

# The molecular basis of parallel adaptation to highland climate in domesticated maize

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**ABSTRACT** Parallel adaptation is defined as the independent evolution of multiple species/subpopulations to similar environments via adaptive mutations in the same locus. We investigate here the molecular basis of maize adaptation to highland climates in Mexico and South America using genome-wide SNP data. Taking advantage of archaeological data on the arrival of maize to the highlands, we infer demographic models for both populations, identifying evidence of a strong bottleneck and rapid expansion in South America. We use these models to then identify loci showing an excess of differentiation as a means of identifying putative targets of natural selection, and compare our results to expectations from recently developed theory on parallel adaptation. In spite of similar morphologies, we see limited evidence of selection on quantitative traits, and, consistent with predictions across a wide array of parameter space, we see few SNPs showing signs of parallel adaptation. Instead, we show that selection appears to have predominantly acted on standing genetic variation, and that introgression from wild teosinte populations appears to have played a role in adaptation in Mexican maize. We discuss the significance of these results in the context of the molecular basis of adaptation to new environments.

## Introduction

Parallel adaptation is a process in which multiple species or populations independently adapt to distinct regions with similar environments via mutations at the same loci (Wood *et al.* 2005; Arendt and Reznick 2008; Elmer and Meyer 2011). Evolutionary genetic analysis of a wide range of species has provided evidence for multiple pathways to parallel adaptation. One such route occurs when identical mutations arise independently and fix via natural selection in multiple populations. In humans, for example, malaria resistance due to mutations from Glu to Val at the sixth codon of the  $\beta$ -globin gene has arisen independently on multiple unique haplotypes (Curat *et al.* 2002; Kwiatkowski 2005). Parallel adaptation can also be achieved when different mutations arise within the same locus and produce similar phenotypic effects. Grain fragrance in rice appears

to have evolved along these lines, as populations across East Asia have similar fragrances resulting from at least eight distinct loss-of-function alleles in the *BADH2* gene (Kovach *et al.* 2009). Finally, parallel adaptation may arise from natural selection acting on standing genetic variation in an ancestral population. In the three-spined stickleback, natural selection has repeatedly acted to reduce armor plating in independent colonizations of freshwater environments. Adaptation in these populations occurred from standing variation at the *Eda* locus in marine populations (Colosimo *et al.* 2005).

We still know relatively little, however, about how common it is for parallel phenotypic evolution to be driven by parallel genetic changes or the relative frequencies of these different routes of parallel adaptation. Domesticated maize (*Zea mays* ssp. *mays*) provides an excellent opportunity to investigate the molecular basis of parallel adaptation. Maize was domesticated from the wild teosinte *Zea mays* ssp. *parviglumis* (hereafter *parviglumis*) in the lowlands of southwest Mexico ~9,000 years before present (BP) (Matsuoka *et al.* 2002;

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Piperno *et al.* 2009; van Heerwaarden *et al.* 2011). After domestication, maize spread rapidly across the Americas, reaching the lowlands of South America and the high altitudes of the Mexican Central Plateau by ~6,000 BP (Piperno 2006), and the Andean highlands ~2,000 years later (Perry *et al.* 2006; Grobman *et al.* 2012). The transition from lowland to highland habitats spanned similar environmental gradients in Mexico and South America (Figure S1) and presented a host of novel challenges that commonly, if not universally, accompany highland adaptation including reduced temperature, increased ultraviolet radiation, and reduced partial pressure of atmospheric gases (Körner 2007).

Common garden experiments in Mexico reveal that highland maize has successfully adapted to highland conditions (Mercer *et al.* 2008), and phenotypic comparisons between Mexican and South American populations are suggestive of parallel adaptation. Landraces from both populations share a number of phenotypes not found in lowland populations, including dense macrohairs (Wilkes 1977; Wellhausen *et al.* 1957), stem pigmentation (Wilkes 1977; Wellhausen *et al.* 1957), and biochemical response to UV radiation (Casati and Walbot 2005). Genetic analyses of maize landraces from across the Americas indicate that the two highland populations are independently derived from their respective lowland populations (Vigouroux *et al.* 2008; van Heerwaarden *et al.* 2011), so observed patterns of phenotypic similarity are not simply due to recent shared ancestry.

Although there are no wild relatives of maize in South America, the teosinte *Zea mays* ssp. *mexicana* (hereafter *mexicana*) is native to the highlands of central Mexico, where it is thought to have occurred since at least the last glacial maximum (Ross-Ibarra *et al.* 2009; Hufford *et al.* 2012a). Phenotypic differences between *mexicana* and *parviglumis* mirror those between highland and lowland maize (Lauter *et al.* 2004) and population genetic analyses of the two subspecies reveal evidence of natural selection associated with altitudinal differences between *mexicana* and *parviglumis* (Pyhäjärvi *et al.* 2013). Landraces in the highlands of Mexico are often found in sympatry with *mexicana*, and gene flow between the two is thought to have contributed to maize adaptation to the highlands (Hufford *et al.* 2013).

In this paper we set out to address a number of questions regarding highland adaptation in maize: What is the genetic architecture of highland adaptation? Do maize populations in the highlands of Mexico and South America show evidence of parallel adaptation? How do observed patterns of parallel adaptation compare to theoretical expectations? We make use of SNP genotyping to characterize patterns of natural selection in highland maize and compare our results to expectations from theoretical models of parallel adaptation. We find evidence supporting unique demographic histories in the highlands of Mexico and South America, a predominance of independent versus parallel adaptation, and contributions of standing variation and introgression from wild relatives to highland adaptation in

maize.

## Materials and Methods

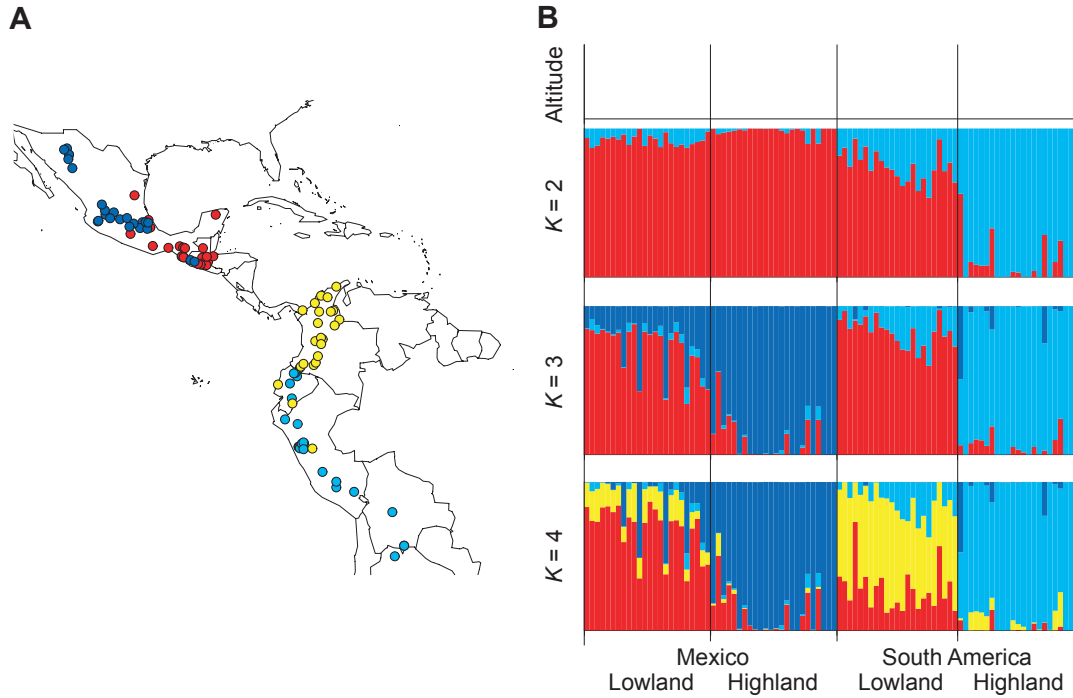
### Materials and DNA extraction

We included one individual from each of 94 open-pollinated landrace maize accessions from high and low elevation sites in Mexico and S. America (Table S1). Accessions were provided by the USDA germplasm repository or kindly donated by Major Goodman (North Carolina State University). Sampling locations are shown in Figure 1A (see also Table S1). Landraces sampled from altitudes <1,700 m were considered lowland, while accessions from >1,700 m were considered highland (Table S1). Seeds were germinated on filter paper following fungicide treatment and grown in standard potting mix. Leaf tips were harvested from plants at the five leaf stage. Following storage at -80°C overnight, leaf tips were lyophilized for 48 hours. Tissue was then homogenized with a Mini-Beadbeater-8 (BioSpec Products, Inc., Bartlesville, OK, USA). DNA was extracted using a modified CTAB protocol (Saghai-Marooft *et al.* 1984). The quality of DNA was ensured through inspection on a 2% agarose gel and quantification of the ratio of light absorbance at 260 and 280 nm using a NanoDrop spectrophotometer (Thermo Scientific, NanoDrop Products, Wilmington, DE, USA).

### SNP data

We generated two complementary SNP data sets for the sampled maize landraces. The first set was generated using the Illumina MaizeSNP50 BeadChip platform, including 56,110 SNPs (Ganal *et al.* 2011). SNPs were clustered with the default algorithm of the GenomeStudio Genotyping Module v1.0 (Illumina Inc., San Diego, CA, USA). Clustering for each SNP was then visually inspected and manually adjusted. These data are referred to as "MaizeSNP50" hereafter. MaizeSNP50 data have high reproducibility and a low proportion of missing data but are subject to ascertainment bias. This array contains SNPs discovered in five ascertainment schemes (Ganal *et al.* 2011); however, the vast majority of SNPs come from two panels: the Syngenta set (14,810 SNPs), derived from polymorphisms distinguishing the parents of the IBM population (the maize lines B73 and Mo17), and the Panzea set, including 40,594 SNPs identified during sequencing of the 25 parents of the NAM population.

The second data set was generated utilizing high-throughput Illumina sequencing data in a method referred to as genotyping-by-sequencing (GBS). **Kelly is up for details.** Average coverage was relatively low (XXX), likely resulting in heterozygotes often being miscalled as homozygotes. However, this data set is relatively free from ascertainment bias. GBS data were obtained for a subset of 87 of the landrace accessions (Table S1).



**Figure 1** (A) Sampling locations of landraces. Red, blue, yellow and light blue dots represent Mexico lowland, Mexico highland, S. America lowland and S. America highland populations, respectively. (B) Results of STRUCTURE analysis of the maizeSNP50 SNPs with  $K = 2 \sim 4$ . The top panel shows the altitude, ranging from 0 to 4,000 m on the y-axes. The colors in  $K = 4$  correspond to those in panel (A).

To assess data quality, we compared genotypes at the 7,197 SNPs that overlap between the MaizeSNP50 and GBS data sets. Excluding missing data, we compared 229,937 genotypes. While only 0.8% of 173,670 homozygous loci in the MaizeSNP50 data set differed from GBS genotypes, 88.6% of 56,267 MaizeSNP50 heterozygotes had different genotypes in the GBS data, being homozygous in nearly all cases. Despite an extremely high heterozygote error rate, our GBS data should be informative given the high correlation in allele frequencies between data sets ( $r = 0.89$ ; Figure SX **change after finishing intro and results**) and a lack of major allele or reference bias (data not shown).

For SNP annotations, we retrieved the filtered gene set from RefGen version 2 of the maize B73 genome sequence (Schnable *et al.* 2009; release 5b.60) from MaizeSequence.org. We excluded genes annotated as transposable elements (84) and pseudogenes (323) from the filtered gene set, resulting in a total of 38,842 genes.

### Structure analysis

We performed a STRUCTURE analysis (Pritchard *et al.* 2000; Falush *et al.* 2003) using synonymous and noncoding SNPs from the MaizeSNP50 data. We assumed free recombination between SNPs without missing data and randomly pruned SNPs closer than 10 kb (alternative distances were tried with nearly identical results). We excluded SNPs in which the num-

ber of heterozygous individuals exceeded homozygotes and where the  $P$ -value for departure from Hardy-Weinberg Equilibrium (HWE) based on a  $G$ -test was smaller than 0.5% using all individuals. Following these data thinning measures, 17,013 biallelic SNPs remained. We conducted three replicate runs of STRUCTURE using the correlated allele frequency model with admixture for  $K = 2$  through 6 populations, a burn-in length of 50,000 iterations and a run length of 100,000 iterations. Results across replicates were nearly identical.

### Demographic inference

We tested three demographic models in which maize was differentiated into high- and lowland populations subsequent to domestication (Figure 2). Observed joint frequency distributions (JFDs) were calculated using the GBS data set due to its lower level of ascertainment bias. A subset of silent SNPs were utilized that had  $\geq 15$  individuals without missing data in both low- and highland populations and did not violate HWE. A HWE cut-off of  $P < 0.005$  was used for each subpopulation due to our under-calling of heterozygotes. In total, we included 18,745 silent SNPs for the Mexican populations in Models IA and IB, 14,508 for the S. American populations in Model I and 11,305 for the Mexican lowland population and the S. American populations in Model II. We obtained similar results under more or less stringent thresholds for significance ( $P < 0.05 \sim 0.0005$ ; data not shown), though the number of



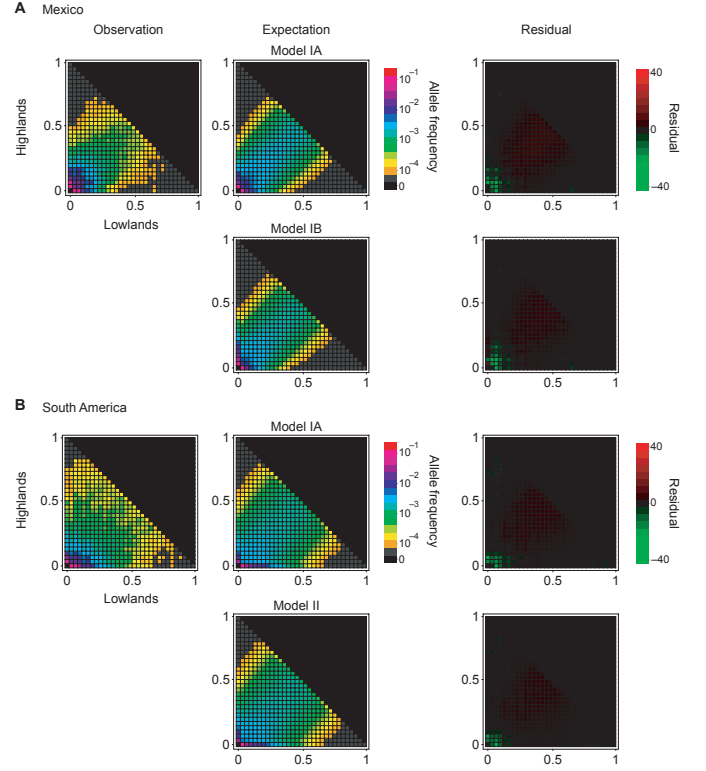
**Figure 2** Demographic models of maize low- and highland populations. Parameters in bold were estimated in this study. See text for details.

SNPs was very small at  $P < 0.05$ . Demographic parameters were inferred using the software *dadi* (Gutenkunst *et al.* 2009), which uses a diffusion method to calculate an expected JFD and evaluates the likelihood of the data using a multinomial assumption.

**Model IA:** This model is applied to the Mexico and S. America populations. We assume the ancestral diploid population representing *parviglumis* follows a standard Wright-Fisher model with constant size. The size of the ancestral population is denoted by  $N_A$ . At  $t_D$  generations ago, the bottleneck event begins at domestication, and at  $t_E$  generations ago, the bottleneck ends. The population size and duration of the bottleneck are denoted by  $N_B$  and  $t_B = t_D - t_E$ , respectively. The population size recovers to  $N_C = \alpha N_A$  in the lowlands. Then, the highland population is differentiated from the lowland population at  $t_F$  generations ago. The size of the low- and highland populations at time  $t_F$  is determined by a parameter,  $\beta$  such that the population is divided by  $\beta N_C$  and  $(1-\beta)N_C$ . We assume that the population size in the lowlands is constant but that the highland population experiences exponential expansion after divergence: its current population size is  $\gamma$  times larger than that at  $t_F$ .

**Model IB:** We expand Model IA for the Mexico populations by incorporating admixture from *mexicana* to the highland Mexican population. The time of differentiation between *parviglumis* and *mexicana* occurs at  $t_{mex}$  generations ago. The size of the *mexicana* population is denoted by  $N_{mex}$  and this size is assumed to be constant. At  $t_F$  generations ago, the Mexico highland population is derived from the Mexico lowland population and admixture with *mexicana*. The proportion of admixture with *mexicana* is denoted by  $P_{mex}$ .

**Model II:** The final model is for the Mexican lowland, S.



**Figure 3** Observed and expected joint distributions of minor allele frequencies in low- and highland populations in (A) Mexico and (B) S. America.

American lowland and highland populations. This model was used for simulating SNPs with ascertainment bias (see below). At time  $t_F$ , the Mexican and S. American lowland populations are differentiated, and the sizes of populations after splitting are determined by  $\beta_1$ . At time  $t_G$ , SA lowland and highland populations are differentiated, and the sizes of populations at this time are determined by  $\beta_2$ . As in Model IA, the S. American highland population is assumed to experience population growth with the parameter,  $\gamma$ .

Estimates of a number of our model parameters were available from previous work.  $N_A$  was determined using estimates of the composite parameter  $4N_A\mu$  and a separate estimate of mutation rate,  $\mu$ , per site per generation.  $4N_A\mu$  was estimated in *parviglumis* to be  $\sim 0.018$  (Eyre-Walker *et al.* 1998; Tenailon *et al.* 2001, 2004; Wright *et al.* 2005; Ross-Ibarra *et al.* 2009). The mutation rate in maize has been estimated to be  $2.9 \sim 3.3 \times 10^{-8}$ , so we assume  $\mu = 3 \times 10^{-8}$  (Clark *et al.* 2005). Thus,  $N_A$  was set to  $0.018/4/(3 \times 10^{-8}) = 150,000$ . The severity of the domestication bottleneck is represented by  $k = N_B/t_B$  (Eyre-Walker *et al.* 1998; Wright *et al.* 2005), and following Wright *et al.* (2005) we assumed  $k = 2.45$  and  $t_B = 1,000$  generations. Taking into account archaeological evidence (Piperno *et al.* 2009), we assume  $t_D = 9,000$  and

$t_E = 8,000$ . We further assumed  $t_F = 6,000$  for Mexican populations in Models IA and II (Piperno 2006),  $t_F = 4,000$  for S. American populations in Model II (Perry *et al.* 2006), and  $t_{mex} = 60,000$ ,  $N_{mex} = 160,000$  (Ross-Ibarra *et al.* 2009), and  $P_{mex} = 0.2$  (van Heerwaarden *et al.* 2011) for Model IB. For both Models IA and IB, we inferred three parameters ( $\alpha$ ,  $\beta$  and  $\gamma$ ), and, for Model II, we fixed  $t_F = 6,000$  and  $t_G = 4,000$  (Piperno 2006; Perry *et al.* 2006) and estimated the remaining four parameters ( $\alpha$ ,  $\beta_1$ ,  $\beta_2$  and  $\gamma$ ).

### Differentiation between low- and highland populations

We used our inferred demographic model to generate a null distribution of  $F_{ST}$  via simulation using the software **ms** (Hudson 2002). The command line options for **ms** are provided in Table S4. Generating the null distribution of differentiation for the MaizeSNP50 data requires accounting for ascertainment bias. Evaluation of genetic clustering in our data (not shown) coincides with previous work (Hufford *et al.* 2012b) in suggesting that the two lines most important in the ascertainment panel are most closely related to Mexican lowland maize. We thus added two additional individuals to the Mexican lowland population and generated our null distribution using only SNPs for which the two individuals had different alleles. For model IA in S. America we added two individuals at time  $t_F$  to the ancestral population of the S. American low- and highland populations because the Mexican lowland population was not incorporated into this model. For each combination of sample sizes in low- and highland populations, we generated  $10^7$   $F_{ST}$  values and used these as a null distribution in order to evaluate our data. We calculated  $F_{ST}$  values for all SNPs that had  $\geq 10$  individuals with no missing data in all four populations and showed no departure from HWE at the 0.5% (GBS) or 5% (MaizeSNP50) level.

### Haplotype scoring test

We performed a pairwise haplotype scoring (PHS) test to detect further evidence of selection, following Toomajian *et al.* (2006). To conduct this test, we first imputed and phased the combined SNP data (both GBS and MaizeSNP50) using the **fastphase** software version 1.4.0 (Scheet and Stephens 2006). As a reference for phasing, we used data (excluding heterozygous SNPs) from an Americas-wide sample of 23 partially inbred landraces that were included in the Hapmap v2 data set (Chia *et al.* 2012). **fastphase** was run with default parameter settings. PHS was calculated for an allele  $A$  at position  $x$  by

$$PHS_{xA} = \sum_{i=1}^{p-1} \sum_{j=i+1}^p Z_{ijx} / \binom{p}{2} - \sum_{i=1}^{n-1} \sum_{j=i+1}^n Z_{ijx} / \binom{n}{2}, \quad (1)$$

where  $n$  is sample size of haploids,  $p$  is the number of haploids carrying the allele  $A$  at position  $x$ , and

$$Z_{ijx} = \frac{d_{ijx} - \bar{d}_{ij}}{\sigma_{ij}}, \quad (2)$$

where  $d_{ijx}$  is the genetic distance over which individuals  $i$  and  $j$  are identical surrounding position  $x$ ,  $\bar{d}_{ij}$  is the genome-wide mean of distances over which individuals are identical, and  $\sigma_{ij}$  is the standard deviation of the distribution of distances. The  $P$ -value for an allele  $A$  with frequency  $p$  at position  $x$  was calculated such that  $\Pr(PHS_{xA} \leq PHS_{null|p})$ , where  $PHS_{null|p}$  are the PHS values for all alleles with frequency  $p$  across the genome.

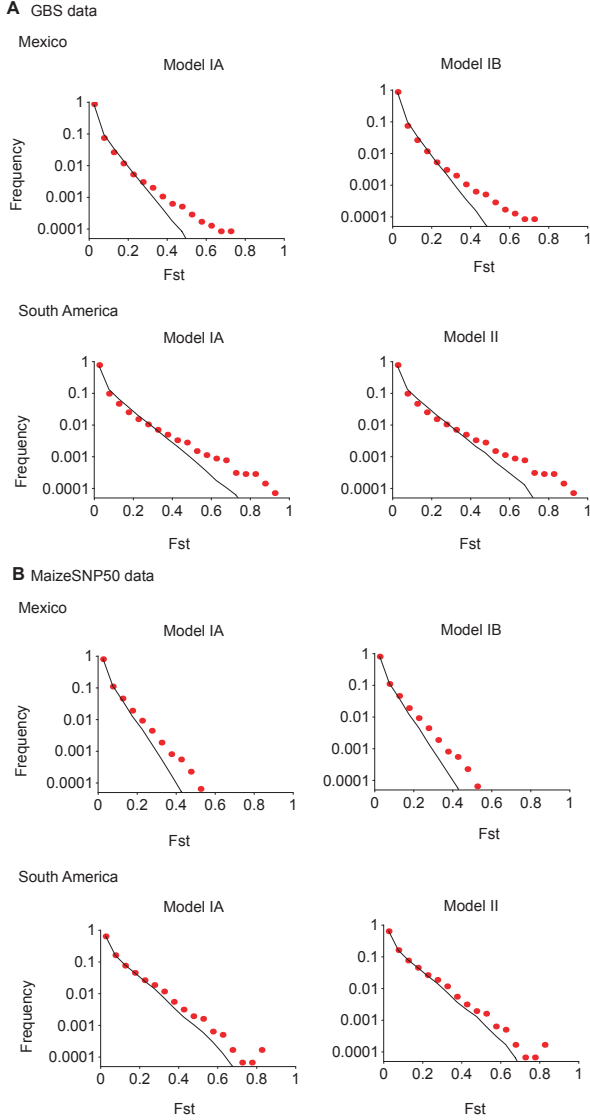
Genetic distances were obtained from the IBM population (Ganal *et al.* 2011). While genetic positions were initially only available for the MaizeSNP50 data set, we fit genetic (cM) and physical (bp) distances to a tenth degree polynomial curve, and calculated cM for all SNPs.

### Theoretical evaluation of parallel adaptation

We suggest below that many of the high- $F_{ST}$  alleles are locally adaptive, and the degree of coincidence between highland regions informs us about whether these adaptations occurred in parallel, or if alleles were transmitted between the two by migration. To see if the abundance and degree of coincidence is consistent with what is known about the population history of maize, we evaluated the rate at which we expect an allele that provides a selective advantage at higher altitude to arise by new mutation in a highland region ( $\lambda_{mut}$ ), and the rate at which such an allele already present in the Mexican highlands would transit the intervening lowlands and fix in the Andean highlands ( $\lambda_{mig}$ ). In each case we assume alleles adapted in the highlands are slightly deleterious at lower altitude. This assumption is consistent with empirical findings in reciprocal transplants of highland and lowland maize in Mexico (Mercer *et al.* 2008). These numbers depend most strongly on the population density, the selection coefficient, and the rate at which seed is transported long distances and replanted. We evaluated these rates using new and existing theory, and validated by simulation. Here we describe the mathematical details; readers may skip to the results without loss of continuity.

To calculate the rate at which new mutations appear and fix in a highland population,  $\lambda_{mut}$ , we multiplied the total population size of the highlands by the mutation rate per generation. To do this, we followed van Heerwaarden *et al.* (2010) in constructing a detailed demographic model for domesticated maize. Fields of  $N = 10^5$  plants are replanted each year from  $N_f = 561$  ears, either from completely new stock (with probability  $p_e = 0.068$ ), from partially new stock (a proportion  $r_m = 0.2$  with probability  $p_m = 0.02$ ), or entirely from the same field otherwise. Each plant is seed parent to all kernels of its own ears, but can be pollen parent to kernels in many





**Figure 4** Observed and expected distributions of  $F_{ST}$  values in GBS (A) and MaizeSNP50 data (B). The x-axes represent  $F_{ST}$  values. The y-axes represent the frequency of SNPs with  $F_{ST}$  values within a bin of 0.05 size. Red dots and solid lines indicate observed and expected distributions.

other ears; a proportion  $m_g = 0.0083$  of the pollen-parent kernels are in other fields. Wild-type plants have an average of  $\mu_E = 3$  ears per plant, and ears have an average of  $N/N_f$  kernels; each of these numbers are Poisson distributed. The mean number of pollen-parent kernels, and the mean number of kernels per ear, is assumed to be  $(1 + s_b)$  times larger for individuals heterozygous for the selected allele. Migration is mediated by seed exchange – when fields are replanted, the seed is chosen from a random distance away with mean  $\sigma_s = 50\text{km}$ , but plants only pollinate other plants belonging to the same village (distance 0). Each individual can have offspring in three cat-

egories: local seed, local pollen, and migrant seed; the mean numbers of each of these are determined by the condition that the population is stable (so wild-type, diploid individuals have on average 2 offspring) except that heterozygotes have on average  $(1 + s_b)$  offspring that carry the selected allele. Each ear has a small chance of being chosen for replanting, so the number of ears replanted of a given individual is Poisson, and assuming that pollen is well-mixed, the number of pollen-parent kernels is Poisson as well. Each of these numbers of offspring has a mean that depends on whether the field is replanted with new stock, and whether ears are chosen from this field to replant other fields, so the total number of offspring is actually a mixture of Poissons; these means, and more details of the computations, are found in Appendix 1.

At these parameter values, we compute that the variance in number of offspring,  $\xi^2$ , is between 20 (for wild-type) and 30 (for  $s_b = 0.1$ ), and the dispersal distance (mean distance between parent and offspring) is  $\sigma = 1.8\text{km}$ .

The rate at which new mutations appear and fix in a highland population, which we denote  $\lambda_{\text{mut}}$ , is equal to the total population size of the highlands, multiplied by the mutation rate per generation and by the chance that a single such mutation successfully fixes (i.e. is not lost to drift). The latter probability, that a single new mutant allele providing benefit  $s_b$  to heterozygotes at high elevation will fix locally in the high elevation population, is approximately  $2s_b$  divided by the variance in offspring number (Jagers 1975). The calculation above is not quite correct, as it neglects migration across the altitudinal gradient, but exact numerical calculation of the chance of fixation of a mutation as a function of the location where it first appears indicates that the approximation is quite good (see figure 1); for theoretical treatment see Pollak (1966) or Barton (1987).

Concretely, the probability that a new mutation destined for fixation will arise in a patch of high-elevation habitat of area  $A$  in a given generation is a function of the density of maize per unit area  $\rho$ , the selective benefit  $s_b$  it provides, the mutation rate  $\mu$ , and the variance in offspring number  $\xi^2$ . In terms of these parameters, the rate of appearance is

$$\lambda_{\text{mut}} = \frac{2\mu\rho A s_b}{\xi^2}. \quad (3)$$

A corresponding expression for the chance that an allele moves from one highland population to another is harder to intuit, and is addressed in more depth in (Ralph and Coop 2013). If an allele is beneficial at high elevation, and fixed in the Mexican highlands, but deleterious at low elevations, then it will be present at low frequency in nearby lowland populations, maintained at migration-selection balance (Slatkin 1973). This equilibrium frequency decays exponentially with distance, so that the highland allele is present at distance  $R$  from the highlands at frequency  $C \exp(-R\sqrt{2s_m}/\sigma)$ , where  $s_m$  is the deleterious selection coefficient for the allele in low elevation,  $\sigma$  is the mean dispersal distance, and  $C$  is a constant depending on geography ( $C \approx 1/2$  is close). Multiplying this fre-

**Table 1 Silent site  $F_{ST}$  from GBS SNPs**

		Mexico		South America	
		Lowlands	Highlands	Lowlands	Highlands
Mexico	Lowlands	–			
	Highlands	0.0244	–		
SA	Lowlands	0.0227	0.0343	–	
	Highlands	0.0466	0.0534	0.0442	–

quency by a population size gets the predicted number (average density across a large number of generations) of individuals carrying the allele in that population. Therefore, in a lowland population of size  $N$  at distance  $R$  from the highlands,  $(N/2) \exp(-R\sqrt{2s_m}/\sigma)$  is equal to the probability that there are any highland alleles present, multiplied by the expected number of these, given that there are some present. Since the latter is at least 1, the chance there are any present in a given generation is no more than  $(N/2) \exp(-R\sqrt{2s_m}/\sigma)$ , and so this puts an upper bound on  $\lambda_{\text{mig}}$ . Therefore, we would need to wait  $T_{\text{mig}} = (2/N) \exp(R\sqrt{2s_m}/\sigma)$  generations for a rare such excursion to occur. In other words, we can bound the rate of migration by

$$\lambda_{\text{mig}} \leq (N/2) \exp(-R\sqrt{2s_m}/\sigma), \quad (4)$$

with  $N$  the total size of the unadapted highland population, and  $R$  the distance from the adapted to the yet-unadapted highland populations. This also omits the probability that such an allele fixes ( $\approx 2s_b/\xi^2$ ), but since such alleles arrive by migration, this omission is unlikely a large effect and is conservative.

To obtain specific predictions, we then computed  $\lambda_{\text{mut}}$  and  $\lambda_{\text{mig}}$  at various parameter values. We also checked these with simulations and more detailed computations, described in the Appendix.

## Results and Discussion

### Samples and data

**for PLoS G** We generated a large set of SNPs in 94 maize accessions that were sampled from the Americas (Table S1; Materials and Methods). These accessions were sampled from the four populations: the lowlands of Mexico/Guatemala ( $n = 24$ ) and northern South America ( $n = 23$ ) and the highlands of the Mexican Central Plateau ( $n = 24$ ) and the Andes ( $n = 23$ ). The SNPs were generated by the two high-throughput methods: genotyping-by-sequencing (GBS) method and MaizeSNP50 Beadchip platform (Materials and Methods). We hereafter refer to the two SNP data sets as “GBS” and “MaizeSNP50”. We used a part of samples ( $n = 87$ ) for generating GBS data, **which is due to computational limitation?**. In total, we obtained 91,779 SNPs after filtering by Hardy-Weinberg criteria with sample size  $\geq 10$  in all the four populations (see Materials and Methods), 67,828 and 23,951 of which were generated by

GBS and MaizeSNP50, respectively. We performed population genomic analyses using these data sets to reveal the molecular basis of parallel highland adaptation in maize.

Our sample included 94 maize landraces from four distinct regions in the Americas: the lowlands of Mexico/Guatemala ( $n=24$ ) and northern South America ( $n=23$ ) and the highlands of the Mexican Central Plateau ( $n=24$ ) and the Andes ( $n=23$ ). Samples were genotyped using the MaizeSNP50 Beadchip platform ( $n=94$ ) and a method referred to as genotyping-by-sequencing (GBS;  $n=87$ ).

### Population structure

We performed a STRUCTURE analysis (Pritchard *et al.* 2000; Falush *et al.* 2003) of our landrace sample, varying the number of groups from  $K = 2 \sim 6$  (Figure 1, Figure S2). Most landraces were assigned to groups consistent with *a priori* population definitions, but admixture between highland and lowland populations was evident at intermediate elevations ( $\sim 1700\text{m}$ ). Consistent with previously described scenarios for maize diffusion (Piperno 2006), we find evidence of shared ancestry between lowland Mexican maize and both Mexican highland and S. American lowland populations. Pairwise  $F_{ST}$  among populations reveals low overall differentiation (Table ), and the higher  $F_{ST}$  values observed in S. America are consistent with decreased admixture seen in STRUCTURE. Archaeological evidence supports a more recent colonization of the highlands in S. America (Piperno 2006; Perry *et al.* 2006; Grobman *et al.* 2012), suggesting that the observed differentiation may be the result of a stronger bottleneck during colonization of the S. American highlands.

### Population differentiation under inferred demography

**Modified for PLoS G** To provide a null expectation for allele frequency differentiation, we used the joint site frequency distribution (JFD) of lowland and highland populations to estimate parameters of two demographic models (Figure 2; see Materials and Methods for details) using the maximum likelihood method implemented in *dadi* (Gutenkunst *et al.* 2009). All models incorporate domestication bottleneck (Wright *et al.* 2005) and population differentiation between lowland and highland populations. Model IA is common between Mexican and S. America populations. Model IB is specific to Mexican populations, into which we incorporated the admixture from *mexicana* to highlands. Model II is specific to S. America, which includes S. American populations and Mexican lowlands. We introduced the last model to simulate SNPs with ascertainment bias because the discovery panel would be originated from Mexican lowlands (see Materials and Methods for details).

Estimated parameter values are listed in Table ??; while the observed and expected JFDs were quite similar for both mod-

els, residuals indicated an excess of rare variants in the observed JFDs in all cases (Figure 3). Under both models IA and IB, we found expansion in the highland population in Mexico to be unlikely, but a strong bottleneck followed by population expansion is supported in S. American maize in both models IA and II. The likelihood value of model IB was higher than the likelihood of model IA by 850 units of log-likelihood (Table ??), consistent with analyses suggesting that introgression from *mexicana* played a significant role during the spread of maize into the Mexican highlands (Hufford *et al.* 2013).

In addition to the parameters listed in Figure 2, we investigated the impact of varying the domestication bottleneck size ( $N_B$ ). Surprisingly,  $N_B$  was estimated to be equal to  $N_C$ , the population size at the end of the bottleneck, and the likelihood of  $N_B < N_C$  was much smaller than for alternative parameterizations (Table ??, Table S2).

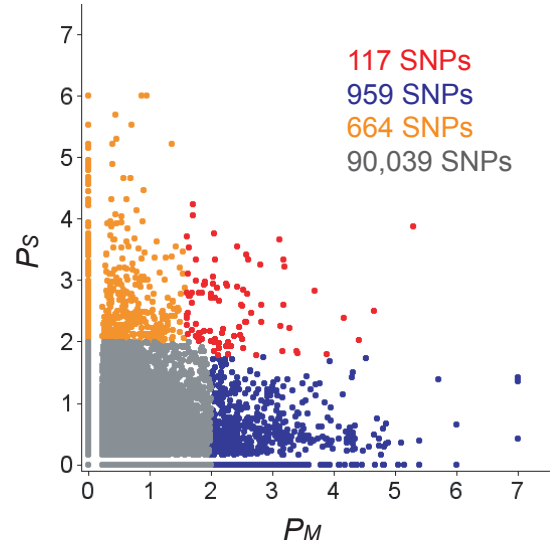
This result appears to contradict earlier work using sequences from coding regions to infer a maize domestication bottleneck (Eyre-Walker *et al.* 1998; Tenaillon *et al.* 2004; Wright *et al.* 2005). One explanation for this discrepancy may be the action of purifying selection in coding regions, which could act to retard the recovery of diversity and lead to estimates of a stronger bottleneck Hufford *et al.* (2012b). Consistent with Hufford *et al.* (2012b), our genome-wide SNP data show an excess of rare variants relative to expectations under Wright *et al.* (2005)'s bottleneck model (Figure 3), suggesting a domestication model involving a weaker bottleneck or more rapid population growth.

Comparing our empirical  $F_{ST}$  values to the null expectation simulated under our demographic models allowed us to identify significantly differentiated SNPs between low- and highland populations. In all cases, observed  $F_{ST}$  values were quite similar to those generated under our null models (Figure 4A), and model choice – including the parameterization of the domestication bottleneck – had little impact on the distribution of estimated p-values (Figure S4). We chose  $P < 0.01$  as an arbitrary cut-off for significant differentiation between low- and highland populations, and identified 1,040 SNPs in Mexico (1,040/76,989=0.0135) and 756 SNPs in South America (756/63,160=0.0120) as outliers.

## Patterns of adaptation

### Adaptation via mutation versus standing variation:

In order to characterize patterns of adaptation, we first determined whether SNPs showing high differentiation between the lowlands and the highlands arose primarily through new mutations or standing genetic variation. We found that these putatively adaptive variants in both Mexico and South America tended to segregate in lowland populations more often than other SNPs (84.6% vs. 74.8% in Mexico, Fisher's exact test (FET)  $P < 10^{-11}$  and 87.3% vs 81.8% in South America,  $P < 10^{-3}$ ). ("segregate in" – are these percentages of SNPs that are polymorphic (as opposed to fixed for either allele) in the relevant population?) **yes. No fixed al-**



**Figure 5** Scatter plot of  $-\log_{10} P$ -values of observed  $F_{ST}$  values, based on simulation from (which model), in Mexico ( $P_M$  on x-axes) and South America ( $P_S$  on y-axes). Red, blue, orange and gray dots represents SNPs showing significance in both Mexico and South America, only in Mexico, only in South America, respectively (see text for details). The number of SNPs in each category is shown in the same color of dots.

**lele between Mexico and S. America** (I don't think I understand. I'd expect SNPs with high frequency differences between high and lowland to have different chances of polymorphism in lowland populations, somehow. Why is this meaningful?) We extended this analysis to standing variation in *parviglumis* by retrieving SNP data from 14 *parviglumis* inbred lines included in the Hapmap v2 data set, using only SNPs with  $n \geq 10$  (Chia *et al.* 2012; Hufford *et al.* 2012b). Again we found that putatively adaptive variants were more likely to be polymorphic in *parviglumis* (81.1% vs. 72.1% in Mexico, FET  $P < 10^{-6}$  and 81.2% vs 72.7% in South America,  $P < 10^{-4}$ ).

**add para** These results suggest that maize adaptation to high altitudes has largely made use of standing genetic variation. Recently, examples of adaptation from standing variation have been increased (Reviewed in Barrett and Schluter 2008; Messer and Petrov 2013), and genome scan studies indicated that soft sweeps are plentiful in *Drosophila* (Garud *et al.* 2013) and human (Turchin *et al.* 2012; Peter *et al.* 2012). Our result is consistent with this view. In the case of maize, the divergence events occurred very recently (Piperno 2006; Perry *et al.* 2006; Grobman *et al.* 2012). Thus, it would be unlikely that adaptation via *de novo* mutations frequently occur, which requires a longer waiting time until new beneficial mutations are arisen. Theoretically, the situation of maize would be consistent with standing variation scenario. Selection from standing variation is expected to be common when the scaled mutation rate (the product of effective population size, mutation rate and target size),  $\Theta \geq 1$ , as long as the scaled selection coefficient (product of effective population size and selection coefficient)  $Ns$  is



large enough (Hermisson and Pennings 2005). Maize should have large  $\Theta$  and  $Ns$  because the effective population size is relatively large (synonymous nucleotide diversity = 0.014, (e.g., Tenaillon *et al.* 2004; Wright *et al.* 2005; Ross-Ibarra *et al.* 2009)).

#### **Highland versus lowland adaptation:**

Given the historical spread of maize from an origin in the lowlands, it is tempting to assume that significant population differentiation should be primarily due to an increase in frequency of adaptive alleles in the highlands. To test this hypothesis, we sought to identify the adaptive allele at each locus using comparisons between Mexico and S. America as well as to *parviglumis* (Text S1). Consistent with predictions, we infer that differentiation at 67.5% (414) and 75.9% (453) of SNPs in Mexico and S. America is due to adaptation in the highlands, with only 32.5% (199) and 24.1% (144) of SNPs inferred to be due to lowland adaptation after excluding the SNPs with ambiguous patterns (probably due to recombination). The majority of these SNPs show patterns of haplotype variation (by PHS test) consistent with our inference (Text S1 and Table S3).

#### **Adaptation through introgression:**

A marked difference between highland adaptation of maize in Mexico and S. America is the potential for adaptation through introgression from wild relatives. While maize in Mexico grows in sympatry with both the lowland taxon *parviglumis* and the highland taxon *mexicana*, maize in South America is outside the range of wild *Zea* species. (Pyhäjärvi *et al.* 2013) recently assessed the potential for local adaptation in *parviglumis* and *mexicana* populations, characterizing differentiation between these subspecies using an  $F_{ST}$ -outlier approach. We observed a significant excess of overlap between our putatively adaptive SNPs in Mexican maize and those identified in the (Pyhäjärvi *et al.* 2013) analysis (Table ??;  $P < 0.01$  by FET). Similar to that paper, we also find that SNPs with significant  $F_{ST}$   $P$ -values are enriched in intergenic regions compared to non-significant SNPs (51.3% vs. 44.2%; FET  $P < 10^{-8}$ ). Significant overlap was also observed between significant SNPs in S. America and teosinte ( $P < 0.01$ ), but the proportion of SNPs was lower than observed in Mexico. These data suggest that adaptations in Mexican maize may have been obtained through gene flow with wild relatives. To more fully explore this hypothesis we evaluated our data in light of introgression identified by (Hufford *et al.* 2013) from *mexicana* into maize in the Mexico highlands. The proportion of significant SNPs in introgressed regions in Mexico is significantly higher than found in S. America (FET  $P \ll 0.001$ ). Outside introgressed regions, the Mexican and S. American populations did not show marked differences in the proportion of significant SNPs (Fisher's exact test,  $P > 0.7$ ). These results combined with those from (Hufford *et al.* 2013) suggest that SNPs in introgressed regions have indeed been under selection.

#### **No evidence for parallel adaptation:**

While maize adaptation in Mexico and S. America are likely distinguished by unique histories of gene flow with wild rel-

atives, the potential remains for parallel adaptation in these two regions. SNPs showing significant differentiation between low- and highland populations in both Mexico and S. America are likely candidates for parallel adaptation. We identify 56 SNPs with  $F_{ST}$   $P$ -values in Mexico ( $P_M$ ) and S. America ( $P_S$ ) both  $< 0.01$ . This number was significantly larger than the random expectation ( $48,370 \times 0.01 \times 0.01 \approx 4.8$ ;  $\chi^2$ -test,  $P \ll 0.001$ ). Furthermore, the distribution of  $P_M$  in the 712 SNPs with  $P_S < 0.01$  was highly skewed toward zero (Figure S4A), and a similar tendency was observed in  $P_S$  given  $P_M < 0.01$  (935 SNPs; Figure S4AB). Thus, we converted the  $P$ -values in one population given  $P < 0.01$  in the other population into  $q$ -values. At a false discovery rate of 0.2 we found 117 SNPs with  $P_M < 0.01 \cap P_S < 0.0169$  or  $P_M < 0.0247 \cap P_S < 0.01$ , and these SNPs were considered our candidates for parallel adaptation. We found 959 SNPs showing significant population differentiation only in Mexico ( $P_M < 0.01 \cap P_S > 0.0169$ ) and 664 SNPs only in South America ( $P_M > 0.0247 \cap P_S < 0.01$ ). The scatter plot of  $P_M$  and  $P_S$  is shown in Figure 5. For a subset of 67 of the SNPs showing putative evidence of parallel adaptation we also had data from *parviglumis* and were able to infer based on patterns of segregation whether these SNPs were potentially adaptive under lowland or highland conditions (Text S1). Surprisingly, SNPs identified as targets of parallel adaptation in Mexico and South America more frequently show segregation patterns consistent with lowland adaptation (62 SNPs) than highland adaptation (5 SNPs).

In addition to evaluating parallel adaptation at the SNP level, we investigated how often different SNPs in the same gene may have been targeted by selection. To search for this pattern, we define a “genetic unit” or GU as all SNPs within 10kb of a transcript. SNPs in an miRNA or second transcript within 10kb of the transcript of interest were excluded. We classified SNPs showing significance in Mexico, S. America or in both regions into 1,277 GUs. Of these, 95 GUs contained at least one SNP with a pattern of differentiation suggesting parallel adaptation, whereas only 12 GUs contained both Mexico-specific and SA-specific significant SNPs. Overall, fewer GUs showed evidence of parallel adaptation than expected by chance (permutation test;  $P < 10^{-5}$ ), with more than 700 and 470 GUs showing Mexico-specific and SA-specific significant SNPs, respectively. Despite similar phenotypes and environments, we thus see little evidence for parallel adaptation at either the SNP or the gene (GU) level.

**Need your comments!!** Our result of few parallel adaptation in maize contrasts with data from humans (Tennissen and Akey 2011) showing frequent evidence of selection on the same genes in multiple pairs of tropical and temperate human populations. It is common in maize and human that the majority of adaptive variants to high altitudes would be derived from standing variation (Tennissen and Akey 2011). On the other hand, one difference between these two species is an effective population size. The effective size of maize (on the order of  $10^5$ )

is an order of magnitude larger than that in human (Takahata and Satta 1997). Human would have less potential to possess genetic variants as a source of adaptation, so it could be more likely that the same variants are selected in multiple subpopulations (as long as  $s$  is enough large and initial frequency is, for example,  $> 0.1$ ). On the other hand, maize would maintain a larger amount of variants in the ancestral lowland population. In this case, if genetic variants have almost the same phenotypic effect, the each highland population might pick up one of them randomly. Or if Mexican and S. American highlands have slightly different climate condition, it is feasible that different variants are selected. The target size of mutations can also increase the variants for adaptation, but there is no data of this size in maize and human. (You are discussing adaptation from standing variation; what about new mutation? This wouldn't require postulating lots of equivalent variants?)

Indeed, there are lines of evidence of adaptation from multiple standing variants in maize. One example is *grassy tillers 1 (gt1)* genes in maize (Wills *et al.* 2013). There are at least two artificially selected mutations on this gene that reduces the number of ears and would be beneficial for the domesticated maize (easy to harvest). *parviglumis* possesses the two mutations as standing variation with low frequency, and both were spread across maize by selection after domestication.

Because linkage disequilibrium in maize decays rapidly (Remington *et al.* 2001; Tenailon *et al.* 2001) as in our data (Figure S5), it is plausible that a number of hard sweeps – strong selection on new mutations – would be missed by our data, but several lines of evidence suggest to us that this is unlikely.

### Comparison to theory

For a final point of comparison, we assessed the degree of parallelism expected under a spatially explicit population genetic model. We estimate the (maize) population density  $\rho$  of the highlands to be around  $(0.5 \text{ people/km}^2) \times (0.5 \text{ ha field/person}) \times (2 \times 10^4 \text{ plants per field ha}) = 5,000 \text{ plants per km}^2$ . The area of the Andean highlands is around  $A = 500 \text{ km}^2$ , leading to a total population of  $A\rho = 2.5 \times 10^6$ . Combined with an offspring variance of  $\xi^2 = 30$ , we can compute the rate  $\lambda_{\text{mut}}$  at which newly adapted alleles arise in the population. We observe that even if there is strong selection for an allele at high elevation ( $s_b = 0.1$ ), a single-base mutation with mutation rate  $\mu = 10^{-8}$  would still take at least 6,000 generations to appear and fix. On the other hand, a kilobase-sized target with mutation rate  $\mu = 10^{-5}$  with this selection coefficient would appear and begin to fix in only 6 generations, while more weakly selected alleles with  $s_b$  of  $10^{-2}$  or  $10^{-3}$  would take hundreds or thousands of generations, respectively. (Note that the time scales linearly with the selection coefficient: at these values  $T_{\text{mut}} = 1/\lambda_{\text{mut}} \approx \mu s_b \times 1.6 \times 10^5$ .) Therefore, we might expect to see parallel changes of similar effect at the level of genes (e.g. disabling mutations), but would not expect to see

adaptive SNPs that arise through independent mutation in the two populations.

Parallel SNP changes seem unlikely from new mutation; what about gene flow between the highlands? From the demographic model above we have estimated that  $\sigma \approx 1.8$  kilometers per generation, so with  $10^{-1} \geq s_m \geq 10^{-4}$  the distance  $\sigma/\sqrt{2s_m}$  over which the frequency of a highland-adaptive, lowland-deleterious allele decays into the lowlands is still short: between 4 and 150 kilometers. Since the Mexican and Andean highlands are around 4,000 km apart, the time needed for a rare allele, with selective cost  $s_m = 10^{-3}$  in the lowlands, to transit between the two highlands is  $T_{\text{mig}} \approx 5 \times 10^{34}$  generations. In other words, from these calculations it is almost impossible that an allele that is deleterious at low elevation with  $s_m = 10^{-3}$  would ever transit from the Mexican to the Andean highlands. If the selection against the allele is even weaker ( $s_m = 10^{-4}$ ) it is still expected to take  $T_{\text{mig}} = 1.8 \times 10^8$  generations. However, shorter distances could be transited by very weakly deleterious alleles – if the distance between highland patches  $R$  is 1,000 km (or if  $\sigma$  is four times larger) then with  $s_m = 10^{-4}$  the time  $T_{\text{mig}}$  is about 1.6 generations – so, adaptation by migration is certain in the known timeframe of maize diffusion. This is strongly dependent on the magnitude of the deleterious selection coefficient: for example, with  $s_m = 10^{-3}$ ,  $T_{\text{mig}}$  is  $2.3 \times 10^6$  generations.

This suggests that even when highland-adaptive mutations are weakly deleterious in the lowlands, gene flow will not result in shared adaptations. The situation where these are neutral in the lowlands is more difficult to model, but we can make some informed guesses. For maize in the Andean highlands to have inherited a highland-adapted allele from the Mexican highlands, those Andean plants must be directly descended from highland Mexican plants that lived more recently than the appearance of the adaptive allele. In other words, the ancestral lineages along which the modern Andean plants have inherited at that locus must trace back to the Mexican highlands. If the allele is neutral in the lowlands, we can treat the movement of these lineages as a neutral process, using the framework of coalescent theory (Wakeley 2005). To do this, we need to follow all of the  $N \approx 2.5 \times 10^6$  lineages backwards; these quickly coalesce to fewer  $m$  lineages in approximately  $\sum_{k=m}^N \frac{2N}{\xi^2 k(k+1)} \approx 1.25 \times 10^5/m$  generations, leaving about 1000 lineages after 100 generations that are spread over a larger area. The displacement of a lineage after  $m$  generations has variance  $m\sigma^2$  and is approximately Gaussian. If we assume that  $n$  lineages are independent, and  $Z_n$  is the distance to the furthest lineage, then  $\mathbb{P}\{Z_n/\sqrt{m\sigma^2} \leq x/\sqrt{2\log n} + \sqrt{2\log n} - (1/2)(\log \log n + \log 4\pi)/\sqrt{2\log n}\} \approx \exp(-e^{-x})$  (Berman 1964). With  $n = 1000$ , the typical distance to the furthest displacement after  $m = 1000$  generations is  $\sqrt{2\sigma^2 m \log n} \approx 212 \text{ km}$ ; after  $m = 6000$  generations it is  $\approx 518 \text{ km}$ . In either case, the chance that the maximum is larger than 1,000 km after 6,000 generations is well less than  $10^{-4}$ . Of course, this is under an equilibrium population model; and maize reached the An-

dean highlands only around 4,000 years ago. Nonetheless, this suggests that even highland-adapted allele that are merely neutral in the lowlands would have difficulty moving between the Mexican and Andean highlands in a few thousand generations.

Based on our spatially explicit population genetic model, parallel adaptation involving identical nucleotide changes is quite unlikely under either scenarios of independent mutation or transit of Central America by undirected (diffusive) sharing of seed. However, independent mutations could be expected in kilobase-sized targets, suggesting there might be signal for genes that share adaptive changes. These conclusions could change if we drastically underestimate the rate of very-long-distance sharing of seed, e.g. if sharing across hundreds of kilometers was common at some point.

## Conclusions

1. We successfully inferred demography and detected the candidates of adaptive loci to highland climates in Mexico and South America by utilizing GBS and 55-k chip.

2. The main conclusion is parallel adaptation is rare in maize highland adaptation.

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## Literature Cited

- Arendt, J., and D. Reznick, 2008 Convergence and parallelism reconsidered: what have we learned about the genetics of adaptation? *Trends Ecol. Evol.* 23: 26–32.
- Barrett, R. D., and D. Schluter, 2008 Adaptation from standing genetic variation. *Trends Ecol. Evol.* 23: 38–44.
- Barton, N. H., 1987 The probability of establishment of an advantageous mutant in a subdivided population. *Genetics Research* 50: 35–40.
- Berman, S. M., 1964 Limit theorems for the maximum term in stationary sequences. *Ann. Math. Statist.* 35: 502–516.
- Casati, P., and V. Walbot, 2005 Differential accumulation of maysin and rhamnosylisoorientin in leaves of high-altitude landraces of maize after uv-b exposure. *Plant, Cell & Environment* 28: 788–799.
- Chia, J. M., C. Song, P. J. Bradbury, D. Costich, N. de Leon, *et al.*, 2012 Maize hapmap2 identifies extant variation from a genome in flux. *Nat. Genet.* 44: 803–807.
- Clark, R. M., S. Tavaré and J. Doebley, 2005 Estimating a nucleotide substitution rate for maize from polymorphism at a major domestication locus. *Mol. Biol. Evol.* 22: 2304–2312.
- Colosimo, P. F., K. E. Hosemann, S. Balabhadra, D. Villarreal, G. M., *et al.*, 2005 Widespread parallel evolution in sticklebacks by repeated fixation of Ectodysplasin alleles. *Science* 307: 1928–1933.
- Currat, M., G. Trabuchet, D. Rees, P. Perrin, R. M. Harding, *et al.*, 2002 Molecular analysis of the  $\beta$ -globin gene cluster in the Niokholo Mandenka population reveals a recent origin of the  $\beta^s$  senegal mutation. *Am. J. Hum. Genet.* 70: 207–223.
- Elmer, K. R., and A. Meyer, 2011 Adaptation in the age of ecological genomics: insights from parallelism and convergence. *Trends Ecol. Evol.* 26: 298–306.
- Eyre-Walker, A., R. L. Gaut, H. Hilton, D. L. Feldman and B. S. Gaut, 1998 Investigation of the bottleneck leading to the domestication of maize. *Proc. Natl. Acad. Sci. USA* 95: 4441–4446.
- Falush, D., M. Stephens and J. K. Pritchard, 2003 Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164: 1567–1587.
- Ganal, M. W., G. Durstewitz, A. Polley, A. Bérard, E. S. Buckler, *et al.*, 2011 A large maize (*Zea mays* L.) SNP genotyping array: development and germplasm genotyping, and genetic mapping to compare with the B73 reference genome. *PLoS One* 6: e28334.
- Garud, N. R., P. W. Messer, E. O. Buzbas and D. A. Petrov, 2013 Soft selective sweeps are the primary mode of recent adaptation in *Drosophila melanogaster*. *ArXiv* p. 1303.0906.
- Grobman, A., D. Bonavia, T. D. Dillehay, D. R. Piperno, J. Iriarte, *et al.*, 2012 Preceramic maize from Paredones and Huaca Prieta, Peru. *Proc. Natl. Acad. Sci. USA* 109: 1755–1759.
- Gutenkunst, R. N., R. D. Hernandez, S. H. Williamson and C. D. Bustamante, 2009 Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data. *PLoS Genet.* 5: e1000695.
- Hermisson, J., and P. S. Pennings, 2005 Soft sweeps: molecular population genetics of adaptation from standing genetic variation. *Genetics* 169: 2335–2352.
- Hudson, R. R., 2002 Generating samples under a Wright-Fisher neutral model of genetic variation. *Bioinformatics* 18: 337–338.

- Hufford, M. B., P. Lubinsky, T. Pyhäjärvi, M. T. Devengenz, N. C. Ellstrand, *et al.*, 2013 The genomic signature of crop-wild introgression in maize. *PLoS Genet.* 9: e1003477.
- Hufford, M. B., E. Martinez-Meyer, B. S. Gaut, L. E. Eguiarte and M. I. Tenaillon, 2012a Past and present distributions of wild and domesticated *Zea mays*: a chance to revisit maize history. *PLoS One* 7: e47659.
- Hufford, M. B., X. Xu, J. van Heerwaarden, T. Pyhäjärvi, J. M. Chia, *et al.*, 2012b Comparative population genomics of maize domestication and improvement. *Nat. Genet.* 44: 808–811.
- Jagers, P., 1975 *Branching processes with biological applications*. Wiley-Interscience [John Wiley & Sons], London Wiley Series in Probability and Mathematical Statistics—Applied Probability and Statistics.
- Körner, C., 2007 The use of 'altitude' in ecological research. *Trends Ecol. Evol.* 22: 569–574.
- Kovach, M. J., M. N. Calingacion, M. A. Fitzgerald and S. R. McCouch, 2009 The origin and evolution of fragrance in rice (*Oryza sativa* L.). *Proc. Natl. Acad. Sci. USA* 106: 14444–14449.
- Kwiatkowski, D. P., 2005 How malaria has affected the human genome and what human genetics can teach us about malaria. *Am. J. Hum. Genet.* 77: 171–192.
- Lauter, N., C. Gustus, A. Westerbergh and J. Doebley, 2004 The inheritance and evolution of leaf pigmentation and pubescence in teosinte. *Genetics* 167: 1949–1959.
- Matsuoka, Y., Y. Vigouroux, M. M. Goodman, J. Sanchez G, E. Buckler, *et al.*, 2002 A single domestication for maize shown by multilocus microsatellite genotyping. *Proc. Natl. Acad. Sci. USA* 99: 6080–6084.
- Mercer, K., A. Martínez-Vásquez and H. R. Perales, 2008 Asymmetrical local adaptation of maize landraces along an altitudinal gradient. *Evolutionary Applications* 1: 489–500.
- Messer, P. W., and D. A. Petrov, 2013 Population genomics of rapid adaptation by soft selective sweeps. *Trends Ecol. Evol.*
- Perry, L., D. H. Sandweiss, D. R. Piperno, K. Rademaker, M. A. Malpass, *et al.*, 2006 Early maize agriculture and interzonal interaction in southern Peru. *Nature* 440: 76–79.
- Peter, B. M., E. Huerta-Sanchez and R. Nielsen, 2012 Distinguishing between selective sweeps from standing variation and from a *de novo* mutation. *PLoS Genet.* 8: e1003011.
- Piperno, D. R., 2006 Quaternary environmental history and agricultural impact on vegetation in Central America. *Annals of the Missouri Botanical Garden* 93: 274–296.
- Piperno, D. R., A. J. Ranere, I. Holst, J. Iriarte and R. Dickau, 2009 Starch grain and phytolith evidence for early ninth millennium B.P. maize from the Central Balsas River Valley, Mexico. *Proc. Natl. Acad. Sci. USA* 106: 5019–5024.
- Pollak, E., 1966 On the survival of a gene in a subdivided population. *Journal of Applied Probability* 3: 142–155.
- Pritchard, J. K., M. Stephens and P. Donnelly, 2000 Inference of population structure using multilocus genotype data. *Genetics* 155: 945–959.
- Pyhäjärvi, T., M. B. Hufford, S. Mezouk and J. Ross-Ibarra, 2013 Complex patterns of local adaptation in teosinte. *Genome Biol. Evol.* 5: 1594–1609.
- Ralph, P., and G. Coop, 2013 Adaptation by migration in a patchy environment. in progress will be on arxiv or submitted.
- Remington, D. L., J. M. Thornsberry, Y. Matsuoka, L. M. Wilson, S. R. Whitt, *et al.*, 2001 Structure of linkage disequilibrium and phenotypic associations in the maize genome. *Proc. Natl. Acad. Sci. USA* 98: 11479–11484.
- Ross-Ibarra, J., M. Tenaillon and B. S. Gaut, 2009 Historical divergence and gene flow in the genus *Zea*. *Genetics* 181: 1399–1413.
- Saghai-Marouf, M. A., K. M. Soliman, R. A. Jorgensen and R. W. Allard, 1984 Ribosomal DNA spacer-length polymorphisms in barley - Mendelian inheritance, chromosomal location, and population-dynamics. *Proc. Natl. Acad. Sci. USA* 81: 8014–8018.
- Scheet, P., and M. Stephens, 2006 A fast and flexible statistical model for large-scale population genotype data: applications to inferring missing genotypes and haplotypic phase. *Am. J. Hum. Genet.* 78: 629–644.
- Schnable, P. S., D. Ware, R. S. Fulton, J. C. Stein, F. Wei, *et al.*, 2009 The B73 maize genome: complexity, diversity, and dynamics. *Science* 326: 1112–1115.
- Slatkin, M., 1973 Gene flow and selection in a cline. *Genetics* 75: 733–756.
- Takahata, N., and Y. Satta, 1997 Evolution of the primate lineage leading to modern humans: phylogenetic and demographic inferences from DNA sequences. *Proc. Natl. Acad. Sci. USA* 94: 4811–4815.
- Tenaillon, M. I., M. C. Sawkins, A. D. Long, R. L. Gaut, J. F. Doebley, *et al.*, 2001 Patterns of DNA sequence polymorphism along chromosome 1 of maize (*Zea mays* ssp. *mays* L.). *Proc. Natl. Acad. Sci. USA* 98: 9161–9166.

- Tenaillon, M. I., J. U'Ren, O. Tenaillon and B. S. Gaut, 2004 Selection versus demography: a multilocus investigation of the domestication process in maize. *Mol. Biol. Evol.* 21: 1214–1225.
- Tennessen, J. A., and J. M. Akey, 2011 Parallel adaptive divergence among geographically diverse human populations. *PLoS Genet.* 7: e1002127.
- Toomajian, C., T. T. Hu, M. J. Aranzana, C. Lister, C. Tang, *et al.*, 2006 A nonparametric test reveals selection for rapid flowering in the *Arabidopsis* genome. *PLoS Biol.* 4: e137.
- Turchin, M. C., C. W. Chiang, C. D. Palmer, S. Sankararaman, D. Reich, *et al.*, 2012 Evidence of widespread selection on standing variation in Europe at height-associated SNPs. *Nat. Genet.* 44: 1015–1019.
- van Heerwaarden, J., J. Doebley, W. H. Briggs, J. C. Glaubitz, M. M. Goodman, *et al.*, 2011 Genetic signals of origin, spread, and introgression in a large sample of maize landraces. *Proc. Natl. Acad. Sci. USA* 108: 1088–1092.
- van Heerwaarden, J., F. van Eeuwijk and J. Ross-Ibarra, 2010 Genetic diversity in a crop metapopulation. *Heredity* 104: 28–39.
- Vigouroux, Y., J. C. Glaubitz, Y. Matsuoka, M. M. Goodman, D. Jesús Sánchez G, *et al.*, 2008 Population structure and genetic diversity of new world maize races assessed by dna microsatellites. *Am. J. Bot.* 95: 1240–1253.
- Wakeley, J., 2005 *Coalescent Theory, an Introduction*. Roberts and Company, Greenwood Village, CO.
- Wellhausen, E. J., A. O. Fuentes, A. H. Corzo and P. C. Mangelsdorf, 1957 *Races of Maize in Central America*. National Academy of Science, National Research Council, Washington, D. C.
- Wilkes, H. G., 1977 Hybridization of maize and teosinte, in Mexico and Guatemala and improvement of maize. *ECO. BOT.* 31: 254–293.
- Wills, D. M., C. J. Whipple, S. Takuno, L. E. Kursel, L. M. Shannon, *et al.*, 2013 From many, one: genetic control of prolificacy during maize domestication. *PLoS Genet.* 9: e1003604.
- Wood, T. E., J. M. Burke and L. H. Rieseberg, 2005 Parallel genotypic adaptation: when evolution repeats itself. *Genetica* 123: 157–170.
- Wright, S. I., I. V. Bi, S. G. Schroeder, M. Yamasaki, J. F. Doebley, *et al.*, 2005 The effects of artificial selection on the maize genome. *Science* 308: 1310–1314.



# 1 Details of the demographic model

Throughout we use in many ways the *branching process approximation* – if an allele is locally rare, then for at least a few generations, the fates of each offspring are nearly independent. So, if the allele is locally deleterious, the total numbers of that allele behave as a subcritical branching process, destined for ultimate extinction. On the other hand, if the allele is advantageous, it will either die out or become locally common, with its fate determined in the first few generations. If the number of offspring of an individual with this allele is the random variable  $X$ , with mean  $\mathbb{E}[X] = 1 + s$  (selective advantage  $s > 0$ ), variance  $\text{Var}[X] = \xi^2$ , and  $\mathbb{P}\{X = 0\} > 0$  (some chance of leaving no offspring), then the probability of local nonextinction  $p_*$  is approximately  $p_* \approx 2s/\xi^2$  to second order in  $s$ . The precise value can be found by defining the generating function  $\Phi(u) = \mathbb{E}[u^X]$ ; the probability of local nonextinction  $p_*$  is the minimal solution to  $\Phi(1 - u) = 1 - u$ . (This can be seen because:  $1 - p_*$  is the probability that an individual's family dies out; this is equal to the probability that the families of all that individual's children die out; since each child's family behaves independently, if the individual has  $x$  offspring, this is equal to  $(1 - p_*)^x$ ; and  $\Phi(1 - p_*) = \mathbb{E}[(1 - p_*)^X]$ .)

If the selective advantage ( $s$ ) depends on geographic location, a similar fact holds: index spatial location by  $i \in 1, \dots, n$ , and for  $u = (u_1, u_2, \dots, u_n)$  define the functions  $\Phi_i(u) = \mathbb{E}[\prod_j u_j^{X_{ij}}]$ , where  $X_{ij}$  is the (random) number of offspring that an individual at  $i$  produces at location  $j$ . Then  $p_* = (p_{*1}, \dots, p_{*n})$ , the vector of probabilities that a new mutation at each location eventually fixes, is the minimal solution to  $\Phi(1 - p_*) = 1 - p_*$ , i.e.  $\Phi_i(1 - p_*) = 1 - p_{*i}$ .

Here we consider a linear habitat, so that the selection coefficient at location  $\ell_i$  is  $s_i = \min(s_b, \max(-s_d, \alpha \ell_i))$ . There does not seem to be a nice analytic expression for  $p_*$  in this case, but since  $1 - p_*$  is a fixed point of  $\Phi$ , the solution can be found by iteration:  $1 - p_* = \lim_{n \rightarrow \infty} \Phi^n(u)$  for an appropriate starting point  $u$ .

## 1.1 Maize model

Specifically, the migration and reproduction dynamics we use are as follows. On a large scale, fields of  $N$  plants are replanted each year from  $N_f$  ears, either from completely new stock (with probability  $p_e$ ), from partially new stock (a proportion  $r_m$  with probability  $p_m$ ), or entirely from the same field. Plants have an average of  $\mu_E$  ears per plant, and ears have an average of  $N/N_f$  kernels; so a plant has on average  $\mu_E N/N_f$  kernels, and a field has on average  $\mu_E N$  ears and  $\mu_E N^2/N_f$  kernels. We suppose that a plant with the selected allele is pollen parent to  $(1 + s)\mu_E N/N_f$  kernels, and also seed parent to  $(1 + s)\mu_E N/N_f$  kernels, still in  $\mu_E$  ears. The number of offspring a plant has depends on how many of its offspring kernels get replanted. Some proportion  $m_g$  of the pollen-parent kernels are in other fields, and may be replanted; but with probability  $p_e$  no other kernels (i.e. those in the same field) are replanted. Otherwise, with probability  $1 - p_m$  the farmer chooses  $N_f$  of the ears from this field to replant (or,  $(1 - r_m)N_f$  of them, with probability  $p_m$ ); this results in a mean number  $N_f/N$  (or,  $(1 - r_m)N_f/N$ ) of the plant's ears of seed children being chosen, and a mean number  $1 + s$  of the plant's pollen children kernels being chosen. Furthermore, the field is used to completely (or partially) replant another's field with chance  $p_e/(1 - p_e)$  (or  $p_m$ ); resulting in another  $N_f/N$  (or  $r_m N_f/N$ ) ears and  $1 + s$  (or  $r_m(1 + s)$ ) pollen children being replanted elsewhere. Here we have assumed that pollen is well-mixed within a field, and that the selected allele is locally rare. Finally, we must divide all these offspring numbers by 2, since we look at the offspring carrying a particular haplotype, not of the diploid plant's genome.

The above gives mean values; to get a probability model we assume that every count in sight is Poisson. In other words, we suppose that the number of pollen children is Poisson with random mean  $\lambda_P$ , and the number of seed children is a mixture of  $K$  independent Poissons with mean  $(1 + s)N/N_f$  each, where  $K$  is the random number of ears chosen to replant, which is itself Poisson with mean  $\mu_K$ . By Poisson additivity, the numbers of local and migrant offspring are Poisson, with means  $\lambda_P = \lambda_{PL} + \lambda_{PM}$  and  $\mu_K = \mu_{KL} + \mu_{KM}$  respectively. With probability  $p_e$ ,  $\lambda_{PM} = m_g(1 + s)$  and  $\mu_K = \lambda_{PL} = 0$ . Otherwise, with probability  $(1 - p_e)(1 - p_m)$ ,  $\mu_{KL} = N_f/N$  and  $\lambda_{PL} = (1 + s)(1 - m_g)$ ; and with probability  $(1 - p_e)p_m$ ,  $\mu_{KL} = (1 - r_m)N_f/N$  and  $\lambda_{PL} = (1 - r_m)(1 + s)(1 - m_g)$ . The migrant means are, with probability  $(1 - p_e)p_e/(1 - p_e) = p_e$ ,  $\mu_{KM} = N_f/N$  and  $\lambda_{PM} = 1 + s$ ; while with probability  $(1 - p_e)p_m$ ,  $\mu_{KM} = r_m N_f/N$  and  $\lambda_{PM} = (1 + s)(r_m(1 - m_g) + m_g)$ , and otherwise  $\mu_{KM} = 0$  and  $\lambda_{PM} = m_g(1 + s)$ .

complete seed stock replacement prob	$p_e$	0.068
pollen migration rate	$m_g$	0.0083
number of plants per field	$N$	$10^5$
number of ears used to replant	$N_f$	561
mean ears per plant	$\mu_E$	3
partial stock replacement prob	$p_m$	0.02
mean proportion stock replaced	$r_m$	0.2
pollen migration distance	$\sigma_p$	0 km
seed replacement distance	$\sigma_s$	50 km
distance between demes	$a$	15 km
width of altitudinal cline	$w$	62km
deleterious selection coefficient	$s_d$	varies
beneficial selection coefficient	$s_b$	varies
slope of selection gradient	$\alpha$	$(s_d + s_b)/w$
variance in offspring number	$\xi^2$	varies
maize population density	$\rho$	$5 \times 10^3$
area of highland habitat	$A$	500 km <sup>2</sup>
mean dispersal distance	$\sigma$	1.8 km

**SUPPLEMENTAL TABLE 1** Parameter estimates used in calculations, and other notation.

## 1.2 Math

The generating function of a Poisson with mean  $\lambda$  is  $\phi(u; \lambda) = \exp(\lambda(u - 1))$ , and the generating function of a Poisson( $\mu$ ) sum of Poisson( $\lambda$ ) values is  $\phi(\phi(u; \lambda); \mu)$ . Therefore, the generating function for the diploid process, ignoring spatial structure, is

$$\Phi(u) = p_e \phi(u; m_g(1 + s)) \quad (1)$$

$$\begin{aligned}
& + \{(1 - p_e)(1 - p_m) \phi(u; (1 + s)(1 - m_g)) \phi(\phi(u; (1 + s)N/N_f); N_f/N) \\
& + (1 - p_e)p_m \phi(u; (1 + s)(1 - r_m)(1 - m_g)) \phi(\phi(u; (1 + s)N/N_f); (1 - r_m)N_f/N)\} \\
& \times \{p_e/(1 - p_e) \phi(u; 1 + s) \phi(\phi(u; (1 + s)N_f/N); N_f/N) \\
& + p_m \phi(u; (1 + s)(r_m(1 - p_e)(1 - m_g) + m_g)) \\
& \times \phi(\phi(u; (1 + s)N/N_f); r_m N_f/N) \\
& + (1 - p_e/(1 - p_e) - p_m) \phi(u; m_g(1 + s))\} \\
& = \phi(u; m_g(1 + s)) (p_e \\
& + \{(1 - p_e)(1 - p_m) \phi(u; (1 + s)(1 - m_g)) \phi(\phi(u; (1 + s)N/N_f); N_f/N) \\
& + (1 - p_e)p_m \phi(u; (1 + s)(1 - r_m)(1 - m_g)) \phi(\phi(u; (1 + s)N/N_f); (1 - r_m)N_f/N)\} \\
& \times \{p_e/(1 - p_e) \phi(u; (1 + s)(1 - m_g)) \phi(\phi(u; (1 + s)N_f/N); N_f/N) \\
& + p_m \phi(u; (1 + s)r_m(1 - m_g)) \\
& \times \phi(\phi(u; (1 + s)N/N_f); r_m N_f/N) \\
& + (1 - p_e/(1 - p_e) - p_m)\} ) \quad (2)
\end{aligned}$$

To get the generating function for a haploid, replace every instance of  $1 + s$  by  $(1 + s)/2$ .

As a quick check, the mean total number of offspring of a diploid is

$$\begin{aligned}
& (1 + s) (m_g + (1 - p_e) \{(1 - p_m)((1 - m_g) + 1) + p_m((1 - r_m)(1 - m_g) + (1 - r_m))\} \\
& + \{p_e((1 - m_g) + 1) + p_m(1 - p_e)(r_m(1 - m_g) + r_m)\}) \quad (3)
\end{aligned}$$

$$= (1 + s) (m_g + (1 - p_e)(2 - m_g)(1 - p_m r_m) + (p_e(2 - m_g) + p_m r_m(1 - p_e)(2 - m_g))) \quad (4)$$

$$= (1 + s) (m_g + (2 - m_g)((1 - p_e)(1 - p_m r_m) + p_e + p_m r_m(1 - p_e))) \quad (5)$$

$$= (1 + s) (m_g + (2 - m_g)) \quad (6)$$

$$= 2(1 + s). \quad (7)$$

Check!

We show numerically later that the probability of establishment is very close to  $2s$  over the variance in reproductive number (as expected). It is possible to write down an expression for the variance, but it's a big, ugly one that doesn't lend itself to intuition.

### 1.3 Migration and spatial structure

To incorporate spatial structure, suppose that the locations  $\ell_k$  are arranged in a regular grid, so that  $\ell_k = ak$ . Recall that  $s_k$  is the selection coefficient at location  $k$ . If the total number of offspring produced by an individual at  $\ell_i$  is  $\text{Poisson}(\lambda_i)$ , with each offspring independently migrating to location  $j$  with probability  $m_{ij}$ , then the number of offspring at  $j$  is  $\text{Poisson}(m_{ij}\lambda_i)$ , and so the generating function is

$$\phi(u; \lambda, m) = \prod_j \exp(\lambda_i m_{ij}(u_j - 1)) \quad (8)$$

$$= \exp \left\{ \lambda_i \left( \left( \sum_j m_{ij} u_j \right) - 1 \right) \right\}. \quad (9)$$

We can then substitute this expression into equation (1), with appropriate migration kernels for pollen and seed dispersal.

For migration, we need migration rates and migration distances for both wind-blown pollen and for farmer seed exchange. The rates are parameterized as above; we need the typical dispersal distances, however. One option is to say that the typical distance between villages is  $d_v$ , and that villages are discrete demes, so that pollen stays within the deme (pollen migration distance 0) and seed is exchanged with others from nearby villages; on average  $\sigma_s$  distance away in a random direction. The number of villages away the seed comes from could be geometric (including the possibility of coming from the same village).

### 1.4 Dispersal distance

The dispersal distance – the mean distance between parent and offspring – is the average of the pollen and seed mean dispersal distances. With the above assumptions, the pollen dispersal distance is zero, and the seed dispersal distance is the chance of inter-village movement multiplied by the mean distance moved. This is

$$\sigma = \frac{1}{2}(p_e + (1 - p_e)p_m r_m)\sigma_s = 1.7932\text{km} \quad (10)$$

at the parameter values above.

### 1.5 Results

Iterating the generating function above finds the probability of establishment as a function of distance along the cline. This is shown in figure 1. Note that the approximation  $2s$  divided by the variance in offspring number is pretty darn close.

## 2 Adaptation by mutation

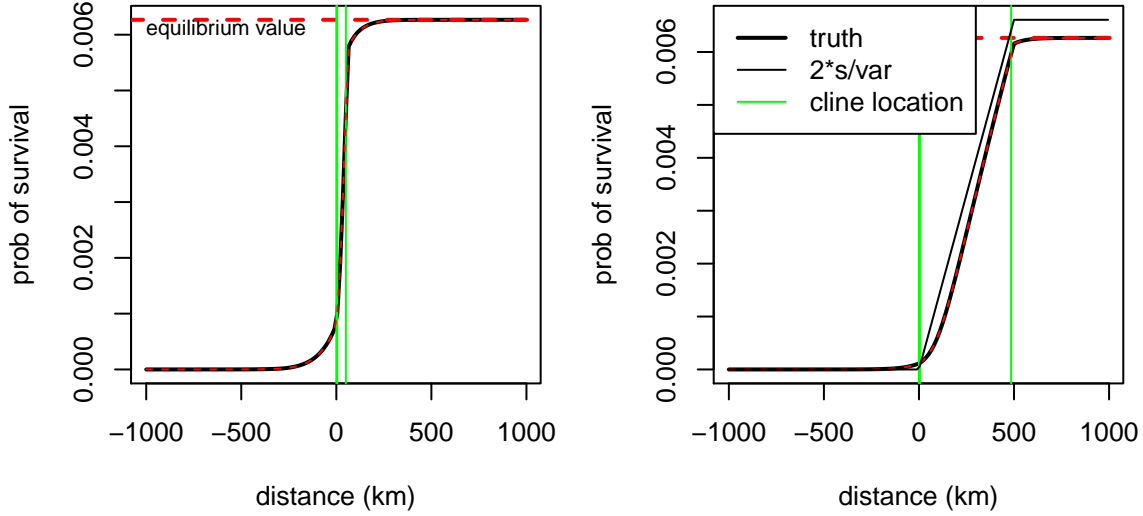
*(just a placeholder for now; to be merged in)*

First, we'd like to compute how difficult is it for the beneficial adaptation to arise by new mutation. The rate of appearance of mutant alleles is a Poisson process, and we can assume that each is successful or not independently, so the time until the new mutant appears and fixes is exponentially distributed, with rate equal to the mutation rate multiplied by the probability of establishment integrated over the population. Referring to figure 1, we see that this is pretty close to  $((\text{area of high altitude}) + (1/2 \text{ area of altitudinal gradient})) \times (\text{population density}) \times (\text{prob of establishment at high altitude})$ .

Let  $A$  denote  $(\text{area of high altitude}) + (1/2 \text{ area of altitudinal gradient})$ . The population density  $\rho$  is roughly  $0.5\text{--}5$  people per  $\text{km}^2 \times (0.5 \text{ ha field/person}) \times (2 \times 10^4 \text{ plants per field ha}) = (5000\text{--}50000 \text{ plants per km}^2)$ . As a check, the other set of numbers was “one village per 15  $\text{km}^2$ ”; i.e. per square with 15km on a side, which is  $0.444$  people per  $\text{km}^2$ .

Since the probability of establishment at high altitude is approximately  $2s_b/\xi^2$ , with  $\xi^2$  the variance in offspring number, the rate of appearance is just

$$\lambda_{\text{mut}} = 2\rho A s_b \mu / \xi^2.$$



**SUPPLEMENTAL FIGURE 1** *(make this look better)* Probability of establishment, as a function of distance along and around an altitudinal cline, whose boundaries are marked by the green lines. **(A)** The parameters above; with cline width 62km; **(B)** the same, except with cline width 500km.

At the values above, with  $.1 \leq s_b \leq .001$ , the factor  $2\rho As_b/\xi^2$  multiplying the mutation rate varies between  $10^2$  and  $10^5$ , implying that a single-base mutation with  $\mu = 10^{-8}$  would have to wait between  $10^4$  and  $10^6$  generations to fix, but a mutation with a larger target, say  $\mu = 10^{-5}$ , would fix in tens to thousands of generations, depending on the selection coefficient.

### 3 Adaptation by migration

As we show in the theory paper, the rate of adaptation by diffusive migration is roughly

$$\lambda_{\text{mig}} = \rho \frac{s_b \sqrt{2s_m}}{2\xi^2} \exp\left(-\frac{\sqrt{2s_m}R}{\sigma}\right).$$

We can talk about this more and give some simulations. But for now, let's interpret.

First note that for  $10^{-1} \leq s_m \leq 10^{-4}$ , the value  $1/\sqrt{2s_m}$  is between 2 and 70 – so the exponential decay of the chance of migration falls off on a scale of between 2 and 70 times the dispersal distance. Above we have estimated the dispersal distance to be  $\sigma \approx 2$  km, and far below the mean distance  $\sigma_s$  to the field that a farmer replants seed from, when this happens, which we have as  $\sigma_s = 50$  km. Taking  $\sigma = 2$  km, we have that  $4 \leq \sigma/\sqrt{2s_m} \leq 150$  km. A very conservative upper bound might be  $\sigma \leq \sigma_s/20$  (if farmers replaced 10% of their seed with long-distance seed every year). At this upper bound, we would have  $5 \leq \sigma/\sqrt{2s_m} \leq 175$  km, which is not very different. This makes the exponential term very small since  $R$  is on the order of 1,000 km.

Taking  $\sigma = 2$  km, we then compute that if  $s_m = 10^{-4}$  (very weak selection in the lowlands), then for  $R = 1,000$  km, the migration rate is  $\lambda_{\text{mig}} \leq 10^{-5}$ , i.e. it would take on the order of 100,000 generations (years) to get a successful migrant only 1,000 km away, under this model of undirected, diffusive dispersal. For larger  $s_m$ , the migration rate is much smaller.

### 4 Conclusion

It seems unlikely that any alleles that are adaptive in the highlands and deleterious at all in the lowlands would have transited central America by undirected (diffusive) sharing of seed. The conclusions could change if we drastically underestimate the rate of very long distance sharing of seed, e.g. if sharing across hundreds of kilometers was common at some point.

Both calculations are very pessimistic about the chance of shared single-base changes through either migration or independent mutation. However, independent mutations could be expected in kilobase-size targets, suggesting there might be signal for genes that share adaptive changes.