

The limits of parallelism in adaptation due to domestication in the grasses

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Abstract

The selection of desirable traits in crops during domestication has been well studied. Many crops share a suite of modified phenotypic characteristics collectively known as the domestication syndrome. In this sense, crops have convergently evolved. Previous work has demonstrated that, at least in some instances, convergence for domestication traits has been achieved through parallel molecular means. However, both demography and selection during domestication may have placed limits on evolutionary potential and reduced opportunities for convergent adaptation during post-domestication migration to new environments. Here we review current knowledge regarding trait convergence in the cereal grasses and consider whether the complexity and dynamism of cereal genomes (e.g., transposable elements, polyploidy, genome size) helped these species overcome potential limitations due to domestication and achieve broad subsequent adaptation.

Introduction

Certain species of plants have been continually selected over the last 10,000 years to better meet the needs of humans. Similar selection pressure has favored traits that consistently distinguish these domesticated crops from their wild progenitors [16], distinctions that are shared even among distantly related species such as maize and sunflower. These traits include increased yield, apical dominance or lack of branching, loss of seed dormancy, loss of bitterness, and loss of shattering or seed dispersal. Collectively, this suite of shared traits is known as the domestication syndrome [36].

Trait sharing among diverged species such as maize and sunflower (their last common ancestor was 150 MYA [11]) is an example of the phenomenon of convergence. Convergent traits can arise from unrelated genes in different enzymatic pathways, such as fruit/seed indehiscence in both dicot and monocot crops (reviewed in [17]). But if a convergent trait is caused by repeated modification of the *same* molecular pathway, ortholog, or nucleotide, we define this as parallelism [85] (Figure 1). We expect that parallelism is more likely to occur in closely related species due to their similar complement of genes and pathways [79], and less likely to occur in substantially diverged species that contain fewer orthologous loci and pathways [100, 79].

After the initial wave of crop domestication yielded convergence in many of the aforementioned domestication syndrome traits, another period of trait evolution ensued—the adaptation of crop

species to varied environmental conditions and pathogens during global expansion. A variety of maize bred for cultivation at sea level, for instance, may not necessarily thrive in the colder, higher UV environment of the Andes mountain range. Therefore, cultivators in the Andes must have looked for individuals in the existing domesticated maize population that were hardy under these new conditions. However, crop adaptation occurred under genetic limitations not experienced during domestication of wild progenitors [97].

Only a subset of genome-wide diversity was retained in initial domesticates and additional diversity was lost through subsampling events during crop expansion. Furthermore, selection on particular alleles coding for domestication traits often resulted in dramatic reductions in diversity in particular chromosomal regions. The effects of this loss of genetic diversity on the potential for adaptation has been documented. For example, a dramatic genetic bottleneck in the “lumper” variety of potato led to a catastrophic outbreak of *Phytophthora infestans*, resulting in the infamous Potato Famine in Ireland in the 1840s [33]. The Potato Famine demonstrated that, by divesting a crop cultivar of its diversity, the cultivar loses its ability to adapt to newly encountered environmental pressures, because the alleles that code for adaptive traits such as, for instance, disease resistance are lost.

This review will consider the extent to which selection and bottlenecks during domestication have affected the potential for parallel adaptation post-domestication. We will focus mainly on cereal grass crops since the major domesticates—maize, rice, sorghum, wheat, barley, and millet—include a range of divergence times conducive to parallel adaptation and evolution of domestication syndrome traits. The cereals also share a specific domestication phenotype whereby the end product is a millable grain. While the cereals have documented loss of diversity due to domestication and subsequent expansion, they possess dynamic genomes with frequent polyploidization, transposable element (TE) activity, and labile genome size. These features may have provided cereals with an advantage in escaping the limits of domestication by generating novel diversity.

The effects of domestication on adaptation in the cereals

Domestication in the cereals

Cereal grasses have often been studied as a cohesive genetic group [7, 26], and there are many reasons why they present a compelling system for studying crop domestication. The grass clade is thought to have arisen around 75 MYA [9, 51], eventually leading to the rice, wheat, barley, millet, maize, and sorghum lineages (Figure 2). Prior to the radiation of the grasses, however, a genome duplication event occurred approximately 70 MYA [77], which is shared among all grass crops (Figure 2). Subsequently, both maize and wheat have undergone additional, lineage-specific polyploidy events (Figure 2) [60]. These polyploidy events, followed by selective and ongoing fractionation, present an opportunity for grass genomes to evolve subfunctionalized homeologs; this, along with relatively high transposon activity (particularly in maize and wheat) that can give rise to functional mutation [103, 63], make the grasses a useful system for studying the potential for adaptation after a domestication bottleneck.

Additionally, most grass crops were domesticated within the latitudinal boundaries of the equator and 35 N [42, 30], featuring both wet and dry seasons [42], which means that many domesticated grasses shared similar environmental pressures such as temperature, precipitation and day length, despite the fact that each of these cereals has been cultivated in separate geographic locations, including maize (Americas), sorghum (Africa), rice (Asia), millet (Eurasia), and wheat and barley (the Middle East) [32]. Taken together, these features make domesticated grass species especially conducive to the meaningful study of convergence.

A number of domestication genes have been characterized in Table 1, [a table which was originally featured in \[59\] and which we adapted and modified for this review](#). Many of the genes in this table have orthologs within the cereal grasses, some of which are found in all cereals, some of which are species-specific. These are among the genes that were probably selected for during cereal domestication, and it is helpful to delineate domestication vs adaptive genes going forward.

Post-domestication adaptation in the cereals

An adaptive trait is one that interacts or responds to the environment in a way that helps an organism to thrive. By this definition, adaptive traits can include (but are not limited to) flowering time, drought tolerance, cold tolerance, soil salinity, and pathogen defense. For domesticated crops, however, adaptive traits that reverse desired domestication phenotypes such as yield, fragrance, flavor, or reduced shattering would not be considered favorable; therefore, we will narrow the definition of an adaptive trait to one that interacts or responds to the environment favorably but does not detract from desired domestication traits.

Perhaps it is also necessary to define what specifically is meant by “environment”. A straightforward (and admittedly simplistic) way would be to break “environment” down to discrete features, which can include, for example, the level of carbon dioxide in the air, the level of UV radiation, temperature, day length, humidity, rainfall, wind, soil nutrient load, and soil salinity. By dividing the environment into these discrete elements, we can address each element individually by asking what sort of adaptive trait we would expect to observe in response to each, how many of these adaptive traits are expressed in the same genetic pathways as known domestication genes, and which represent entirely distinct physiological processes.

Selection during domestication on genes relevant to adaptation during expansion could constrain adaptation and affect the likelihood that adaptation to similar environmental conditions occurs in parallel across species. Genome-wide loss of diversity during genetic bottlenecks associated with both initial domestication and later crop expansion can also constrain adaptation by reducing the diversity in cereal crop populations. Domestication bottlenecks are a demographic process in which cultivators derive a domesticate from a subset of wild populations and has been well documented (*e.g.*, [97]). Massive loss of nucleotide diversity during domestication is reported in domesticated bread wheat [37], maize (with an increase in deleterious alleles) [21, 97], rice [116], Sorghum [35], and barley [52] compared with wild relatives, demonstrating that loss of diversity is widespread in cultivated grasses and is a phenomenon that is distinct from uncultivated wild relatives. It would seem that domestication itself is responsible for the loss of diversity, and because of this, attempts to adapt domesticated grasses to new environments could be constrained by recent demography. We propose that both demographic bottlenecks and selection during domestication can affect the likelihood that adaptive traits would be selected in parallel, since these depend on whether adaptive alleles are retained across taxa post-domestication.

Predicting the likelihood of parallelism in post-domestication cereal adaptation

If the process of domestication reduces the chances of parallel adaptation in cereal crops, are there ways that the cereals can escape from these constraints and generate adaptive alleles? And if so, can we predict what sorts of adaptation are likely to be parallel? The likelihood that an adaptive trait will be selected in parallel is summarized in Figure 3. Here, we will focus primarily on our expectations for post-domestication parallel selection of adaptive traits in the cereals relative to (1) whether an adaptive gene is orthologous in other species; (2) whether an adaptive gene functions also as a domestication gene; (3) mutation rate; and (4) mutational target size; and how the dynamics of cereal crop genomes may uniquely influence some of these expectations.

Adaptive genes that have orthologs in other species

A relatively simple way to predict the possibility of parallel adaptation is whether a gene characterized as functioning in an adaptive capacity is orthologous across taxa. An ever-increasing number of causal genes for adaptation are being identified both within and outside of the grasses; some of these genes are listed in Table 1. In this table, adaptation genes that have been characterized can be categorized based on whether they occur strictly within a species, share orthologs across the grasses, share orthologs within and outside of the grasses, or share orthologs entirely outside of the grasses (Column 5). This gives us an opportunity to form hypotheses regarding the likelihood of parallelism for a certain trait based on its known orthology across taxa (Column 8, Table 1). If an adaptive gene is orthologous across taxa, there is possibility of parallel adaptation.

One example of a gene thought to confer adaptation is *ZmCCT9* in maize, which appears to be involved in flowering under the long days of higher latitudes. More specifically, a transposon insertion upstream of *ZmCCT9* in domesticated maize cultivars led to reduced photoperiod sensitivity, which has allowed domesticated maize to expand its range [39]. This gene has orthologs in barley and wheat (Column 3, Table 1); therefore, there is a good chance that the ortholog exists in other cereal crops as well (where it has yet to be characterized), and thus we can estimate that parallel convergence of this trait is possible in those species. Another adaptive gene is the maize *ZmVPP1* gene, where an upstream insertion is linked to drought tolerance [99]. Since this gene has an ortholog linked to drought tolerance in Arabidopsis, *AVP1* [29], orthologs may exist elsewhere in the cereals as well. Wheat and barley share a small family of cold-tolerance genes including *Wcs19* [12], *Wcor14* [95] and *Bcor14b* [14], all of which encode chloroplast-targeted COR proteins analogous to the Arabidopsis protein *COR15a* [89, 92]. The LEA protein orthologs *HVA1* and *Wrab 18/19* in barley and wheat, respectively, are also associated with cold tolerance [38, 20]. Transcript and protein levels of the barley *HvPIP2* aquaporin gene were found to be down-regulated in roots but up-regulated in the shoots of plants under salt stress [48]. *HvPIP2* has an ortholog in maize, *ZmPIP2-4* [115], and in spinach, *PM28A* [24]. There are also the ASR (abscisic acid, stress, and ripening-induced) genes that are associated with salinity tolerance in rice [46], *Setaria* (millet) [61], and tomato [53].

However, another drought-tolerance gene in rice, *OsAHL1* [113], does not appear to have a characterized drought-tolerant ortholog in any other species at the time of this writing. While this ortholog may certainly exist undiscovered in other grasses, there are some adaptive traits, specifically traits involved in pathogen resistance and stress response, that are less likely to have orthologs, even in closely related species. There are examples of shared orthologs for pathogen defense and stress response genes in the grasses (Table 1), but by and large, genes that code for traits involved in plant defense and stress response are frequently orphan genes, or genes that are specific to a particular lineage and share no defined orthologs with any outgroup [105]; reviewed in [1]. Orphan genes tend to be very dynamic, arising and becoming lost much faster than their basal counterparts [27]. Orphan genes can arise via transposon exaptation [18] and propagate through trans duplication [27, 1], including retrotransposition [98]. Therefore, movement of these genes to a new region whose local euchromatic status can confer novel expression patterns to the mobilized gene can be a strong source of adaptation, especially since it has been shown that stressful environments can stimulate activation of transposable elements [6, 66] reviewed in [73]. This is one way that cereal crops might be able to escape the legacy of reduced diversity due to domestication in order to adapt. If an adaptive trait such as pathogen resistance is dependent on these orphan-type genes, which quite often are unique even in individual cultivars within the same crop species, then we would not expect to see parallel selection of this trait at the allelic level in cereal adaptation, since each species—indeed, each cultivar—would be expected to have its own unique, "outward-facing" suite of orphan genes that would confer environmental adaptation uniquely to its niche.

Domestication genes that have adaptive components

Table 1 provides a starting point to predict which adaptive genes are likely to be found across the grasses, and which traits in the grasses are likely to be selected in parallel. In addition to enhancing our basic understanding of the repeatability of evolution, this is useful if we wish to breed wild grass relatives for adaptive traits, or create hybrids among existing cultivars, since we can now associate favorable phenotypes and QTL with orthologs across species by simple comparative genomics. But to what extent can this knowledge help us to understand how domestication has impacted a crop's ability to adapt to new environments and the extent to which adaptation is in parallel across crops? We propose that a gene involved in domestication is less likely to be selected for in adaptation, if the adaptive function reverses the domestication phenotype. Therefore, it is useful to define genes that are known to function as domestication genes versus those that have been characterized as adaptive (Column 1, Table 1). Table 1 collates examples of adaptation traits to domestication traits, where probable, using the definition of adaptation as described above.

There are a number of adaptive traits described previously, such as drought tolerance, cold tolerance, soil salinity, and pathogen defense, that are unlikely to have a domestication component, since they appear unrelated to previously described domestication syndrome traits. Some of these adaptive traits have characterized genes described in Table 1. However, there are genes described in Table 1 that can be potentially associated with both adaptation and domestication during crop expansion. For example, the *Ghd7* gene in rice has been associated with agronomic traits such as grains per panicle, plant height and heading date; however, natural variants with reduced function allow rice to be cultivated in cooler regions [108], which is an adaptive phenotype. Another example of a domestication trait with an adaptive component is pigmentation. Loss of pigmentation

has been favored in a variety of cereal cultivars, from rice to maize, as a cultural preference during domestication. As it turns out, pigment assists with UV tolerance in cereals and other plant species, particularly at high elevation [88, 34]. Therefore, pigmentation could lead to greater tolerance of UV radiation in cereals colonizing high elevation post-domestication [80]. Loss of allelic diversity due to selection during domestication may reduce adaptive potential when the same genes control domestication and adaptation phenotypes. Thus it may be less likely that genes that are selected during domestication would also be selected in parallel for adaptive traits, and we would not expect that orthologs to these genes across taxa would undergo parallel adaptation.

But there is one way that a genome may escape from this constraint, and that is through polyploidy. Whole-genome duplication events can result in homeologs that may undergo subfunctionalization or neofunctionalization and give rise to adaptive loci. Neofunctionalization of homeologs is widespread in maize [40] and in bread wheat [78], which have both undergone recent, lineage-specific polyploidy events (Figure 2). To some extent, it can be predicted which homeolog in a post-polyploid cereal is likely to be adaptive. It is known that of the two retained post-polyploidy subgenomes in maize, one undergoes less fractionation and is more highly expressed than the other (i.e. the dominant subgenome) [106, 86], and there is evidence that fractionation is biased not only in maize, but in wheat as well [19]. Schnable and Freeling found that of the characterized genes that have a known mutant phenotype, the majority are on the less fractionated subgenome [87]. Many of these genes, such as *tb1*, *Waxy*, *Opaque2*, and several starch synthesis and coloration genes not in Table 1, have a domestication syndrome phenotype in maize. Additionally, recent work has suggested that the genes on the more highly expressed subgenome in maize contribute more to phenotypic variation than the less expressed subgenome across a wide variety of traits, including those linked to adaptation [83]. Indeed, two genes associated with adaptive phenotypes in maize from Table 1, *ZmVPP1* (drought tolerance) and *ZmPIP2-4* (soil salinity) are both found on the less fractionated subgenome [87]; and genes associated with adaptation phenotypes such as disease resistance have also been observed on the more dominant subgenome in [83]. Parallelism in recent polyploids, therefore, may be more likely within the more dominant subgenome.

Mutation rate

As we have seen, selection for adaptive traits in crop species can be fundamentally constrained by demography during domestication, primarily due to the population bottleneck that frequently accompanies domestication. This factor may have limited the extent of parallelism during adaptation in the cereals relative to more diverse, wild species. However, this limitation imposed by the domestication bottleneck in grass crops may to some extent be reversed due to their dynamic genomes, particularly their high transposon activity relative to other crop species, which can lead to a higher mutation rate and a larger mutational target size.

We have seen that grasses tend to have relatively active transposons, and this transposon activity may permit a higher mutation rate in cereals [103]. In Table 1, several adaptive phenotypes are due to a transposon insertion somewhere in the functional region of a gene, such as *ZmCCT9* and *ZmVVP1* in maize. However, a comprehensive review of TEs and plant evolution [64] suggests that our understanding of the role of transposable element activity in crop adaptation is largely anecdotal and might be overstated, but perhaps can be better elucidated by harnessing the recent advances in genomics such as more sophisticated TE annotation protocols, whole-genome sequencing, and comparative algorithms. Using these advances in genome biology, a recent study

by Lai and coworkers found that transposon insertions may have played an important role in creating the variation in gene regulation that enabled the rapid adaptation of domesticated maize to diverse environments [58]. We propose that a higher mutation rate in cereal crops due to transposon insertion increases the chances for new beneficial adaptive mutations at a given locus, and thus increases the likelihood of parallelism of an adaptive orthologous gene or pathway compared to other crop species.

Mutational target size

Transposable elements may also result in meaningful differences in genome size across cereal crops. Transposons are known to contribute to the expansion of genome size in maize and other plant species [93] (reviewed in [64]). A recent review [69] suggests that larger genomes may affect the process of adaptation by increasing the number and location of potentially functional mutations, thus expanding the regulatory space in which functional mutations may arise. This may increase the likelihood that a given orthologous gene or pathway could be selected in parallel for adaptive traits, despite losses of diversity experienced during domestication. In this way, cereal grasses may be more poised than other crop species to reverse the effects of their domestication bottlenecks, and increase the chances of parallel adaptation, due to their high rates of transposon activity.

Conclusions

This review set out to explore how domestication has influenced the potential for subsequent adaptation in the grasses, and the extent to which we could predict parallel adaptation in cereal crops. Demographic bottlenecks and targeted selection during domestication have removed potentially adaptive variation which may, in turn, reduce the extent of parallelism observed during adaptation. We hypothesize that parallelism in adaptation in cereal crops is affected by: (1) whether an adaptive gene is orthologous across taxa; (2) whether an adaptive trait is related to the domestication syndrome; (2) the strength of the domestication bottleneck in a particular species; and (3) the level of plasticity across the genome affecting gene copy number, mutation rate, and mutation target size. As demonstrated in Table 1, the causal loci underlying adaptation in the grasses are increasingly becoming clear. Comparative genomic analyses of cereals and their wild relatives combined with comparative studies of uniquely adapted populations will help further distinguish genes involved in these processes and characterize whether selection occurred in parallel. The genomic study of time-stratified archaeological samples will help further clarify the timing of selection and the extent to which parallelism in adaptation is conditioned on initial selection during domestication. Crops in the grass family have been very successful in adapting to a wide range of environmental conditions despite limitations in adaptive potential due to domestication, perhaps due to their active TEs, their history of polyploidy, and their large genomes. As the genetic basis of adaptation becomes more clear, genes involved in adaptation across both wild and domesticated grasses can be compared to fully evaluate the limits domestication places on parallelism in adaptation.

Authors' Contributions

M. Hufford devised the theme and general concepts of domestication, adaptation, and parallelism. M. Woodhouse devised the sections relating to grass genome plasticity, orthology, and orphan genes. M. Woodhouse and M. Hufford contributed equally to the drafting and the editing of the article.

Competing Interests

The authors report no competing interests.

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Table 1: Parallel or Convergent Orthologies (adapted from Lenser and Theissen, 2013 [59])

Trait type	Phenotypic trait	Crop species	Ortholog phylogeny	Phylogeny of domestication trait	Orthologous gene(s)	Gene product	Potentially parallel?	References
domestication	Determinate growth	Tomato, soybean, common bean	Family/above family	outside the cereals	SP, Drl1, PvTFL1y	Signaling protein	parallel	[16, 84, 65, 57, 94]
domestication	Dwarfism	Rice, barley	Family	grass-wide	OsGA20ox-2, HvGA20ox-2	Metabolic enzyme	parallel	[3, 2, 44]
domestication	Dwarfism	Sorghum, pearl millet	Family	grass-wide	dw3, d2	Transporter protein	parallel	[70, 76]
domestication	Dwarfism	Wheat	Species	species-specific, grass	Rht-1	SH2-TF	unknown	[16]
domestication	Fragrance	Rice, soybean	Species/family	cereals and beyond	BADH2, GmBADH2	Metabolic enzyme	parallel	[55, 47]
domestication	Glutinous seeds	Rice, wheat, maize, foxtail millet, barley, amaranth, sorghum, broomMaize millet	Species/family/above family	cereals and beyond	GBSSI, Waxy	Metabolic enzyme	parallel	[43, 22, 49, 50, 41, 75]
domestication	Grain quality	Maize	Species	species-specific, grass	Opaque2	bZIP-TF	unknown	[67]
domestication	Shatter resistance	Sorghum, rice, maize	Family	grass-wide	Sh1, OsSh1, ZmSh1	YABBY-like TF	parallel	[62]
both	Coloration	Pea, potato	Above family	outside the cereals	flavonoid 3',5'-hydroxylase	Metabolic enzyme	parallel	[67]
both	Coloration	Rice, potato	Species/above family	cereals and beyond	Rd/DFR, DFR	Metabolic enzyme	parallel	[28, 112]
both	Coloration	Blood orange	Species	species-specific, outside cereals	Ruby	MYB-TF	unknown	[10]
both	Coloration	Rice	Species	species-specific, grass	Bh4	Transporter protein	unknown	[114]
both	Coloration	Soybean	Species	species-specific, outside cereals	R	MYB-TF	unknown	[31]
both	Coloration	Rice	Species	species-specific, grass	Rc	bHLH-TF	unknown	[67]
both	Coloration	Grapevine	Species	species-specific, outside cereals	VvMYBA1-3	MYB-TF	unknown	[67]
both	Flowering time	Barley, pea, strawberry	Above family	cereals and beyond	HvCEN, PsTFL1c, FvTFL1	Signaling protein	parallel	[13, 25, 54]
both	Flowering time	Rice, barley, pea, lentil	Family/above family	cereals and beyond	Hd17, EAM8, Mat-a, HR, LeELF3	Circadian clock	parallel	[102, 68, 111, 23]
both	Flowering time	Rice, wheat, sunflower, barley	Family/above family	cereals and beyond	Hd3a (Heading date 3a), VRN3/TaFT, HsFT1, HvFT	Signaling protein	parallel	[109, 91, 8]
both	Flowering time	Sorghum, rice	Family	grass-wide	Ghd7, SbGhd7	CCT domain protein	parallel	[108, 72]
both	Flowering time	Turnip, Brassica oleracea	Family	outside the cereals	BtFLC2, BoFLC2	MADS domain TF	parallel	[107, 110, 74]
both	Flowering time	Barley, wheat, ryegrass	Species/family	grass-wide	VRN1, BM5, TmAP1, WAP1, LpVRN1	MADS domain TF	parallel	[4]
both	Flowering time	Rice, barley, wheat, sorghum, sugar beet	Species/family/above family	cereals and beyond	OsPRR37, Ppd-H1, Ppd1, SbPRR37, BvBTC1	Circadian clock	parallel	[71, 96, 45, 5, 104, 15]
both	Flowering time	Rice	Species	species-specific, grass	Hd1	Zinc finger TF	unknown	[67]
both	Plant architecture	Maize, pearl millet, barley	Family	grass-wide	tb1, Pgtb1, INT-C	TCP-TF	parallel	[90, 82, 81]
both	Plant architecture	Barley	Species	species-specific, grass	VRN1	Homeodomain-TF	unknown	[67]
adaptation	Cold tolerance	Barley, wheat	Family	grass-wide	HVA1, Wrb18, Wrb19	LEA protein	parallel	[38, 20]
adaptation	Cold tolerance	Wheat, barley	Family	grass-wide	Wcs19, Wcor14, Wcor15, Bcor14b	Cor protein	parallel	[92]
adaptation	Drought tolerance	Maize, Arabidopsis	Above family	cereals and beyond	ZmVPP1, AVP1	H(+) pyrophosphatase	parallel	[99]
adaptation	Drought tolerance	Rice	Species	species-specific, grass	OsAHL1	AT-hook PPC domain	unknown	[113]
adaptation	Flowering time	Barley, wheat, maize	Species/family	grass-wide	VRN2, ZCCT1, ZmCCCT9	CCT domain protein	parallel	[39]
adaptation	Metal tolerance	Wheat, rye	Family	grass-wide	TaALMT1, ScALMT1	Transporter protein	parallel	[67]
adaptation	Metal tolerance	Sorghum, Maize	Family	grass-wide	SbMATE1, ZmMATE1	Transporter protein	parallel	[67]
adaptation	Pathogen resistance	Wheat, rice, sorghum	Family	grass-wide	LR34	ABC transporter	parallel	[56]
adaptation	Pathogen resistance	Maize	Species	species-specific, grass	Rp3	NBS-LRR	unknown	[101]
adaptation	Soil salinity	Barley, maize, spinach	Above family	cereals and beyond	HvPIP2:1, ZmPIP2-4, PM28A	Aquaporin	parallel	[48, 115, 24]
adaptation	Soil salinity	Rice, foxtail millet, tomato	Above family	cereals and beyond	OsASR1, OsASR3, SiASR1, SiASR1	ABA stress ASR protein	parallel	[61, 53]

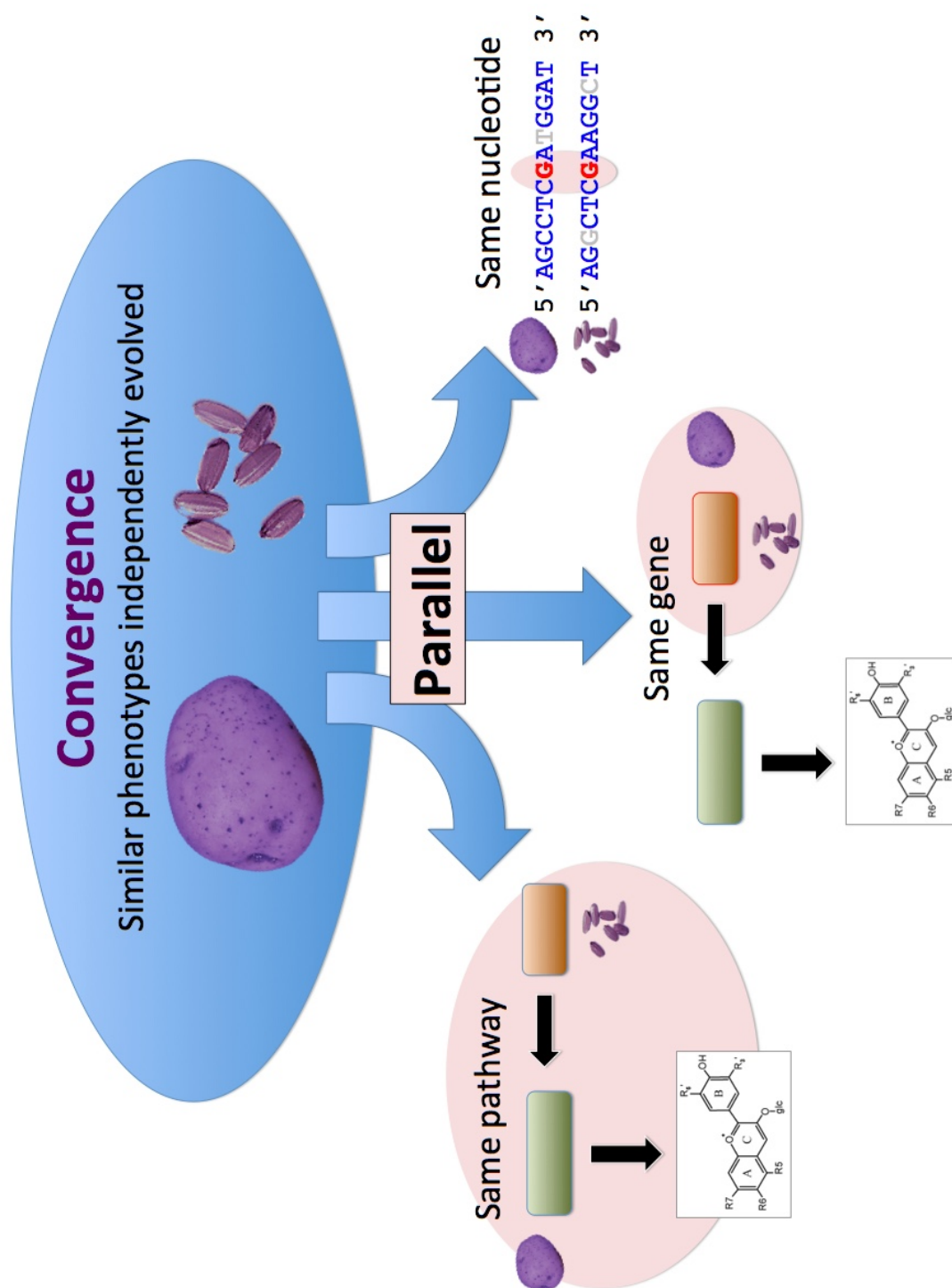


Figure 1: Figure describing parallelism in convergence. Convergence is the phenomenon whereby similar traits, such as purple pigmentation in potato and rice in this example, arise independently in different species. Parallelism is when convergent traits are caused by modification of the same molecular pathways, genes, or nucleotides.

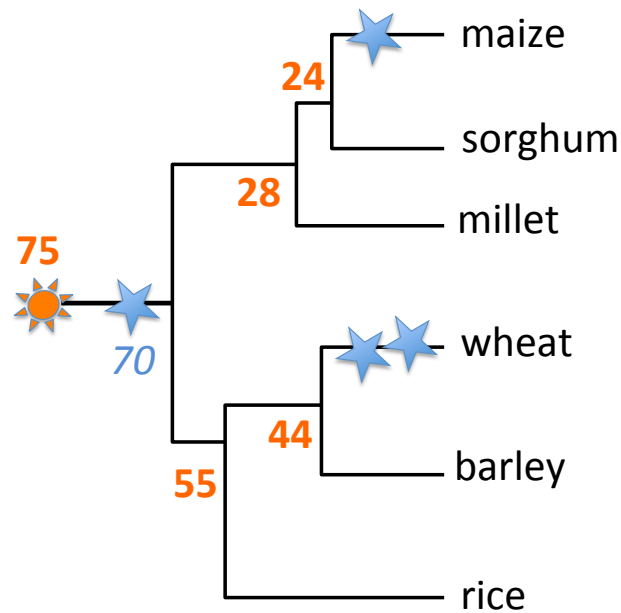


Figure 2: Simple cladogram of major cereal speciation. Numbers are in MYA (millions of years ago). Orange sun: grass speciation event 75 MYA. Blue stars: polyploidy events; the major grass polyploidy event immediately after the grass speciation event occurred approximately 70 MYA. The Ehrhartoideae clade, which includes rice, arose approximately 55MYA. The Pooideae clade, which includes wheat and barley, arose around 44MYA; Chloridoideae which contains foxtail millet 28 MYA, and the Panicoids, which include maize and sorghum, arose approximately 24MYA. The branch length is not proportional to the number of substitutions per site.

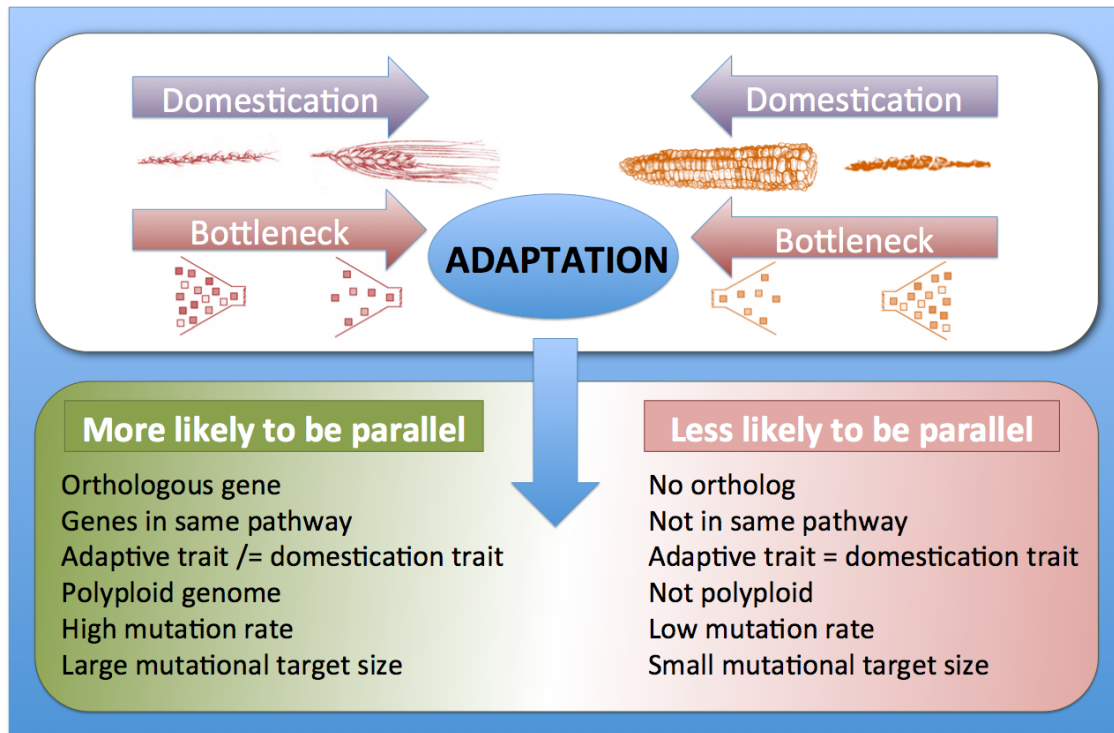


Figure 3: Figure describing the likelihood that post-domestication adaptation would be parallel. The top panel describes a simple representation of spike domestication in wheat (top left) and maize (top right). Alongside the domestication of each crop is the resulting bottleneck. After the domestication of both crops, any adaptation must result from a population with lower diversity in each crop species. The likelihood of parallel adaptation is compromised due to this lower diversity, but parallelism may still result if certain criteria are met (bottom panel, on the left).