

Review: Adaptive Introgression Expanded the Genetic Base of Crops during post-Domestication Spread

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The process of domestication is often conceptualized as geographically constrained, with crops originating from a wild progenitor within one or more defined centers followed by expansion to the modern-day extent of cultivation [1]. However, archaeological and genetic evidence are beginning to reveal that, in many cases, domestication has been temporally protracted and geographically diffuse [2, 3, 4, 5, 6]. An additional important aspect of the emerging complexity of domestication is beneficial gene flow (*i.e.*, adaptive introgression) from locally adapted wild relatives during crop expansion following initial domestication.

Adaptive introgression has three components: hybridization between two genomes, backcrossing to one of the parents, and selection on different recombinant genotypes with progressively diminished linkage drag [7, 8]. In domesticated species, adaptive introgression would consist of crop/wild hybrids backcrossing to a crop, retention and increase in frequency of adaptive wild haplotypes in the crop, and selection against undesirable wild background. To date, the literature on crop-wild gene flow has largely focused on the risk of transgene introgression from domesticated crops into wild relatives (for a review, [9]) and on modern plant breeding efforts to introgress desired traits from wild relatives (for a review, [10]). The history of natural and potentially adaptive introgression of wild alleles into domesticated crops over evolutionary timescales has received considerably less attention. However, new tools and methods have recently been employed to detect genome-wide patterns of introgression, granting new insights into the prevalence of adaptive introgression in crop histories. Preliminary results suggest there is a need to expand our conception of domestication to include a broadening of the genetic base of crops that occurred through adaptive gene flow with newly encountered wild relatives during post-domestication expansion.

In this review, we will: 1) briefly describe recently developed methods for detecting adaptive introgression and provide a summary of how they can be applied to detect crop-wild introgression, 2) present case studies suggesting wild-to-crop introgression has conferred local adaptation, 3) consider how introgression bears upon fundamental questions of domestication, and 4) describe future advances in both basic and applied genetics that can be made through the study of introgression in agroecosystems.

Introgression methods and their application

The decreasing cost of genome-wide resequencing and availability of reduced-representation genotyping (*e.g.*, GBS and RAD-Seq), combined with new analytical methods, has facilitated comprehensive study of introgression across a number of species (**Table 1**). High-density marker data can

be used with haplotype-based and other methods to assign specific genomic regions to a taxon of origin and identify introgression across taxa [11, 12, 13, 14, 15, 16]. The methods reviewed here do not include those marginally estimating introgression/migration rate as a component of demographic history (*e.g.*, Approximate Bayesian Computation (ABC) [17], diffusion approximations for demographic inference ($\delta a \delta i$) [18], isolation with migration models [19], and a series of methods utilizing the sequentially Markovian coalescent (PSMC, MSMC and SMC++) [20, 21, 22]). Rather, we focus on methods that explicitly identify introgressed genomic segments based on the extent of differentiation, on patterns of nucleotide/haplotype sharing, and phylogenetic relationships.

First, introgressed segments are expected to show low differentiation from their source population. The F_{st} and d_{XY} statistics and their derivatives including G_{min} [16] and RND_{min} [15] gauge differentiation. The former two statistics are insensitive to rare migrants and therefore lack power to detect recent introgression, while the latter two overcome this limitation. Additionally, RND_{min} accounts for variable mutation rate, which is detected based on branch length to an outgroup [15]. These statistics have recently been further developed by adding differentiation between both non-admixed (A) and admixed populations (B) and a source population (C) [23]. For example, the $U_{A,B,C(w,x,y)}$ statistic summarizes number of sites where an allele at frequency y in the source population (C) has a frequency higher than x in the admixed population (B) and lower than w in the non-admixed population (A). A similar statistic, $Q95_{A,B,C(w,y)}$, sets a hard cutoff at the 95th percentile of allele frequencies in the admixed population (B) [23]. Further modifications have allowed specification of more than one source population (see details in [23]).

Second, local ancestry deconvolution (also known as chromosome painting) assigns genomic regions to various source populations based on patterns of allele/haplotype sharing [24]. One form of chromosome painting utilizes hidden Markov models to evaluate ancestry across admixed genomes through comparison to reference, non-admixed individuals (*e.g.*, HAPMIX [12]). Another clusters admixed populations with reference samples using a sliding-window approach (*e.g.*, PCAdmix [25] and LAMP [26]). And finally, introgression can be detected through chromosome painting by using a Bayesian model [27] in which deviations from Hardy-Weinberg equilibrium are minimized through creation of genetic groups (*e.g.*, fineSTRUCTURE [13]).

Third, the ABBA-BABA statistic (also known as the D-statistic) and related statistics are widely applied to introgression detection. These statistics make inferences regarding introgression based on genomic patterns of derived variants that are shared between populations or species. Patterns of allele sharing are interpreted in a phylogenetic context and the method is best suited to detection of introgression at the genome level. Elaborations of the D-statistic capable of localizing introgression to specific genomic regions include \hat{f}_d [11] and the five-taxon D-statistic [14]. The former is quite similar to the D-statistic but uses allele frequencies from each population/species, and the latter detects introgression based on the localized phylogenetic pattern and is capable of determining introgression directionality.

Application of these approaches combined with population genetic statistics to detect selection across a number of plant and animal species suggests introgression can play an adaptive role. For example, based on the sequence divergence, introgression has been detected across *Mimulus* (*i.e.*, monkeyflower) species resulting in adaptation to pollinator preference and contributed to speciation [28]; Jeong et al. [29] utilized HAPMIX to disclose introgression from Sherpa to Tibetan humans at loci controlling high altitude adaptation (reviewed in [30]); ABBA-BABA statistics were employed to reveal introgression of wing coloration loci conferring Müllerian mimicry (a type of mimicry in which two unpalatable species resemble one another, compounding the efficacy of their repellent signal) across butterfly species [31]. .

Crop adaptation through introgression

Genome-wide data from extensive samples of crops and their wild relatives, in combination with the new methods described above, have recently allowed detailed analysis of wild-to-crop introgression in some of the world’s most important crops (**Table 2**). Below we present a summary of findings from maize, barley, rice, and potato, four promising systems in which introgression from wild relatives appears to have played an adaptive role.

1. Maize:

The relationship between maize (*Zea mays* ssp. *mays*) and the teosinte *Zea mays* ssp. *mexicana* (hereafter, *mexicana*) offers a prime case study of adaptive wild-to-crop introgression. Maize was domesticated from *Zea mays* ssp. *parviglumis* (hereafter, *parviglumis*) approximately 9,000 BP in the lowlands of the Balsas River Valley in Mexico [32]. From this domestication center, maize spread into the highlands of the Mexican Central Plateau, where it came into sympatry with *mexicana*. Introgression from *mexicana* to maize in the Central Plateau has been reported based on both morphological [33] and molecular [34, 35] data. However, Hufford et al. [36] first localized *mexicana* introgression to chromosomal regions and provided evidence that it was likely adaptive. The authors identified nine genomic regions in several maize populations which consistently showed evidence of *mexicana* introgression based on chromosome painting methods including HAPMIX (Figure 1). These introgressed segments overlapped with QTLs that had previously been found to control anthocyanin content and leaf macrohairs [37], traits known to be adaptive at high elevation. In a growth chamber experiment, the authors demonstrated that maize populations with *mexicana* introgression showed greater plant height (a proxy for fitness) under highland environmental conditions than populations that lacked introgression. Height differences were not detected under lowland conditions.

Populations of *mexicana* cannot be found outside of the highlands of Mexico, yet maize has colonized and adapted to high elevation in a number of other regions. A recent study [4] employed the ABBA-BABA and \hat{f}_d statistics to evaluate whether maize with *mexicana* introgression was transferred to other highland regions or whether highland adaptation was obtained *de novo* outside of Mexico. Overall, analyses revealed that *mexicana* introgressions were transferred to Meso-American high elevation regions in Guatemala and the southwestern United States, but more distant high elevation regions (*e.g.*, the Andes) showed no *mexicana* ancestry.

Since *mexicana* haplotypes appear to have played an important role historically in adaptation of maize to challenging high-elevation conditions, modern breeding programs may further benefit from drawing on *mexicana* germplasm, particularly in regions like the Andes where *mexicana* alleles are not known to have spread.

2. Barley:

Barley (*Hordeum vulgare* subsp. *vulgare*) was domesticated at least twice roughly 8,000 to 10,000 BP: once from the wild subsp. *spontaneum* in the Fertile Crescent and once from subsp. *spontaneum* var. *agriocrithon* in Tibet [38, 39, 40, 41, 42, 43]. Presently, the distribution of subsp. *spontaneum* stretches from the eastern Mediterranean through the Middle-East to west-central Asia, spanning clines in temperature, precipitation, soil type, and altitude [44]. Barley-*spontaneum* hybrids are fertile and commonly found when these taxa co-occur. Gene flow between wild and domesticated barley is frequent [43], at times occurring over distances greater than a kilometer [45].

Poets and co-authors [46] recently investigated the range-wide contribution of wild barley to landraces, assessing both genome-wide and geographical patterns. This study identified several lines of evidence consistent with wild introgression aiding the dispersal and adaptation of domesticated barley. Genomic regions of shared ancestry were detected linking particular landraces to numerous wild relative populations, suggesting landraces may have received wild introgression on a continual basis during post-domestication expansion. However, barley landraces showed an excess of ancestry from nearby wild relatives, indicating a prevalence of local and potentially adaptive gene flow. Limited linkage disequilibrium and small tracts of identity by state indicated even locally introgressed chromosomal regions are old, perhaps dating to the early expansion of barley post-domestication. While these results are suggestive, wild barley haplotypes have yet to be definitely linked to specific local adaptations in landraces.

3. Asian Rice:

The details of Asian rice (*Oryza sativa*) domestication are still debated. Certain genetic and archaeobotanical evidence point toward independent domestications of the two prominent varietal groups *japonica* and *indica* from the wild species *Oryza rufipogon* (*rufipogon* hereafter) in the Yangtze Basin of China 7000 BP and the Indian Ganges plain 4000 BP, respectively [47], with a potential third domestication event giving rise to *aus* in Bangladesh or central India [48]. Other studies support a single domestication occurring 8,200-13,500 BP in the Yangtze Basin, with later divergence of *japonica* and *indica* [49, 50]. Huang and colleagues [50] developed a genetic map of rice variation, which they used to measure genetic distance between a range-wide sample of wild and domesticated rice, finding *japonica* was domesticated near the Pearl River in Guangxi province, China, and that *indica* was likely the result of hybridization between *japonica* and local *rufipogon* populations in Southern and South-eastern Asia. In a re-examination of these same data, [48] found evidence supporting independent domestications of *japonica*, *indica*, and *aus*, as well as a hybrid origin (*japonica* x *aus*) of *aromatic* rice. A recent third analysis by Choi and co-authors [51] compared these two disparate results and the methods utilized therein, concluding that domestication alleles (including *LABA1*, *PROG1*, and *sh1*) arose via a single domestication event of *japonica*, and that these alleles introgressed into several wild *rufipogon* subpopulations which thereby became the progenitors of other Asian rice varieties.

The findings of [51] run in parallel with a hypothesis posited by Vaughan and colleagues [52]. According to this hypothesis, domestication alleles arose in a single cultivated rice population and subsequently introgressed into diverse cultivated populations (some *japonica*-like, some *indica*-like) in the region. As these fully domesticated populations spread into new environments, they potentially received introgression from locally-adapted wild relatives, retaining alleles that improved fitness.

4. Potato

Modern potato (*Solanum tuberosum*) is believed to have been domesticated in southern Peru in sympatry with a multitude of wild relatives about 6000-10000 BP, although the exact location and formal classification and phylogenetic relationships between these taxa have long been disputed [53, 54, 55, 56]. A distance-based phylogeny assembled from a SNP array from a *Solanum* diversity panel (which included wild, landrace, and cultivated species) formed three groups (North American, South American, and cultivated) and identified *S. candolleianum* as being most probable wild progenitor of the potato [57].

Table 1: List and brief description of recently developed methods and examples of empirical studies employing these methods.

methods	data type	reference	examples
divergence			
Gmin	biallelic SNP	[16]	[70]
RNDmin	phased haplotype	[15]	NA
$U_{A,B,C(w,x,y)}$ and $Q95_{A,B,C(w,y)}$	biallelic SNP	[30]	[71]
chromosome painting			
Hapmix	phased haplotype; reference panel	[12]	[36, 72]
RASPberry	phased haplotype	[73]	[74]
MultiMix	phased/unphased genotype; reference panel	[75]	[76]
PCAdmix	phased haplotype	[25]	[77, 78]
LAMP	phased haplotypes; reference panel	[26]	[79]
phylogenetic relationship			
ABBA-BABA/D-statistics	biallelic SNP	[80]	[31]
fd statistic	biallelic SNP	[11]	[81, 82]
five taxon D statistics	biallelic SNP	[14]	[83, 84]

Although potatoes are usually propagated clonally, farmers also promote sexual hybridization at times to improve disease resistance and develop new cultivars [58]. Farmers continue to grow potatoes in close proximity to wild relatives, resulting in domesticate-weedy-wild hybrid complexes which promote introgressive hybridization [59, 60, 61]. These complexes, combined with a diverse range of biotic and environmental selective pressures and local farming practices (human-mediated migration, isolated farmsteads in fertile valleys, clonal propagation, and intentional maintenance of a variety of landraces), have fostered expansion of genetic diversity within potatoes subsequent to domestication [62]. However, as farmers tend to abandon fields after being used for potato cultivation, it is less likely that hybrids have an opportunity to form stable populations for maintained introgressive gene flow into the domesticated potato gene pool [62]. Also, natural selection may be subverted by farmer preference and artificial selection [63].

Nevertheless, introgressive hybridization is widespread in potatoes [64]. The various cultivars of Andean potatoes are interfertile, forming one large plastic gene pool [58]. In their wild/landrace/domesticated diversity panel, Hardigan and colleagues [65] found a high level of genomic contribution from wild species (including *S. candolleianum*) into Andean tetraploid cultivated landraces and North American cultivars (20.2% and 32.1%, respectively). Genes located within these introgressed regions were more likely to be highly-expressed, stress-inducible, and contained loci related to disease resistance, drought tolerance, and heat tolerance, suggesting that these introgressed regions impart stress response mechanisms critical to survival, possibly facilitating tolerance for new environmental pressures during range expansion. Drought- and frost-resistance genes introgressed from wild relatives are also reported to have expediated the spread of cultivated potatoes into the central Andean Altiplano [66, 67, 68]. Andean potatoes exhibit high ecological versatility, due in part either to allelic diversity in polyploids or introgression of desirable alleles from wild relatives in diploids [69].

Crop	Compatible Wild Relatives	Hybrids and/or Hybridization	Evidence of Crop Introgression	Evidence of Adaptiveness	Source
Maize (<i>Zea mays</i> subsp. <i>mays</i>)	<i>Z. m.</i> subsp. <i>mexicana</i> , <i>Z. m.</i> subsp. <i>parviglumis</i>	X	X	X	[36]
Asian Rice (<i>Oryza sativa</i>)	<i>O. rufipogon</i>	X	X	X	[50]
Barley (<i>Hordeum vulgare</i>)	<i>H. v.</i> subsp. <i>spontaneum</i>	X	X	X	[46]
Sunflower (<i>Helianthus annuus</i>)	<i>H. argophyllus</i> , <i>H. bolanderi</i> , <i>H. debilis</i> , <i>H. petiolaris</i>	X			[85]
Cassava (<i>Manihot esculenta</i>)	<i>M. glaziovii</i>	X	X	X	[86]
Potato (<i>Solanum tuberosum</i>)	many	X	X	X	[65, 66?]
Tomato (<i>Solanum lycopersicum</i>)	<i>S. pimpinellifolium</i>	X	X	X	[87]
Olive (<i>Olea europaea</i> ssp. <i>europaea</i> var. <i>sativa</i>)	<i>O. e.</i> ssp. <i>europaea</i> var. <i>sylvestris</i>	X	X		[88]
Soybeans (<i>Glycine max</i>)	<i>G. soja</i>	X	X		[89]
Common Bean (<i>Phaseolus vulgaris</i>)	<i>P. v.</i> var. <i>aborigineus</i> , <i>P. v.</i> var. <i>mexicanus</i> [[not in this source]]	X	X		[90]
Grapes (<i>Vitis vinifera</i> subsp. <i>vinifera</i>)	<i>V. v.</i> subsp. <i>sylvestris</i>	X	X		[91]
Sorghum (<i>Sorghum bicolor</i> subsp. <i>bicolor</i>)	<i>S. b.</i> subsp. <i>arundinaceum</i> , <i>S. b.</i> subsp. <i>drummondii</i>	X	X		[92]
Wheat (<i>Triticum monococcum</i> , <i>T. dicoccum</i> , <i>T. aestivum</i>)	<i>T. m. boeoticum</i> , <i>T. diocoides</i> , <i>T. urartu</i> , <i>Aegilops speltoides</i> , <i>A. tauschii</i>	X	X		[93]
Apple (<i>Malus domestica</i>)	<i>M. sylvestris</i> , <i>M. orientalis</i> , <i>M. baccata</i> , <i>M. sieversii</i>	X	X		[94]

Re-evaluating domestication

A framework in which crops are domesticated from a single wild population or even a single species is an oversimplification when introgression is extensive during crop geographic expansion. The addition of ongoing gene flow to our understanding of crop demography could therefore bear importantly on fundamental questions of crop domestication:

What is the progenitor of a crop?

Depending on the extent of post-domestication gene flow with new wild relatives, identification of a crop’s progenitor can be complicated or confounded entirely. Introgression between a crop and newly-encountered taxa decreases divergence of the crop from these donors. This signal could be mistaken for origin rather than gene flow. For example, when determining a single origin of maize from *parviglumis*, Matsuoka and colleagues [32] identified a paradox: while *parviglumis* is found exclusively in the lowlands of southwest Mexico, maize with allele frequencies most similar to *parviglumis* was found in the highlands of the Mexican Central Plateau. Several years later, van Heerwaarden *et al.* [34] resolved the paradox by determining that widespread introgression in the highlands from *mexicana*, which is closely related to *parviglumis*, has caused maize from this region to appear ancestral. Similarly, extensive post-domestication adaptive introgression from potato wild relatives long obscured this crop’s origin. Recent work has shown that, following the original domestication event of *Solanum tuberosum* in the central Andes, potato received introgression from as many as four additional species during colonization of the highest elevations of the Andes and the lowlands of the Chilean coast [95, 96, 97].

Beyond confounding detection of progenitor taxa, extensive introgression may necessitate a reevaluation of crop origins. In cases like maize and potato it is important to recognize the substantial contributions of introgressing taxa to the genetic base of modern crops. Broad recognition of the role these wild relatives have played in crop adaptation could further their use in breeding and elevate their conservation status.

When was a crop domesticated?

Estimates of the timing of initial domestication are often based on levels of sequence divergence between a crop and populations of its presumed progenitor (*e.g.*, [32, 49]). In highly introgressed domesticates, these estimates will be based on comparison of both crop and introgressant haplotypes to those of the presumed progenitor. In such cases, divergence time is a mixture of time since domestication and time since split of the progenitor and the introgressing taxon. This phenomenon, in combination with divergence of crop samples from true ancestral crop populations, ongoing evolution of crop progenitors, and problems with assuming evolution under a molecular clock [98], may help explain discrepancies between domestication dates based on genetic and archaeological data. More accurate estimates of the timing of domestication may be obtained from genetic data by excluding loci that show signatures of introgression or by explicitly including estimates of introgression when modeling a crop’s demographic history.

How was genome-wide diversity shaped by domestication?

Measurement of the strength of the initial domestication bottleneck may also be impacted by adaptive introgression during the spread of crops. Crop wild relatives have distinct demographies when compared to domesticates and may therefore have contrasting effective population sizes (N_e). The influence of wild relative introgression on estimates of the domestication bottleneck will depend on a number of factors including the magnitude of gene flow, the N_e of the introgressing taxon, and the strength of selection on haplotypes following introgression. For example, substantial introgression at neutral loci from a wild taxon with a historically higher N_e will lead to underestimates of the overall strength of the domestication bottleneck.

What candidate genes were targeted by selection during domestication?

Loci targeted by selection during domestication can be identified through so-called “bottom-up” approaches based on population genetic signatures [99]. Ideally, candidate loci will be identified by first constructing a demographic model representing the history of the domesticate. In this approach, diversity data from neutral loci are fit to potential models of a crop’s demography and then statistical tests of selection are used to identify candidate domestication genes under the most likely model. Due to the difficulty of this approach and the uncertainty associated with any given demography, many studies identify domestication loci using a strict outlier approach in which loci showing, for example, the greatest reduction in nucleotide diversity or the highest allele frequency differentiation in the domesticate relative to the wild progenitor are identified as candidates. Introgression during crop expansion may influence candidate gene detection using both demographic-modeling and strict-outlier approaches. For example, *mexicana* introgression into maize described above accounts for approximately 20% of the genome of maize in the highlands of Mexico [34]. Takuno and co-authors [100] have shown that a demographic model incorporating this introgression is a significantly better fit to empirical data than a model lacking introgression. Failure to account for introgression in maize would therefore compromise domestication candidate detection, particularly if a study contained maize samples from the Mexican highlands. Likewise, introgression that increased nucleotide diversity in the domesticate or decreased differentiation at domestication loci would confound a strict outlier approach. However, previous work, also in maize, has shown that known domestication loci are particularly resistant to introgression [36], likely due to ongoing selection favoring the domesticated phenotype.

Future studies in crop-wild introgression

Basic:

Research has so far shown that adaptive crop-wild introgression has played a significant role in the domestication and dispersal of many agronomically-important crops. However, the dynamics of this process are not yet fully understood, especially in the context of individual case examples, and many questions remain.

What is the genomic architecture of this introgression, and does the architecture suggest that it has been adaptive? At what geographic scale is introgression adaptive? *Barley and maize most strongly show geographic patterns that we can talk about here, but I'm not sure how to discuss them again.* To what extent does this depend on the slope of environmental gradients such as temperature, precipitation, and elevation across these ranges? *Refer to the map and bar graph here?* We can look at conservation of genomic architecture across landscapes and between populations, and make predictions about introgressions and their relations to local adaptation. If the genomic architecture of an introgressed region is conserved across a broad ecogeographical region, this suggests that the introgression imparts adaptation to general environmental or climatic variables. On the other hand, if the genomic architecture is conserved within populations but not between nearby populations in the region, this suggests that the introgressed regions offer adaptations to more local selective pressures. If the genomic architecture of an introgressed region is not conserved within a population, there is little evidence that the introgression is adaptive. *Determination of adaptiveness could be accomplished genomically (looking for high LD regions that indicate selective sweeps) or by functional identification?*

After hybridization events that lead to introgression, how long might the detectable genomic signals of introgression persist? Introgressed regions are easier to detect when there has been limited recombination to break them apart. Therefore, introgressions are easiest to detect when they are either recent (few generations means few recombination events) or involve structural variation (which diminishes recombination rate). *involve -> involving* Because recombination progressively breaks apart LD in introgressed regions, measurements of LD can be used to date introgression events (as in [46]).

At what taxonomic scale does introgression occur? When do species become so diverged that introgression is either maladaptive or impossible (due to Dobzhansky-Muller incompatibilities or other mechanisms)? Theory indicates that the most significant limiting factor to gene flow between progenitor and domesticate is divergence time. Over time, diverged populations drift and become increasingly incompatible. Small effective population size, and correspondingly high genetic load, of the introgressive population also limits gene flow. Although perhaps less applicable in crop systems, this effect is seen in other well-documented cases of introgression (for example, Neanderthal introgression into humans, [?]). *I tracked down the sources that indicate that introgression is suppressed around genes. The case example was Neanderthal alleles into humans, the paper titled "The genetic history of Ice Age Europe" [?], cited by the Graham Coop paper. However, I'm unclear if this is a general rule, or simply a consequence of Neanderthal being high in deleterious genetic load. Wouldn't crop systems, with wild relatives harboring putatively adaptive alleles with low load, show a different pattern? I could also talk about cross-incompatibility factors in maize/teosinte hybridization vs. highly compatible asian rice and its relatives. I probably wouldn't need a new source for the rice, but I might need to cite a paper about tcb1, ga1, and ga2.*

Applied:

Our identification and understanding of introgression in agroecosystems would be augmented by the development of wild relative genomic resources, such as annotated genomic sequence assemblies and functional genomic data sets [?]. Additional study of introgression in agroecosystems could

lead to advances in both basic and applied genetics, and specifically the continued improvement of modern crops. Loci underlying the domesticated phenotype can be more clearly identified by removing the confounding population genetic signals of introgression. These loci are potentially beneficial targets for crop improvement. Furthermore, adaptive introgression that is demonstrably tied to a specific environment may include beneficial alleles that can be utilized in crop breeding.

I could here include a handfull of examples of crops that farmers have bred adaptive alleles into. Also, we could mention that identification of wild relatives responsible for valuable agronomic introgressed alleles could inform conservation efforts.

Conclusions

Conclusions

In the same way that Darwin explored natural selection by studying domesticated species (going so far as to feature domestic pigeons as his "special group" at the beginning of his *On the Origin of Species* [101]), we frequently find that modern crop systems, in tandem with their extant wild relatives, offer unparalleled opportunities for the study of several evolutionary questions, including the role of adaptive introgression in dispersal and range expansion. The advent and application of genomics tools has lead to mounting evidence which underscores the prevalence of genetic admixture between crops and wild relatives during and well beyond the initial stages of domestication. Likewise, population genetic theory reinforces the proclivity of wild relatives to provide advantageous, locally-adapted alleles to crops as they disperse beyond their domestication centers into new geographies with new ecological pressures and niches. Within this new conception, the process of crop range expansion is a concurrent element of domestication, rather than a distinct event subsequent to it. This is a revolutionary departure from the prevailing model, and as such, offers new questions and new opportunities for investigation. These questions take on practical importance as well as theoretical. Understanding a crop's history of domestication in terms of selection, adaptation, and admixture empowers efforts at crop development and improvement. As the historic role of wild relatives in the development of many crops is increasingly clarified, it is likely that we may reevaluate the importance of conservation of wild populations (in particular or in general) that harbor agronomically-valuable alleles that may be targeted by pre-breeding efforts. These efforts may be of particular value in the face of future climate volatility and change.

Domesticated crops are among humanity's first and greatest inventions. Interwoven in the genetic history of these crops is the story of our ancestors as they transitioned through the Agronomic Revolution. In this more nuanced and dynamic understanding of crop domestication, we gain insight into the evolutionary journey that crops and humanity took, and continue to take, together.

I let these final few sentences get a little more poetic than I normally would. I think maybe I should reel them back in, or cut them.

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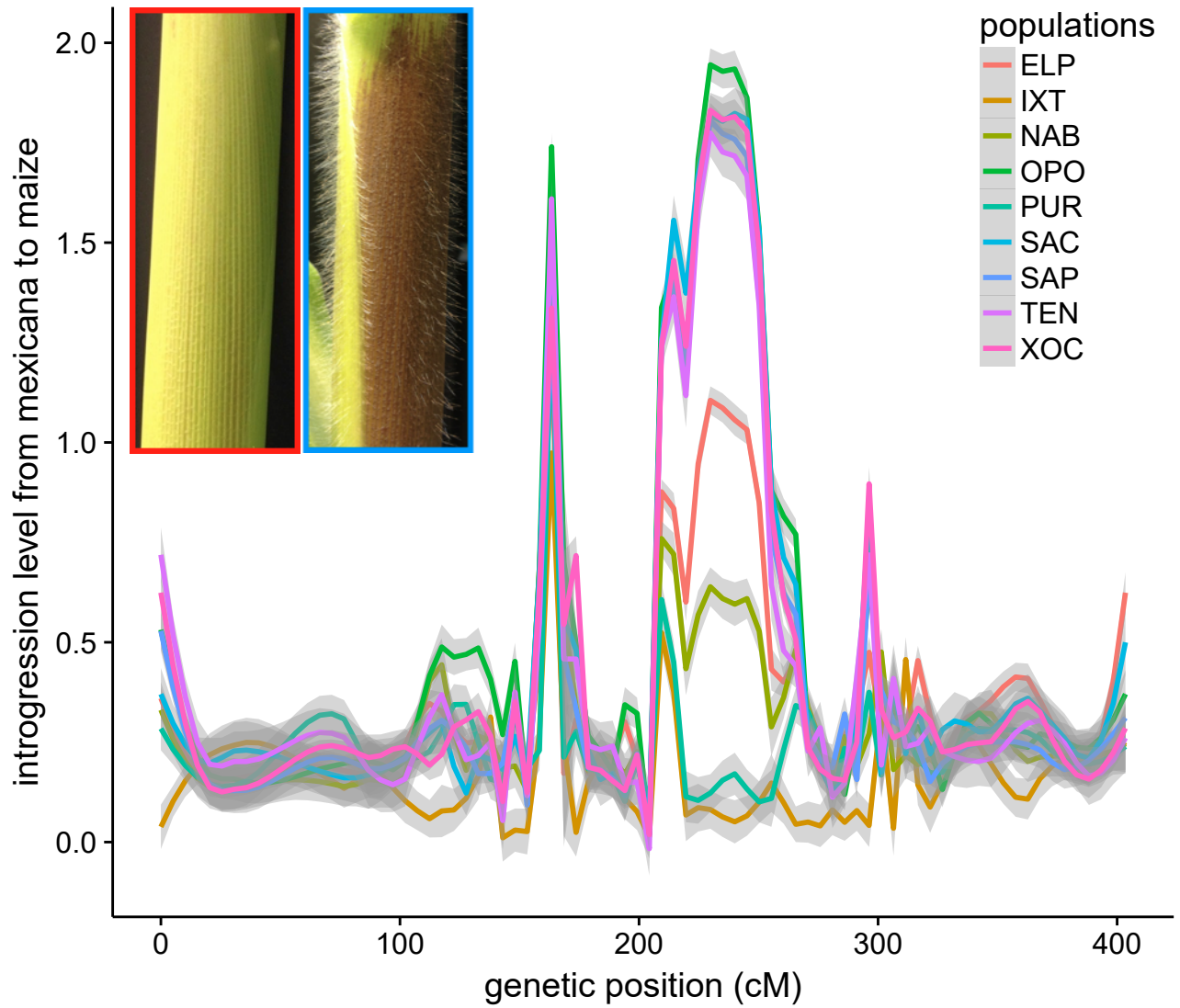


Figure 1: Hapmix vectors indicating introgression level from *mexicana* to Mexican highland maize on chromosome 4. Data adopted from Hufford et al. [36]. ELP: EL Porvenir; IXT: Ixtlan ; NAB: Nabogame; OPO: Opopeo; PUR: Puruandiro; SAC: Santa Clara; SAP: San Pedro; TEN: Tenango del Aire; XOC: Xochimilco. Insets showed the phenotypes of macrohairs on lowland (red) and highland (blue) maize stems.

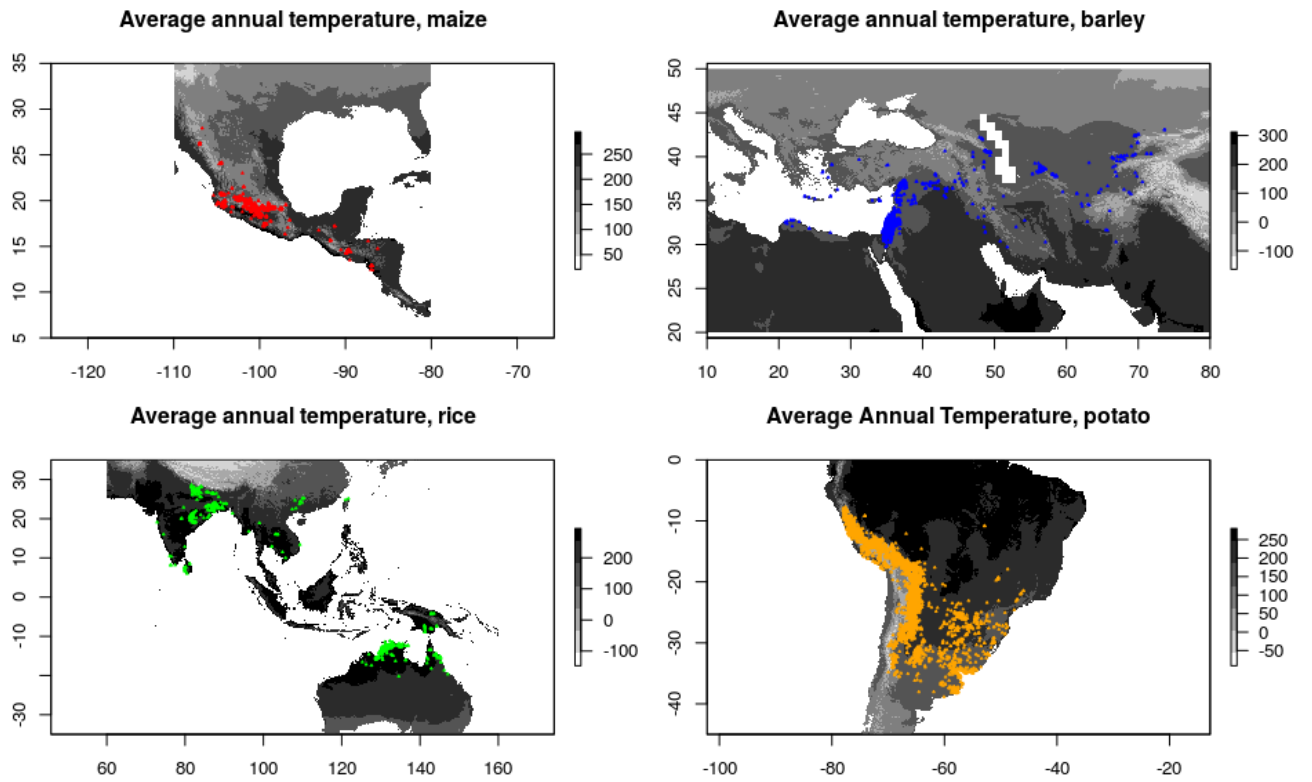


Figure 2: Map of the natural ranges of wild relatives of four domesticated crops, overlaid with average annual temperature. The distribution of average annual temperature experienced in the geographic home ranges of wild relatives interfertile with four crops

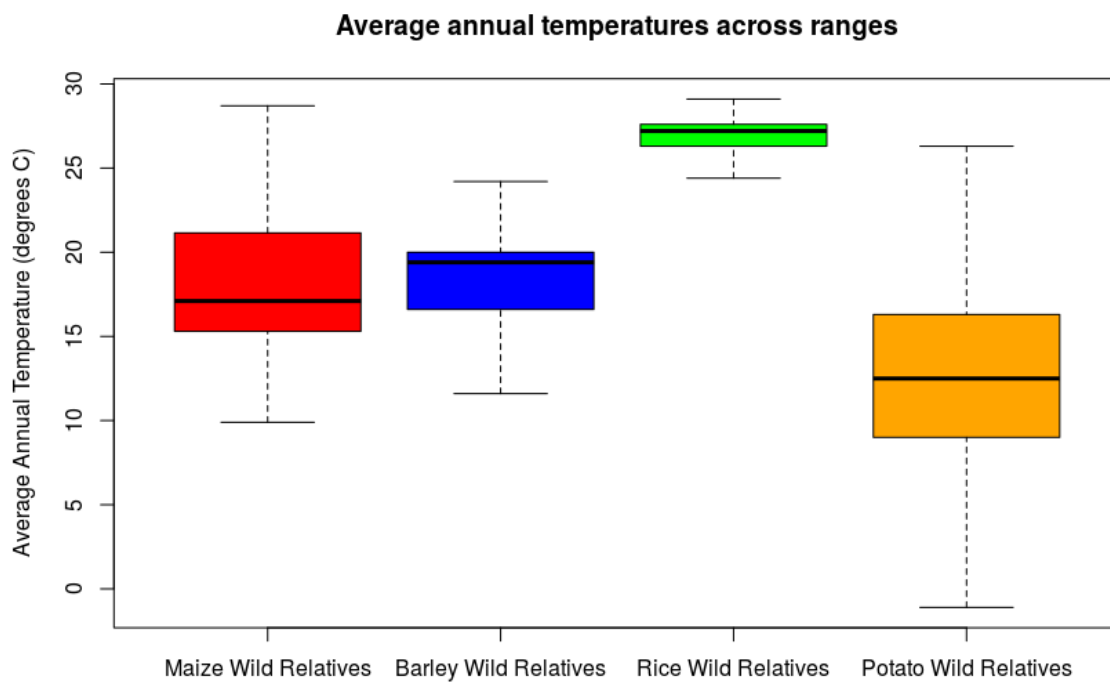


Figure 3: The distribution of average annual temperatures experienced in the geographic home ranges of wild relatives interfertile with four crops