *Rochester University* Daniel Garrigan, Daven C. Presgraves
- *UC Irvine* Anthony (Tony) Long
- *University of Kansas* Stuart MacDonald

Graduate Advisors and Postdoctoral Sponsors (Total: 2)

University of Chicago Manyuan Long
Cornell University Andrew G. Clark

Thesis Advisor and Postgraduate Sponsor (Total: 3)

Postdoctoral: Rebekah R. Rogers **PhD Thesis Advisor:** Julie M. Cridland, Jaleal S. Sanjak

Data Management Plan

Data Types

This proposal will generate genotype and full-genome sequence data, phenotype data, analytical code, germplasm, and publications.

Data Archiving, Plan for Sharing, Public Access Policy

Genotype and Sequence Data EDIT THIS WHOLE DOCUMENT

Dissertation Summary - Kimberly J. Gilbert

A major obstacle in evolutionary biology is the difficulty of population genetic inference in the face of confounding factors, such as demographic history. My dissertation work has focused on several topics related to this broad area of research:

1. Evaluating the ability of statistical genetic methods to estimate effective population sizes in the face of migration (Gilbert and Whitlock, 2015)
2. Assessing the factors related to local adaptation at range edges during species expansion
3. Validating SNP loci under selection for adaptation to climate in lodgepole pine (*Pinus contorta*)

Effective population size, N_e , is a fundamental parameter in population genetics, evolutionary biology, and conservation biology, yet its estimation can be fraught with difficulties. Several methods to estimate N_e from genetic data have been developed that take advantage of various approaches for inferring N_e . The ability of these methods to accurately estimate N_e , however, has not been comprehensively examined. This part of my dissertation work employed seven of the most cited methods for estimating N_e from genetic data (Colony2, CoNe, Estim, MLNe, ONeSAMP, TMVP, and NeEstimator including LDNe) across simulated datasets with populations experiencing migration or no migration. The simulated population demographies were an isolated population with no immigration, an island model metapopulation with a sink population receiving immigrants, and an isolation by distance stepping stone model of populations. We found considerable variance in performance of these methods, both within and across demographic scenarios, with some methods performing very poorly. The most accurate estimates of N_e can be obtained by using LDNe, MLNe, or TMVP; however each of these approaches is outperformed by another in a differing demographic scenario. Knowledge of the approximate demography of population as well as the availability of temporal data largely improves N_e estimates.

Species range edges have boundaries that cannot always be explained ecologically or geographically, which leaves the question of what evolutionary forces may prevent populations at range edges from adapting and expanding the species range further. A large body of theoretical work has investigated many evolutionary parameters' effects on local adaptation in edge populations, but one area lacking in research is that of the interaction of the landscape with the ability to locally adapt. This study investigates how more realistic, heterogeneous environmental gradients (compared to the linear gradients that previous studies investigate) may interact with dispersal distance and the effect size of mutations. I have simulated a range of parameter combinations that show a strong relation of mutation effect size on the ability to spread across the landscape. As environmental heterogeneity increases, migration load (reduction in fitness due to dispersal away from an area previously adapted to) increases, and local adaptation becomes more difficult, especially in smaller populations at the range edge, slowing the speed of expansion across the landscape.

A history of range expansion can confound many inferences that population genetics aims to understand. Identifying the loci that underlie traits contributing to local adaptation is one such inference that is a major goal in evolutionary biology today. The lodgepole pine (*Pinus contorta*) is a major timber tree in the Pacific Northwest which has a history of expansion post-glaciation, and either one or putatively a second glacial refugia from which this expansion occurred. Climate change is spurring foresters to plant trees for future harvest that will be best adapted to future climates for optimal yield, hence identifying loci underlying adaptation to climate change is a key goal. I am conducting a validation study of SNP loci identified through GWAS, genotype-environment association, and F_{ST} outlier tests to assess how often these methods may produce false positives as a result of population structure and spatial autocorrelation of genetic clines due to range expansion with gradients in environmental variables (i.e. temperature and precipitation). I have sampled a provenance trial (common garden study) in British Columbia to compare performance of populations from a range of native temperatures (MAT -3.7°C - 11°C) planted across test sites of varying temperature (MAT -1.4°C - 5°C) from which I will be able to test if predicted alleles do indeed show increased performance in mature, natural-grown trees.