Evolutionary rescue through gene flow despite genetic incompatibilities shaped diversity of the pseudo-cereal grain amaranth

José Gonçalves-Dias[*,†], **Akanksha Singh**[*,†], **Corbinian Graf**[†] **and Markus G Stetter**[*,‡]
[*]These authors contributed equally, [†]Institute of Plant Sciences, University of Cologne, Cologne, Germany, [‡]Cluster of Excellence on Plant Sciences, University of Cologne, Cologne, Germany

Crop domestication and the subsequent expansion of crops have long been thought of as a linear process from a wild ancestor to a domesticate. However, evidence of gene flow from locally adapted wild relatives that provided adaptive alleles into crops has been identified in multiple species. Yet, little is known about the evolutionary consequences of gene flow during domestication and the interaction of gene flow and genetic load in crop populations. We study the pseudo-cereal grain amaranth that has been domesticated three times in different geographic regions of the Americas. We quantify the amount and distribution of gene flow along the genome of the three grain amaranth species and their two wild relatives. Our results show ample gene low between crop species and between crops and their wild relatives. Genetic load in introgressed regions from different donors suggest the potential of evolutionary rescue through decreased genetic load in genomic regions contributed by wild relatives with larger population size. To assess fitness of early hybrids we performed experimental crosses between the three crop species and found genetic incompatibilities between one Central American grain amaranth and the other two crop species. These incompatibilities might have created recent reproductive barriers, and maintain species integrity today. Together, our results show that gene flow played an important role in the domestication and expansion of grain amaranth, despite genetic species barriers. The domestication of plants was likely not linear and created a genomic mosaic by multiple contributors with varying fitness effects for today's crops.

KEYWORDS Gene flow, Genetic load, Evolutionary rescue, Grain amaranth, Hybrid incompatibilities

Introduction

Evolution and speciation has long been viewed as a linear process with a single ancestor giving rise to one or more derived species. Genomic data of large samples have revealed ancestry of different species within modern populations in a number of species (Harris and Nielsen 2016; Niu *et al.* 2019; Chomicki *et al.* 2020; Kozak *et al.* 2021; Orlando *et al.* 2021; Lv *et al.* 2022). Particularly in plants where reproductive barriers are often weak the potential for the exchange of genetic material between related species is rather high (Ostevik *et al.* 2016; Osuna-Mascaró *et al.* 2023; Sheidai and Koohdar 2023). Yet, the observation of exchanging genetic material between species is often seen as an exception and as a minor contribution to the genomic composition of a species.

Gene flow describes the process of exchanging genetic information between populations or even species (Rieseberg and Burke 2001). While interbreeding between populations might be frequent, the manifestation of gene flow between locally adapted populations or even species is thought to be rare as it would decrease fitness. Nevertheless, beneficial gene flow has been shown to be an important source of variation for local adaptation (Crispo 2008; Sexton *et al.* 2011; Ellstrand 2014; Tigano and Friesen 2016; López-Goldar and Agrawal 2021). At least partial fertility of hybrids is required, and compatibility between donor and recipient determines the intensity of gene flow (Aguillon *et al.* 2022). In the course of speciation, the ability to form viable hybrids can be lost, and reproductive barriers that prevent gene flow can evolve. Hence, hybrid incompatibility can hinder gene flow and lead to reproductive isolation. Yet, reproductive isolation in plants is often incomplete or is circumvented by intermediate populations, allowing for gene flow even between different species.

The domestication of crops and animals led to a major transition in human lifestyle and had profound im-

[1] Dept. of Plant Sciences, University of Cologne, Cologne, Germany E-mail: m.stetter@uni-koeln.de

pact on the genetic makeup of the domesticates (Doebley 2006). Crop domestication can be seen as rapid evolution, often leading to speciation. Even more than speciation in general, crop domestication has long been described as a linear process starting from one wild species evolving through strong directional selection into a domesticate. However, this view has been challenged in recent years, where gene flow from wild relatives have been documented in a number of crops, including maize (Ross-Ibarra *et al.* 2009), rice (Yang *et al.* 2012), barley (Civáň *et al.* 2021), sorghum (Smith *et al.* 2019), tomato (Razifard *et al.* 2020), *brassica* (Saban *et al.* 2023) and others (Luo *et al.* 2007; Ding *et al.* 2022; Page *et al.* 2019; Liu *et al.* 2019). Reproductive isolation of the crop from its wild relatives would ensure the maintenance of domestication traits, hence, the success of domestication (Dempewolf *et al.* 2012). Gene flow from wild relatives would have led to a reduction of domestication related phenotypic changes. Early generations of crop-wild hybrids would be rather unfit as wild plant or crops, as their adaptive traits strongly differ (Janzen *et al.* 2019; Stetter 2020). Yet, gene flow from wild relatives could have increased the genetic variation in early crops, which could have been beneficial to increase adaptive potential (Smith *et al.* 2019). In addition, gene flow from locally adapted wild relatives has been shown to have provided alleles that allowed the crop population to establish in novel environments (Van Heerwaarden *et al.* 2011; Hufford *et al.* 2013; Wang *et al.* 2021).

Plant domestication has likely been driven by demographic changes and directional selection. Domestication bottlenecks reduced the effective population size, leading to an accumulation of mildly deleterious alleles in the population (Gaut *et al.* 2018). Selection on major effect domestication genes might have allowed hitchhiking of linked mildly deleterious alleles (Sedivy *et al.* 2017). Together these effects increased genetic load – the accumulation of deleterious alleles – in the crop population (Bertorelle *et al.* 2022). Several studies have assessed the accumulation of genetic load in domesticates compared to their wild relatives, e.g., rice (Lu *et al.* 2006; Xu *et al.* 2006; Nabholz *et al.* 2014), maize (Rodgers-Melnick *et al.* 2015; Gaut *et al.* 2015), and soybean (Kim *et al.* 2021). While an accumulation of genetic load has been detected in many domesticated species, no increase has been detected in sorghum, potentially due to the transition to selfing in the crop (Lozano *et al.* 2021). Gene flow from wild relatives with larger effective population size into crop populations might have reduced the genetic load (Stetter 2020). In sorghum gene flow between landraces resulted in decreased genetic load across landraces (Smith *et al.* 2019). However, such evolutionary rescue by gene flow from wild relatives into domesticates has received little attention. We study the effects of gene flow on genetic load in a three times domesticated crop and its wild relatives to understand the evolutionary role of gene flow and genetic load during crop domestication.

Grain amaranth is a nutritious pseudo-cereal from the Americas that has been domesticated three times from one ancestral species (*A. hybridus*). Two grain amaranths were domesticated in Central America (*A. cruentus, A. hypochondriacus*) and one in South America (*A. caudatus*) (Sauer 1967). The taxonomic complexity of the *Amaranthus* genus led to different domestication scenarios for the crop (Sauer 1967; Kietlinski *et al.* 2014; Stetter *et al.* 2017). Population genetic and genome-wide selection signals suggest subpopulations of *A. hybridus* as ancestors for all three grain amaranths (Stetter *et al.* 2020). In South America, the closely related *A. quitensis* was potentially involved in the domestication process of *A. caudatus* and genome-wide signals of gene flow between grain amaranths and their wild relatives have been detected previously (Kietlinski *et al.* 2014; Stetter *et al.* 2020). While the three grain amaranth species have been cultivated as a crop in different regions of America for thousands of years, all three lack key domestication traits (Stetter *et al.* 2017). A potential reason for the lack of domestication traits might be continuous gene flow from wild relatives that prevented domestication traits to fix (Stetter 2020). Understanding the underlying genomic signatures of gene flow and selection could improve the understanding of evolutionary history of crops (Meyer *et al.* 2012).

In this study, we use population-wide whole genome sequencing data and reveal the mosaic signature of gene flow along the genome of domesticated amaranths. We find strong signals of gene flow even between the three geographically isolated domesticated species. Besides post-domestication gene flow between crops, we also observed high levels of genetic exchange between the South American wild species and the local crop. A hybridization experiment between three crops indicates genetic incompatibility between *A. cruentus* and the other two grain amaranths. This reproductive barrier might be a contributing factor to the different rates of gene flow observed between species despite their geographic distances. Gene flow from the wild ancestor *A. hybridus* into the domesticated amaranths reduced genetic load in the crops but that only few positively selected regions were exchanged through gene flow between crop species. Gene flow might be an important source of genetic variation for crops, not only to provide adaptive alleles but also to reduce genetic load and allow further selection.

Results

Strong post-domestication exchange between crops

Gene flow likely played an important role during the domestication of different crops (Janzen *et al.* 2019). In grain amaranth genome wide signals of gene flow between species have been previously reported (Stetter *et al.* 2017, 2020). In order to quantify gene flow among different domesticated and wild populations, we measured ancient admixture using the D-statistic (ABBA-BABA) for all possible tree topologies using ANGSD (Korneliussen *et al.* 2014) in whole genome sequencing data of six population

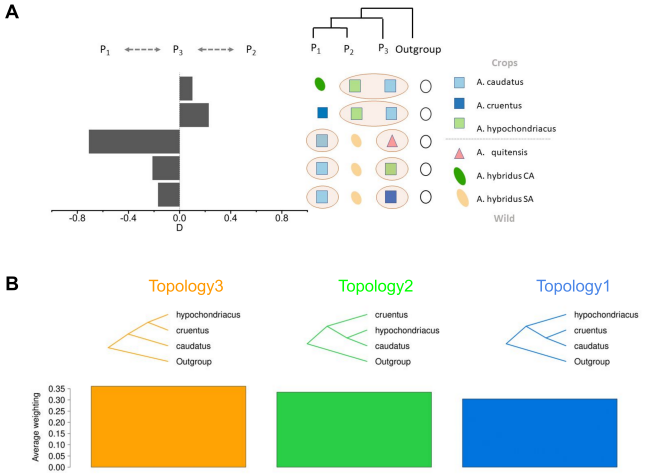

Figure 1 Genome-wide signals of gene flow. A) Gene flow between amaranth populations (exchanging pairs highlighted in yellow). D-value indicate the strength of gene flow. Only significant signals of gene flow are shown. B) Genome-wide summary of tree topologies along the genome inferred by Twisst. Proportion of each of the three topologies observed along the genome shown in bars.

samples of domesticated (caudatus: *A. caudatus*; cruentus: *A. cruentus*; hypochondriacus: *A. hypochondriacus*) and wild amaranth (hybridus_CA: *A. hybridus* from Central America; hybridus_SA: *A. hybridus* from South America and quitensis: *A. quitensis*). We identified gene flow between crop species, and between crops and their wild relatives. We found ample gene flow even between geographically distant crop species (Figure 1A). The strongest signal was identified for the Central American crop hypochondriacus and the South American caudatus. This signal was robust even when changing the third species in the test (Figure 1A and Table S1). The test also identified gene flow between the South American crop species caudatus and the second Central American grain amaranth cruentus. However, the strength of gene flow between them was lower. This is also shown when the three grain species were tested in the same tree, where a significant level of gene flow between caudatus and hypochondriacus was identified (D=0.22; Figure 1 A, second row), showing that the signal of gene flow between the two species is higher than shared variation of the three. As both Central American grain amaranths were domesticated from Central American hybridus and the exact sub populations of the ancestor that gave rise to each crop remain unknown, we could not test directly for gene flow between the two Central American grain species. The high level of exchange of genetic material between species was also shown by tree topology tests using Twisst (Martin and Van Belleghem 2017). While the expected tree topology along the genome with the two Central American crops being closest was most common, the other two alternative topologies were only slightly less abundant (Figure 1B). Altogether, more gene flow was observed between two allopatric crop species caudatus and hypochondriacus, and less gene flow was observed with cruentus.

We tested whether isolation with gene flow between hypochondriacus and caudatus was a better fitting model than a simple split without further gene flow, by simulating demographic histories using Fastsimcoal2 (Excoffier *et al.* 2013). We investigated for three alternative models: population split without gene flow, population split with one-time gene flow and population split with continuous gene flow (Figure S1). The model for a population split with continuous gene flow was obtained as the best model (Table S2), suggesting that this is the most suitable scenario (Figure S1). In addition, this model predicts population splits estimates that coincides with previous observations (Stetter *et al.* 2020).

In addition to gene flow between crop species, we examined gene flow signals between the crops and their wild relatives. We found the strongest signal of gene flow between the sympatric South American grain crop caudatus and the local wild quitensis with a D-value of -0.71, indicating strong gene flow between the local relatives. When testing a scenario where we assumed quitensis as the ancestor of caudatus, which had been suggested previously (Sauer 1967), significant gene flow from South American hybridus was detected (Figure S2), indicating the intermediate role of *A. quitensis* between wild and domesticated species.

Fine-scale gene flow reveals heterogeneous distribution between individuals and along the genome

The genome-wide and population-wide gene flow analysis already showed the complex pattern of exchange of genetic material between the *Amaranthus* species. We found evidence of gene flow for distant and closely related species. To understand the species complex as a whole, we inferred the local ancestry (Lawson *et al.* 2012) along the genome of each population (Figure 2). Summarizing local ancestry on the per-individual basis, showed a varying level of gene flow within species. We observed that the Central American grain species cruentus and hypochondriacus had a less admixed backgrounds, but shared ancestry tracks depending on the different individuals. Both had the highest donated portion from the wild hybridus_CA (Figure 2). Hypochondriacus had heterogeneous contribution from the other species to different individuals (although with proportions less than 0.016 total), while cruentus had more homogeneous contribution among individuals in the population. In South America, the overall pattern observed with population-wide introgression tests were also confirmed by individual based test. The South American populations caudatus and quitensis shared large amounts of ancestry, but this strongly varied between the individuals, between 10.8% and 18.5% of quitensis ancestry in caudatus individuals (Figure 2A), which also varied along the genome (Figure

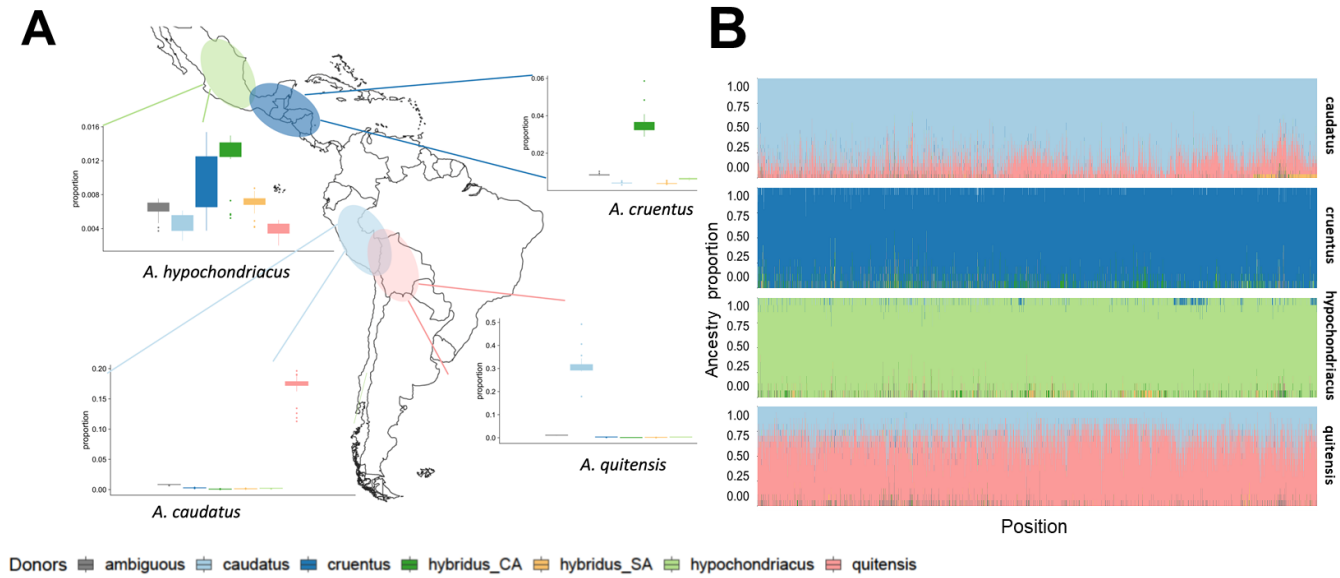

Figure 2 Variable ancestry across individuals and along the genome. A) Contribution of donor populations to individual recipients. Values within boxplots represent contribution by different donor populations to each individual of the recipient population. Y-axis scale differs between plots. Schematic geographic range of populations. B) Population scale ancestry proportion along Scaffold 4. Proportion of most likely donor population at given SNP across all individuals in the recipient population. Each plot represents a recipient population and colors represent donor populations. Donor colors according to figure 1.

2B).

We further wanted to understand whether gene flow is variable along the genome. Comparing ancestry signals along the genome of the different species showed that even the same region can have multiple donors in a species (Figure 2B and Figure S3). Using D-value in genomic windows, we scanned the genomes for gene flow signal in the trees with significant genome wide signals. The comparison between crops showed the presence of gene flow between hypochondriacus and caudatus, and between cruentus and caudatus (Figure 1). We observed similar signals as for global gene flow analysis; stronger gene flow between caudatus and hypochondriacus (D>0.992 for top 1% windows) than between caudatus and cruentus (D < -0.887 for bottom 1% windows) (Figure 3). Windows representing significant gene flow from cruentus or hypochondriacus with caudatus did not overlap suggesting that gene flow occurred independently between species.

To understand the potential reason for the observed high levels of gene flow between grain amaranth species, we combined gene flow signals along the genome with selection scan results (Gonçalves-Dias and Stetter 2021). Despite the genome-wide distribution of gene flow between crop species, only few selective sweeps overlapped with outlier windows of gene flow between caudatus and the other two crop species. We found 13 overlapping windows in total, eight in regions of gene flow between hypochondriacus and caudatus and five between caudatus and cruentus. Despite the relatively low total number, the overlap was higher than expected by chance (p=0.02) suggesting beneficial gene flow between geographically distant crop relatives.

Increased genetic load in domesticated grain amaranths compared to their wild ancestor

In many crop species a reduction in overall genetic diversity between wild relatives and the crop has been observed. This has been associated to population bottlenecks and directional selection during domestication (Gaut *et al.* 2018). Increased genetic drift and hitchhiking with selected alleles can lead to a higher genetic load in the domesticated species (Lu *et al.* 2006; Wang *et al.* 2017). We calculated GERP scores for the *A. hypochondriacus* reference genome from whole genome alignments with 15 diverse plant species of different relatedness as proxy for deleterious alleles (Figure S4). We observed that two domesticated species (caudatus and cruentus) had a significantly higher total genetic load than their wild ancestor hybridus. The third crop species hypochondriacus had higher load than hybridus_SA but lower than hybridus_CA (Figure 4A). This pattern remained even when using the *A. cruentus* reference genome (Ma *et al.* 2021) to calculate GERP scores, showing that the difference is likely not the result of reference bias when calculating GERP scores (Figure S5). The South American relative quitensis showed as high total load as the domesticated species. Partitioning of total genetic load into fixed and segregating load, showed that the domesticated species had a high fixed load, but a lower segregating

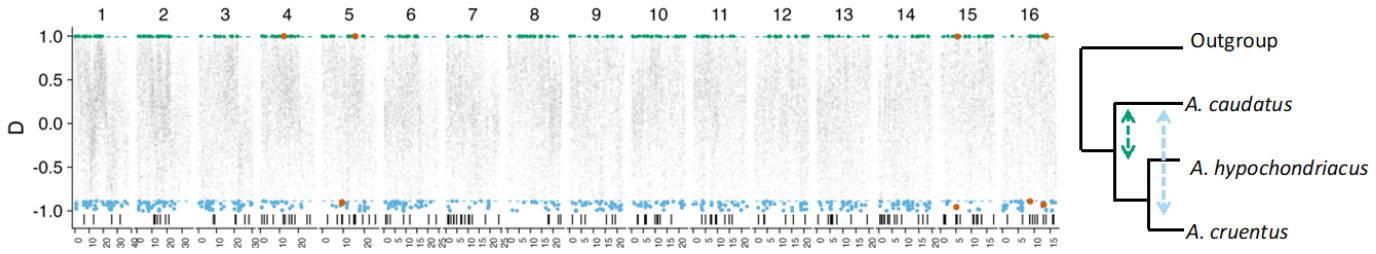

Figure 3 Fine-scale gene flow along the genome between domesticated amaranth populations. We used the D-value to calculate gene flow along the genome in 1000 SNPs windows. Each dot represents the D-value for a tree comparing *A. caudatus* with *A. hypochondriacus* or *A. cruentus*. Positive values are indicative of gene flow between *A. caudatus* and *A. hypochondriacus* and negative values between *A. caudatus* and *A. hypochondriacus*. The top 0.1% of windows in each direction were colored. The bars at the bottom indicate previously detected selective sweep regions detected in *A. caudatus*. Orange dots denote overlaps between selective sweep and top gene flow signal.

load than their wild ancestor (Figure 4B and C). Quitensis showed also high fixed load and low segregating load, in agreement with the small effective population size and low genetic diversity previously documented (Stetter *et al.* 2020).

To investigate if hitchhiking of deleterious alleles with selected loci led to the overall increase in genetic load in the domesticated species, we compared genetic load within selective sweep regions (Gonçalves-Dias and Stetter 2021) with that of random non-sweep regions. We observed that the mean load per site in sweep regions was significantly higher than in control regions for all domesticates, suggesting a hitchhiking effect (Figure 4D). However, mean GERP score per deleterious site in the sweep regions showed lower values than deleterious sites in control regions (Figure 4E). This suggests that mildly deleterious alleles might accumulate within selective sweep regions due to hitchhiking, but strongly deleterious alleles fix or increase in frequency due to increased genetic drift.

Signals of evolutionary rescue in grain amaranth

The abundant gene flow between grain amaranths and their wild relatives is expected to impact the patterns of genetic load. To evaluate the potential effect of gene flow on the accumulation of deleterious alleles, we measure the total load accumulated within gene flow regions from other species into a recipient species as the proportion of introgressed load received per individual. The expected value if gene flow regions carry the same amount of load as random regions would be 0, while the value is positive for deleterious gene flow and negative for beneficial gene flow. The analysis showed that gene flow regions from wild relatives into domesticated reduced genetic load, while gene flow between crops donated higher load in the recipient population (Figure 4F). Gene flow from domesticated donors into the wild species resulted in higher genetic load. These results might suggest that gene flow from populations with higher effective population sizes (wild relatives) could provide evolutionary rescue for the smaller populations (crops).

Hybrid incompatibilities between grain amaranths

All gene flow begins with the inter-mating between individuals of different populations. To further understand the process of gene flow and differences in observed levels of gene flow, we crossed multiple inbred lines of the three crop species. We selected three accessions from each crop species and crossed them within and between species including selfings. All crosses produced viable F_1 seeds. Selfings and intra-specific F_1 plants grew without complications and set seeds (Figure 5, Table S3). The inter-specific F_1 plants of the 5 crosses between *A. caudatus* and *A. hypochondriacus* developed healthy and fertile plants. For crosses between *A. cruentus* and *A. hypochondriacus*, one of the three crosses led to a lethal phenotype, with unhealthy seedlings that did not survive juvenile stage (Figure 5). Yet, both parents of this cross produced healthy and fertile offspring with other crossing partners, suggesting that incompatibility is the result of a specific allelic combination rather than an individual unfit parent (Table S3). All of the six crosses between *A. caudatus* and *A. cruentus* resulted in the lethal phenotype, suggesting a genetic incompatibility between these species. The difference in hybrid compatibility between grain amaranth species likely contributed to the observed patterns of gene flow.

Discussion

Crop populations that we observe today are the result of different evolutionary processes. While selection and demographic changes have been extensively studied, gene

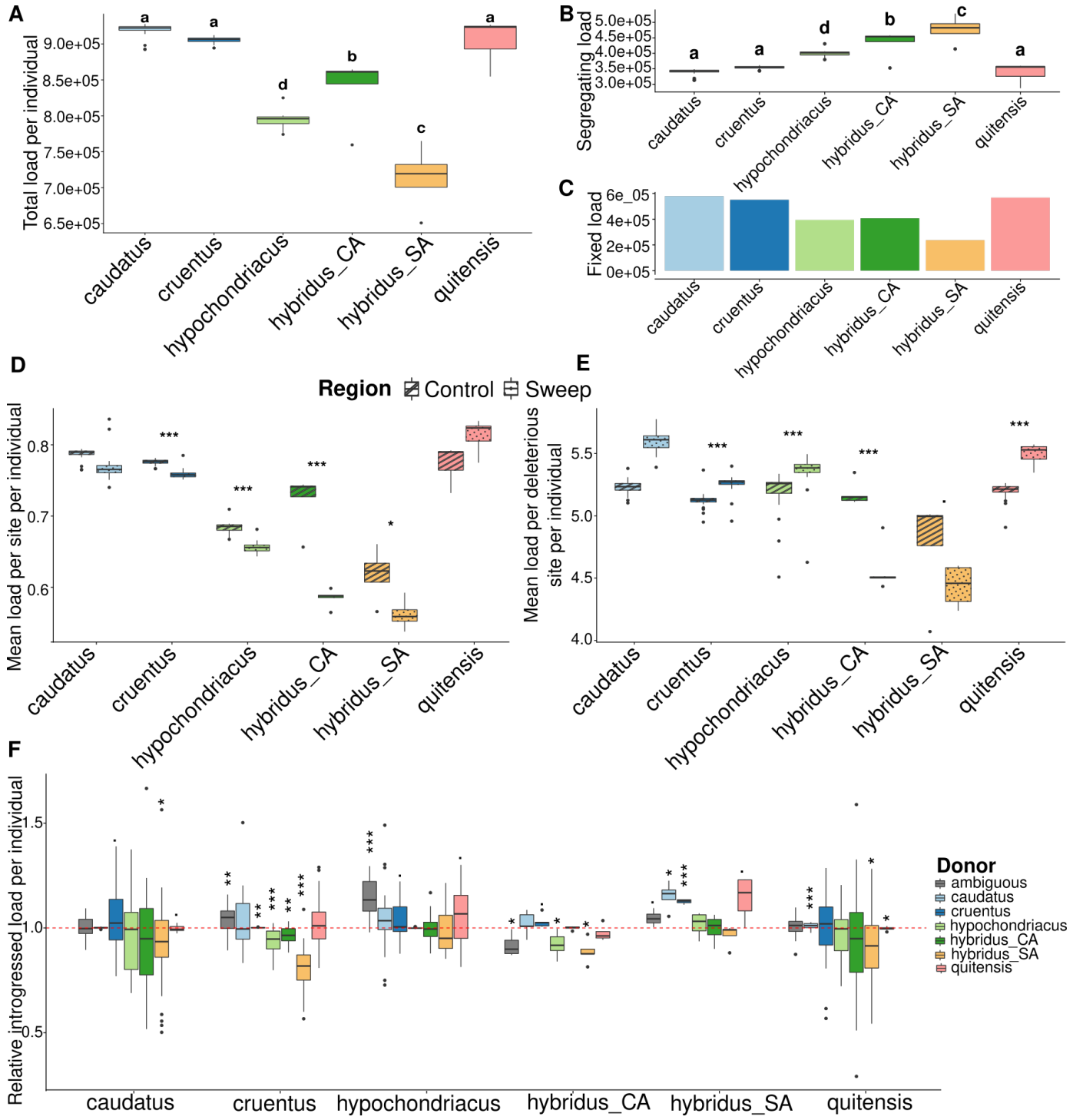

Figure 4 Distribution of genetic load during domestication of grain amaranth. Genetic load was calculated as sum of GERP scores for derived allele per individual. A) Total genetic load per individual in domesticated and wild populations of grain amaranth.The letters above the box-plot represented the Tukey's post hoc test. B) Segregating genetic load and C) fixed genetic load within a populations. D) and E) Accumulation of deleterious alleles in selective sweep regions and control regions (rest of the genome). D) plot shows average of total load accumulated; E) Mean GERP score of each deleterious allele in the region. The asterisks above the box-plot represent the significance level. F) Relative introgressed genetic load; total load in introgressed regions relative to gene flow received from the donor. A value greater than one represents increased load through gene flow, while a value lower than one shows reduction in load through gene flow compared to the amount of gene flow. A value of 1 shows equal load and gene flow proportion (denoted by red dotted line). The asterisks above box plot represent significance level for one sample t-test.

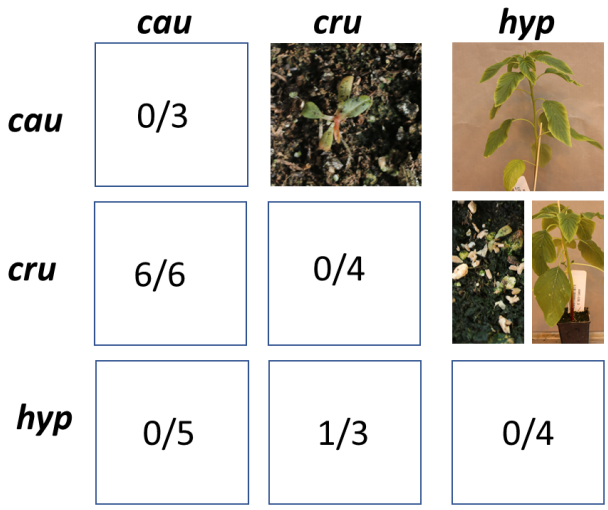

Figure 5 Proportion of lethal F_1 phenotypes. Lower triangle shows the number of lethal combinations between accessions out of total number of combinations. Upper triangle shows example images of phenotypes of inter specific crosses. cau: *A. caudatus*, cru: *A. cruentus* , hyp: *A. hypochondriacus*

flow and its role in the fitness of crops has only received attention in recent years. This is partially due to technical advances in plant genomics, but might also have resulted from the conceptual assumption of a linear process from one wild ancestor. The complex makeup of modern grain amaranth shows that gene flow between crop populations even over long geographic distances was prevalent (Figure 1). Gene flow between crop lineages of species that were domesticated multiple times has also contributed to diversity in rice (Yang *et al.* 2012), tomato (Razifard *et al.* 2020) and common bean (Rendón-Anaya *et al.* 2017). Not only does such gene flow between closely related crop populations occur, it is also heterogeneous between individuals and along the genome (Figure 2).

A potential reason for lower genetic exchange between specific pairs of grain amaranth could have been the reported difference in chromosome number between *A. cruentus* with 17 chromosomes in comparison to 16 chromosomes in the other 4 species (EJ and Poggio 1994; Ma *et al.* 2021). Yet, this would only lead to infertile F_1 plants, rather than necrotic, non-viable plants that die in the seedling stage. Instead, *A. cruentus* formed fertile hybrids with two out of three *A. hypochondriacus* accessions, suggesting incompatibility not because of difference in chromosome numbers but rather a genetic incompatibility (Figure 5). Our crossing experiment revealed differential genetic incompatibility between grain amaranth species, consistent with previous observation on interspecific hybrid necrosis (Gupta and Gudu 1991). A potential one-locus underdominance model of hybrid incompatibility would require strong genetic drift in both populations (Wu and Ting 2004), which could be the result of domestication bottlenecks (Stetter *et al.* 2020). The observed reproductive barrier could also be the result of a Dobzhansky-Muller incompatibility (Muller 1942), including more than one locus. The genetic mechanism for incompatibility warrants further investigation, as this has practical implications for potential hybrid breeding using the different crop species as heterotic pools. The complete compatibility between *A. hypochondriacus* and *A. caudatus* is reflected in higher gene flow signals than between these species and *A. cruentus* (Figure 1 and 5). Therefore, *A. hypochondriacus* and *A. caudatus* would be the most promising heterotic pools for future amaranth breeding.

Given the high prevalence of incompatibility between *A. cruentus* and *A. caudatus*, gene flow might have occurred early during the 8,000 year-long domestication history if strong reproductive barriers only developed later in the process. If the hybrid incompatibility arose at the advent of amaranth domestication, it can be expected that gene flow between *A. cruentus* and *A. caudatus* was likely beneficial, given the high fitness disadvantage of F_1 hybrids (Janzen *et al.* 2019; Aguillon *et al.* 2022). We found a low but significant number of introgressed selective sweeps, that might represent such beneficial gene flow between amaranth crop species. Currently, there are only few domestication related QTL known in grain amaranth that would allow linking introgressed regions to phenotypic changes during domestication. The previously reported QTL for the seed color change during amaranth domestication did not show signals of introgression consistent with the previously reported repeated selection for the trait in the three crop species (Stetter *et al.* 2020). More quantitative genetic and functional analyses could reveal additional QTLs that could indicate the adaptive potential of introgressed regions between grain amaranths.

Adaptive gene flow from wild relatives into crops has previously been associated to environmental adaptation in crops. For instance, in maize the introgression of the wild relative *Zea mays spp. mexicana* has been associated with the adaptation of maize to highland conditions and colder climates (Wang *et al.* 2017). Recent work even suggests a prevalent role of *Zea mays spp. mexicana* in the domestication of maize (Yang *et al.* 2023). While we cannot associate gene flow from wild relatives with positive selection, we find decreased genetic load in regions that were introgressed from wild relatives (Figure 4). This could be due to higher effective population size of wild relatives (Stetter *et al.* 2020). The wild ancestor *A. hybridus* showed lower genetic load than the domesticates (Figure 4), which might be the result of less demographic change during its recent past. Post-domestication gene flow between crops and their wild ancestor could consequently reduce the frequency of deleterious alleles. A similar correlation of genetic load and gene flow from a wild relative has also been shown in maize, where gene flow regions from the wild relative showed reduced ge-

netic load (Wang *et al.* 2017). Similarly, work in humans has shown that gene flow from a relative with small population size (Neanderthal) into a population with larger population size (modern humans) led to increased genetic load (Harris and Nielsen 2016), as we observe for gene flow from domesticated amaranths into *A. hybridus*. The accumulation of genetic load in populations with small effective population sizes can even lead to the extinction of populations or species as a whole (Rogers and Slatkin 2017). Hence, gene flow from relatives with large population size not only provides adaptive variation but can also lead to evolutionary rescue of the small population (Carlson *et al.* 2014). Despite the amelioration of genetic load through gene flow with wild relatives, crop-wild hybrids are expected to perform poorly as crop. Gene flow therefore needs to have an overall beneficial effect that is higher than the destruction of domestication traits (Stetter 2020). This might be particularly possible in crops like grain amaranth where the domestication syndrome is only weakly pronounced (Stetter *et al.* 2020).

For crops that maintain high gene flow with their relatives and are phenotypically less differentiated from wild plants, as it is the case for grain amaranth, the borders between wild and domesticate might be fluid. Strong gene flow between wild and domesticated crops might also allow the domesticate to return to the wild and be viable without human intervention again. Such feralization has been observed for a number plant and animal species (Gering *et al.* 2019). We find particularly strong signals of gene flow between grain amaranth and its wild relatives in South America (Figure 1A). The close relationship between wild species and crop in South America has led to different hypothesis for the domestication of *A. caudatus* suggesting *A. quitensis* as potential wild ancestor (Sauer 1967). While this cannot be completely ruled out, previous work using genome wide makers data suggested *A. hybridus* as ancestor for all three grain amaranths (Kietlinski *et al.* 2014; Stetter *et al.* 2020). The high and genome-wide equally distributed signal of gene flow between *A. caudatus* and *A. quitensis* (Figures 1 and 2) together with the low population size and signs of a strong population bottleneck in *A. quitensis* (Stetter *et al.* 2020) might indicate a feralized status of this species. The clarification of the status of *A. quitensis* will need further work with multiple populations of this species and local crop and wild relatives.

Overall, we show that the relationships between species are beyond linear, with exchanges between populations despite large geographic distances, and reintroduction of genetic material that was potentially lost during speciation. Even with observed genetic incompatibilities and high genetic differentiation between the crop species we found strong signals of gene flow between grain amaranths and between the crops and their wild relatives. Recurrent gene flow from the wild relative into the crops might have allowed evolutionary rescue, counteracting loss of diversity, but likely hindered the fixation of domestication traits leading to the incomplete domestication syndrome observed today for grain amaranth.

Materials and Methods

We studied whole genome resequencing data of 108 domesticated and wild amaranth accessions. The raw reads are available from European Nucleotide Archive (project numbers PRJEB30531) (Stetter *et al.* 2020). The accessions included the three domesticated amaranth; 33 *A. caudatus* L. (caudatus), 21 *A. cruentus* L. (cruentus) and 21 *A. hypochondriacus* (hypochondriacus); as well as 5 wild *A. hybridus* L. from Central America (hybridus_CA), 4 *A. hybridus* L. from South America (hybridus_SA), and 24 *A. quitensis* Kunth. (quitensis) (Table S4). *A. tuberculatus* was used as outgroup for the study (ERR3220318), (Kreiner *et al.* 2019). Raw reads were aligned to amaranth reference genome (Lightfoot *et al.* 2017) using bwa-mem2 (v 2.2.1) (Vasimuddin *et al.* 2019).

Variant calling

For variant calling, we utilized ANGSD (v.0921) (Korneliussen *et al.* 2014), with `-ref` *A. hypochondriacus* V2.1 reference genome (Lightfoot *et al.* 2017) `- doCounts 1, doGeno 3 dovcf 1, gl 2, dopost 2, domajorminor 1` and `domaf 1`. We filtered for missing data and mapping quality using `minInd 73` (max 30 missing data), `minQ 20, minMapQ 30, only_proper_pairs 1 trim 0, SNP_pval 1e-6, setMaxDepthInd 150` and `setminDepth 73`. The resulting VCF file was phased using Beagle (v 5.2) (Browning *et al.* 2021) using default parameters. For linkage disequilibrium (LD) pruning, we used Plink (v 1.9) (Purcell *et al.* 2007) using windows of 50kb with 5kb steps and a r^2 threshold of 0.3. The resulting VCF file had a total of 13,330,082 sites.

Gene flow analysis

We inferred gene flow between populations using D-statistic implemented in ANGSD (v.0921) (Korneliussen *et al.* 2014). We inferred population-wide statistics with the `abbababba` function for calculations of D per individual and `abbababba2` for calculations between populations. For both tests, *A. tuberculatus* was used as outgroup (H4). Only trees with a significant Z-score (absolute value above 3) were included in the results. For fine-scale analysis along the genome we employed Dsuite (Malinsky *et al.* 2021-02). We used the function `Dinvestigate` in windows of 100 SNPs to calculate D between trios along the genome. We also utilized the function `Dtrios` to verify the concordance of the global genome with the results obtained from ANGSD. To overlap regions with gene flow between crop species with selection signals, windows with significant signals of gene flow (1% outlier values) were overlapped with selective sweeps signals in the recipient population. Selective sweeps were previously identified in Gonçalves-Dias and Stetter (2021). The overlaps were tested for significance using a hypergeometric test (*pyhper* function in

R 4.2).

Topology inference

We used Twisst (Martin and Van Belleghem 2017) to infer the topology of each trio along the genome in windows of 100 SNPs, utilizing *A. tuberculatus* as an outgroup. For each window, a topology is assigned; a summary of the proportional windows that each topology appeared is then obtained. This inference allows a blind observation of the relationship between species. In the case, where topologies that differ from a neutral expectation are present in high proportions suggests gene flow between species. We inferred the topology for trios, between which a putative gene flow signal was identified.

Local Ancestry inference

We inferred local ancestry for each individual using finestrucuture v4.1 (Lawson *et al.* 2012). We used a uniform recombination rate generated with the perl script `makeuniformrecfile.pl`. The program was run using parameter `-f 0 0` which considers the populations and iterates through all individuals. We further assigned the most likely donor for each genome region of an individual. The donor for each position per individual was assigned based on the most likely donor population with a likelihood larger than 0.5. Sites that could not meet these likelihood thresholds were called as "ambiguous". Using these thresholds, the proportion of donated region per individual was calculated. In addition, the proportion along the genome within each population was summarized.

Demographic modeling

To estimate whether the identified scenario of gene flow fit best to our data we used simulations using Fastsimcoal2 (Excoffier *et al.* 2013). The joint site frequency spectrum (SFS) was generated using non-coding SNPs having no missing value in any of the individual and a minimum coverage of five reads using a python program easySFS . First, the program was run on preview mode (–preview) to identify the true sample size and the best sample size selected was used for the projection (`-proj`) to generate the joint SFS. Three different models namely, two-population split, two-population split with one migartion event and two-population split with continuous gene flow (Figure S1) were applied to the observed joint SFS. The models were compared using Akaike's Information Criterion (AIC). The best parameter estimate was calculated based on 100 independent runs with 200,000 coalescent simulations and 40 cycles of likelihood maximization algorithm. The 95 percent confidence interval of each parameter was estimated based on 50 non-parametric bootstrapping datasets. Each of the 50 bootstraped datasets were run for 50 times to estimate the best run. These 50 best run parameters were then used to estimate the confidence interval using boot package in R (Canty and Ripley 2017).

Genetic Load

We used Genomic Evolutionary Rate Profiling (GERP) (Davydov *et al.* 2010) scores to account for the effect of deleterious alleles at each site. We aligned 15 repeat-masked genomes of angiosperm species spanning large taxonomic range to the reference genome of *A. hypochondriacus* (v2.1) (Lightfoot *et al.* 2017). We followed the pipeline of Wu *et al.* (2022). Briefly, we aligned genomes of 16 divergent species: *Beta vulgaris* EL10 1.0, *Brachypodium distachyon* v2.1, *Chenopodium quinoa* v1.0, *Glycine max* Wm82.a4.v1, *Helianthus annuus* r1.2, *Medicago truncatula* Mt4.0v1, *Mimulus guttatus* v2.0, *Oryza sativa* v7.0, *Phaseolus vulgaris* v2.1, *Populus trichocarpa* v4.1, *Setaria viridis* v2.1, *Solanum lycopersicum* ITAG4.0, *Sorghum bicolor* v3.1.1, *Spinacia oleracea* (Monoe Viroflay) and *Vitis vinifera* v2.1 from phytozome (Goodstein *et al.* 2012) to the *A. hypochondriacus* reference genome using the LAST aligner (Kiełbasa *et al.* 2011). The tree topology for the species was extracted from the NCBI-phylogeny using the ete3 toolkit (v3.1.2) (Huerta-Cepas *et al.* 2016). Phylofit from phast package (Siepel *et al.* 2005) was used to calculate the branch length of the tree along with four-fold degenerate sites from *A. hypochondriacus* reference annotation file to generate a neutral model. All pairwise alignments were merged using ROAST (https://github.com/multiz/multiz) (Blanchette *et al.* 2004). GERP++ (Davydov *et al.* 2010) was used to calculate the GERP scores for each site using `gerpcol` with `-j` option that projects out the reference genome to avoid bias in the calculation. All sites with negative GERP values were set to 0 as negative values are not informative and misleading. The ancestral allele for each site was defined on the basis of three outgroup species closest to *Amaranthus* in the phylogenetic tree, i.e., *Beta vulgaris*, *Chenopodium quinoa* and *Spinacia oleracea*. Variants among these three species were called from the roast multiple alignment file (maf) using maffilter (version 1.3.1) (Dutheil *et al.* 2014). Sites not covered by any of the three outgroup species were removed. For the remaining sites the major allele among the three species was called the ancestral allele. In case of discrepancy for a majority rule the allele for *Spinacia oleracea* was called as the ancestral allele.

From a total of 13.2 million SNPs, we extracted 1,429,744 sites for which the GERP score and the ancestral alleles could be assigned. We then polarised the SNPs and removed sites where neither the reference nor the alternate allele matched the ancestral one. This yielded a total of 1,145,566 SNPs that were used for genetic load calculation. The GERP scores of the positions having the derived allele were then added to total load of individual using an additive model. The GERP score from sites having derived alleles were then summed to calculate the total genetic load. The genetic load was calculated for each accession individually.

To comment upon the reference bias, the GERP score was also calculated using *A. cruentus* genome as reference, using same method as described above. The variants file

of individuals that used *A. hypochondriacus* as reference was lifted to the *A. cruentus* genome using liftover module of maffilter (version 1.3.1) (Dutheil *et al.* 2014). Individual genetic load was then calculate using GERP score from *A. cruentus* genome for each lifted site as described above.

To overlap genetic load and selective sweeps, the sweep regions for each of the populations were overlapped with the sites with GERP score. Variants from those regions were extracted for the individuals of the respective populations. Any other regions of the genome that were not under the sweep region were considered as the control region. To account for the difference in the sizes of the sweep and control regions, we divided the total load with the total number of sites used in the analysis.

In order to calculate the introgressed load, GERP scores were summed for sites having the derived allele donated by a different population. Introgressed load was expressed as a ratio of load contributed by the introgressed species to the percentage of introgression sites. A value greater than one predicts the contribution of higher load due to gene flow.

Experimental hybridization between grain amaranth species

We selected genetically and morphologically defined accessions for each of the three crop species (*A. caudatus*, *A. cruentus*, and *A. hypochondriacus*) to assess their cross compatibility. We crossed 9 parental accessions (three per species) to create 25 inter - and intraspecific crosses (Table S3). The parental lines were previously selfed for at least three generations to ensure homozygosity. To determine hybrid survival the hybrids were grown alongside their parental accessions in a green house in Cologne (Germany) under long day conditions (16h light, 8h dark) and 25°C. We evaluated the survival of hybrid plants from at least three offspring per cross.

Data Availability

Genomic data is available through Stetter *et al.* (2020) and the associated ENA project. All scripts used in the analysis are available on github.

Author contribution

MGS conceived the study. JGD processed the data, conducted genome-wide analysis of gene flow and local ancestry inferences. AS performed genetic load analysis and demographic modeling. CG performed experimental crosses and executed the incompatibility study together with JGD. JGD, AS and CG prepared figures and tables. MGS, JGD and AS wrote the manuscript. All authors discussed the results, edited, and approved the manuscript.

Acknowledgments

We acknowledge funding by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) under Germany´s Excellence Strategy – EXC-2048/2 – Project ID 390686111 and grant STE 2654/5 to MGS by the DFG.

References

Aguillon, S. M., T. O. Dodge, G. A. Preising, and M. Schumer, 2022 Introgression. Current Biology **32**: R865–R868.

Bertorelle, G., F. Raffini, M. Bosse, C. Bortoluzzi, A. Iannucci, *et al.*, 2022 Genetic load: genomic estimates and applications in non-model animals. Nature Reviews Genetics pp. 1–12.

Blanchette, M., W. J. Kent, C. Riemer, L. Elnitski, A. F. Smit, *et al.*, 2004 Aligning multiple genomic sequences with the threaded blockset aligner. Genome Research **14**: 708–715.

Browning, B. L., X. Tian, Y. Zhou, and S. R. Browning, 2021 Fast two-stage phasing of large-scale sequence data. The American Journal of Human Genetics **108**: 1880–1890.

Canty, A. and B. Ripley, 2017 Package 'boot'. Bootstrap Functions. CRAN R Proj .

Carlson, S. M., C. J. Cunningham, and P. A. Westley, 2014 Evolutionary rescue in a changing world. Trends in Ecology & Evolution **29**: 521–530.

Chomicki, G., H. Schaefer, and S. S. Renner, 2020 Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics and archaeology. New Phytologist **226**: 1240–1255.

Civáň, P., K. Drosou, D. Armisen-Gimenez, W. Duchemin, J. Salse, *et al.*, 2021 Episodes of gene flow and selection during the evolutionary history of domesticated barley. BMC Genomics **22**: 1–17.

Crispo, E., 2008 Modifying effects of phenotypic plasticity on interactions among natural selection, adaptation and gene flow. Journal of Evolutionary Biology **21**: 1460–1469.

Davydov, E. V., D. L. Goode, M. Sirota, G. M. Cooper, A. Sidow, *et al.*, 2010 Identifying a high fraction of the human genome to be under selective constraint using gerp++. PLOS Computational Biology **6**: e1001025.

Dempewolf, H., K. A. Hodgins, S. E. Rummell, N. C. Ellstrand, and L. H. Rieseberg, 2012 Reproductive isolation during domestication. The Plant Cell **24**: 2710–2717.

Ding, Y.-M., Y. Cao, W.-P. Zhang, J. Chen, J. Liu, *et al.*, 2022 Population-genomic analyses reveal bottlenecks and asymmetric introgression from Persian into iron walnut during domestication. Genome Biology **23**: 1–18.

Doebley, J., 2006 Unfallen grains: how ancient farmers turned weeds into crops. Science **312**: 1318–1319.

Dutheil, J. Y., S. Gaillard, and E. H. Stukenbrock, 2014 Maffilter: a highly flexible and extensible multiple genome alignment files processor. BMC Genomics **15**: 1–10.

EJ, G. and L. Poggio, 1994 Karyological studies in grain amaranths. Cytologia **59**: 25–30.

Ellstrand, N. C., 2014 Is gene flow the most important evolutionary force in plants? American Journal of Botany

101: 737–753.

Excoffier, L., I. Dupanloup, E. Huerta-Sánchez, V. C. Sousa, and M. Foll, 2013 Robust demographic inference from genomic and SNP data. PLOS Genetics **9**: e1003905.

Gaut, B. S., C. M. Díez, and P. L. Morrell, 2015 Genomics and the contrasting dynamics of annual and perennial domestication. Trends in Genetics **31**: 709–719.

Gaut, B. S., D. K. Seymour, Q. Liu, and Y. Zhou, 2018 Demography and its effects on genomic variation in crop domestication. Nature Plants **4**: 512–520.

Gering, E., D. Incorvaia, R. Henriksen, J. Conner, T. Getty, *et al.*, 2019 Getting back to nature: feralization in animals and plants. Trends in Ecology & Evolution **34**: 1137–1151.

Gonçalves-Dias, J. and M. G. Stetter, 2021 PopAmaranth: A population genetic genome browser for grain amaranths and their wild relatives. G3: Genes, Genomes, Genetics .

Goodstein, D. M., S. Shu, R. Howson, R. Neupane, R. D. Hayes, *et al.*, 2012 Phytozome: a comparative platform for green plant genomics. Nucleic Acids Research **40**: D1178–D1186.

Gupta, V. and S. Gudu, 1991 Interspecific hybrids and possible phylogenetic relations in grain amaranths. Euphytica **52**: 33–38.

Harris, K. and R. Nielsen, 2016 The genetic cost of Neanderthal introgression. Genetics **203**: 881–891.

Huerta-Cepas, J., F. Serra, and P. Bork, 2016 ETE 3: Reconstruction, analysis, and visualization of phylogenomic data. Molecular Biology and Evolution **33**: 1635–1638.

Hufford, M. B., P. Lubinksy, T. Pyhäjärvi, M. T. Devengenzo, N. C. Ellstrand, *et al.*, 2013 The genomic signature of crop-wild introgression in maize. PLOS Genetics **9**.

Janzen, G. M., L. Wang, and M. B. Hufford, 2019 The extent of adaptive wild introgression in crops. New Phytologist **221**: 1279–1288.

Kiełbasa, S. M., R. Wan, K. Sato, P. Horton, and M. C. Frith, 2011 Adaptive seeds tame genomic sequence comparison. Genome Research **21**: 487–493.

Kietlinski, K. D., F. Jimenez, E. N. Jellen, P. J. Maughan, S. M. Smith, *et al.*, 2014 Relationships between the weedy *Amaranthus hybridus* (Amaranthaceae) and the grain amaranths. Crop Science **54**: 220–228.

Kim, M.-S., R. Lozano, J. H. Kim, D. N. Bae, S.-T. Kim, *et al.*, 2021 The patterns of deleterious mutations during the domestication of soybean. Nature Communications **12**: 97.

Korneliussen, T. S., A. Albrechtsen, and R. Nielsen, 2014 ANGSD: Analysis of Next Generation Sequencing Data. BMC Bioinformatics **15**: 356.

Kozak, K. M., M. Joron, W. O. McMillan, and C. D. Jiggins, 2021 Rampant genome-wide admixture across the *Heliconius* radiation. Genome Biology and Evolution **13**: evab099.

Kreiner, J. M., D. A. Giacomini, F. Bemm, B. Waithaka, J. Regalado, *et al.*, 2019 Multiple modes of convergent adaptation in the spread of glyphosate-resistant *Amaranthus tuberculatus*. Proceedings of the National Academy of Sciences **116**: 21076–21084.

Lawson, D., G. Hellenthal, S. Myers, and D. Falush, 2012 Inference of population structure using dense haplotype data. PLOS Genetics **8**.

Lightfoot, D., D. Jarvis, T. Ramaraj, R. Lee, E. Jellen, *et al.*, 2017 Single-molecule sequencing and Hi-C-based proximity-guided assembly of amaranth (*Amaranthus hypochondriacus*) chromosomes provide insights into genome evolution. BMC Biology **15**: 74.

Liu, S., A. Cornille, S. Decroocq, D. Tricon, A. Chague, *et al.*, 2019 The complex evolutionary history of apricots: Species divergence, gene flow and multiple domestication events. Molecular Ecology **28**: 5299–5314.

López-Goldar, X. and A. A. Agrawal, 2021 Ecological interactions, environmental gradients, and gene flow in local adaptation. Trends in Plant Science **26**: 796–809.

Lozano, R., E. Gazave, J. P. Dos Santos, M. G. Stetter, R. Valluru, *et al.*, 2021 Comparative evolutionary genetics of deleterious load in sorghum and maize. Nature Plants **7**: 17–24.

Lu, J., T. Tang, H. Tang, J. Huang, S. Shi, *et al.*, 2006 The accumulation of deleterious mutations in rice genomes: A hypothesis on the cost of domestication. Trends in Genetics **22**: 126–131.

Luo, M.-C., Z.-L. Yang, F. You, T. Kawahara, J. Waines, *et al.*, 2007 The structure of wild and domesticated emmer wheat populations, gene flow between them, and the site of emmer domestication. Theoretical and Applied Genetics **114**: 947–959.

Lv, F.-H., Y.-H. Cao, G.-J. Liu, L.-Y. Luo, R. Lu, *et al.*, 2022 Whole-genome resequencing of worldwide wild and domestic sheep elucidates genetic diversity, introgression, and agronomically important loci. Molecular Biology and Evolution **39**: msab353.

Ma, X., F. E. Vaistij, Y. Li, W. S. Jansen van Rensburg, S. Harvey, *et al.*, 2021 A chromosome-level *Amaranthus cruentus* genome assembly highlights gene family evolution and biosynthetic gene clusters that may underpin the nutritional value of this traditional crop. The Plant Journal **107**: 613–628.

Malinsky, M., M. Matschiner, and H. Svardal, 2021-02 Dsuite - Fast *D* -statistics and related admixture evidence from VCF files. Molecular Ecology Resources **21**: 584–595.

Martin, S. H. and S. M. Van Belleghem, 2017 Exploring evolutionary relationships across the genome using topology weighting. Genetics **206**: 429–438.

Meyer, R. S., A. E. DuVal, and H. R. Jensen, 2012 Patterns and processes in crop domestication: an historical review and quantitative analysis of 203 global food crops. New Phytologist **196**: 29–48.

Muller, H. J., 1942 Isolating mechanisms, evolution, and temperature. In *Biol Symp*, volume 6, pp. 71–125.

Nabholz, B., G. Sarah, F. Sabot, M. Ruiz, H. Adam, *et al.*, 2014 Transcriptome population genomics reveals severe

bottleneck and domestication cost in the African rice (*Oryza glaberrima*). Molecular Ecology **23**: 2210–2227.

Niu, S., Q. Song, H. Koiwa, D. Qiao, D. Zhao, *et al.*, 2019 Genetic diversity, linkage disequilibrium, and population structure analysis of the tea plant (*Camellia sinensis*) from an origin center, guizhou plateau, using genome-wide snps developed by genotyping-by-sequencing. BMC Plant Biology **19**: 1–12.

Orlando, L., R. Allaby, P. Skoglund, C. Der Sarkissian, P. W. Stockhammer, *et al.*, 2021 Ancient DNA analysis. Nature Reviews Methods Primers **1**: 14.

Ostevik, K. L., R. L. Andrew, S. P. Otto, and L. H. Rieseberg, 2016 Multiple reproductive barriers separate recently diverged sunflower ecotypes. Evolution **70**: 2322–2335.

Osuna-Mascaró, C., R. Rubio de Casas, J. M. Gómez, J. Loureiro, S. Castro, *et al.*, 2023 Hybridization and introgression are prevalent in southern european *Erysimum* (brassicaceae) species. Annals of Botany **131**: 171–184.

Page, A., J. Gibson, R. S. Meyer, and M. A. Chapman, 2019 Eggplant domestication: pervasive gene flow, feralization, and transcriptomic divergence. Molecular Biology and Evolution **36**: 1359–1372.

Purcell, S., B. Neale, K. Todd-Brown, L. Thomas, M. A. R. Ferreira, *et al.*, 2007 PLINK: A tool set for whole-genome association and population-based linkage analyses. The American Journal of Human Genetics **81**: 559–575.

Razifard, H., A. Ramos, A. L. Valle, C. Bodary, E. Goetz, *et al.*, 2020 Genomic evidence for complex domestication history of the cultivated tomato in latin america. Molecular Biology and Evolution .

Rendón-Anaya, M., J. M. Montero-Vargas, S. Saburido-Álvarez, A. Vlasova, S. Capella-Gutierrez, *et al.*, 2017 Genomic history of the origin and domestication of common bean unveils its closest sister species. Genome Biology **18**: 1–17.

Rieseberg, L. H. and J. M. Burke, 2001 The biological reality of species: gene flow, selection, and collective evolution. Taxon **50**: 47–67.

Rodgers-Melnick, E., P. J. Bradbury, R. J. Elshire, J. C. Glaubitz, C. B. Acharya, *et al.*, 2015 Recombination in diverse maize is stable, predictable, and associated with genetic load. Proceedings of the National Academy of Sciences **112**: 3823–3828.

Rogers, R. L. and M. Slatkin, 2017 Excess of genomic defects in a woolly mammoth on Wrangel island. PLOS Genetics **13**: e1006601.

Ross-Ibarra, J., M. Tenaillon, and B. S. Gaut, 2009 Historical divergence and gene flow in the genus *Zea*. Genetics **181**: 1399–1413.

Saban, J. M., A. J. Romero, T. H. Ezard, and M. A. Chapman, 2023 Extensive crop-wild hybridisation during *Brassica* evolution, and selection during the domestication and diversification of *Brassica* crops. Genetics p. iyad027.

Sauer, J. D., 1967 The Grain Amaranths and Their Relatives: A Revised Taxonomic and Geographic Survey. Annals of the Missouri Botanical Garden **54**: 103–137.

Sedivy, E. J., F. Wu, and Y. Hanzawa, 2017 Soybean domestication: the origin, genetic architecture and molecular bases. New Phytologist **214**: 539–553.

Sexton, J. P., S. Y. Strauss, and K. J. Rice, 2011 Gene flow increases fitness at the warm edge of a species' range. Proceedings of the National Academy of Sciences **108**: 11704–11709.

Sheidai, M. and F. Koohdar, 2023 Evidence for ancient introgression and gene flow in the genus *Tamarix* L. (amicaceae): a computational approach. Genetic Resources and Crop Evolution pp. 1–9.

Siepel, A., G. Bejerano, J. S. Pedersen, A. S. Hinrichs, M. Hou, *et al.*, 2005 Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research **15**: 1034–1050.

Smith, O., W. V. Nicholson, L. Kistler, E. Mace, A. Clapham, *et al.*, 2019 A domestication history of dynamic adaptation and genomic deterioration in sorghum. Nature Plants **5**: 369–379.

Stetter, M. G., 2020 Limits and constraints to crop domestication. American Journal of Botany **107**: 1617–1621.

Stetter, M. G., T. Müller, and K. J. Schmid, 2017 Genomic and phenotypic evidence for an incomplete domestication of South American grain amaranth (*Amaranthus caudatus*). Molecular Ecology **26**: 871–886.

Stetter, M. G., M. Vidal-Villarejo, and K. J. Schmid, 2020 Parallel seed color adaptation during multiple domestication attempts of an ancient new world grain. Molecular Biology and Evolution **37**: 1407–1419.

Tigano, A. and V. L. Friesen, 2016 Genomics of local adaptation with gene flow. Molecular Ecology **25**: 2144–2164.

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. Proceedings of the National Academy of Sciences **108**: 1088–1092.

Vasimuddin, M., S. Misra, H. Li, and S. Aluru, 2019 Efficient architecture-aware acceleration of bwa-mem for multicore systems. In *2019 IEEE International Parallel and Distributed Processing Symposium (IPDPS)*, pp. 314–324, IEEE.

Wang, L., T. M. Beissinger, A. Lorant, C. Ross-Ibarra, J. Ross-Ibarra, *et al.*, 2017 The interplay of demography and selection during maize domestication and expansion. Genome Biology **18**: 1–13.

Wang, L., E. B. Josephs, K. M. Lee, L. M. Roberts, R. Rellán-Álvarez, *et al.*, 2021 Molecular parallelism underlies convergent highland adaptation of maize landraces. Molecular Biology and Evolution **38**: 3567–3580.

Wu, C.-I. and C.-T. Ting, 2004 Genes and speciation. Nature Reviews Genetics **5**: 114–122.

Wu, Y., L. Johnson, B. Song, C. Romay, M. Stitzer, *et al.*, 2022 A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. The Plant Genome **15**: e20204.

Xu, J.-L., J.-M. Wang, Y.-Q. Sun, L.-J. Wei, R.-T. Luo, *et al.*, 2006 Heavy genetic load associated with the subspecific differentiation of japonica rice (*Oryza sativa ssp. japonica L.*). Journal of Experimental Botany **57**: 2815–2824.

Yang, C.-c., Y. Kawahara, H. Mizuno, J. Wu, T. Matsumoto, *et al.*, 2012 Independent domestication of asian rice followed by gene flow from japonica to indica. Molecular Biology and Evolution **29**: 1471–1479.

Yang, N., Y. Wang, X. Liu, M. Jin, M. Vallebueno-Estrada, *et al.*, 2023 Two teosintes made modern maize. bioRxiv pp. 2023–01.

Supplement

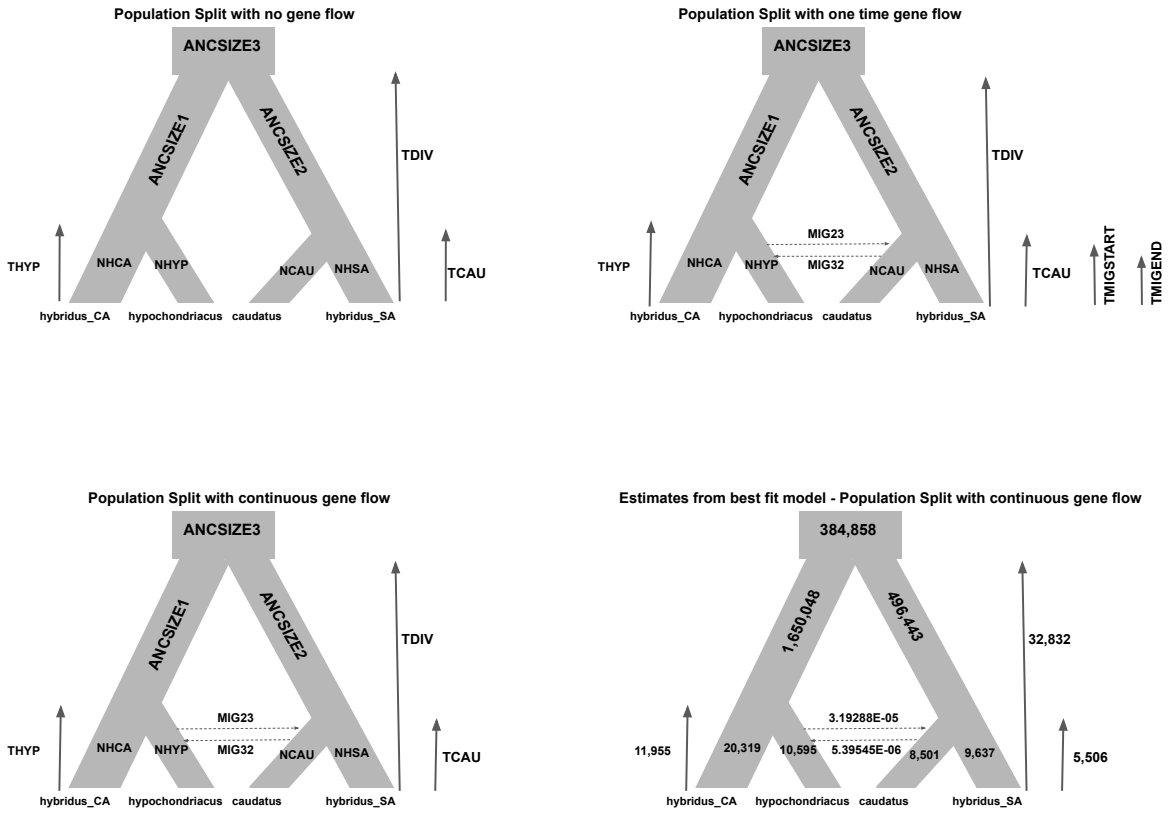

Figure S1 Different demographic models used in Fastsimcoal2 to predict the best scenario. The model of population split with continuous gene flow was predicted to be best model. Also see Table S2 for detailed demographic parameters for each model.

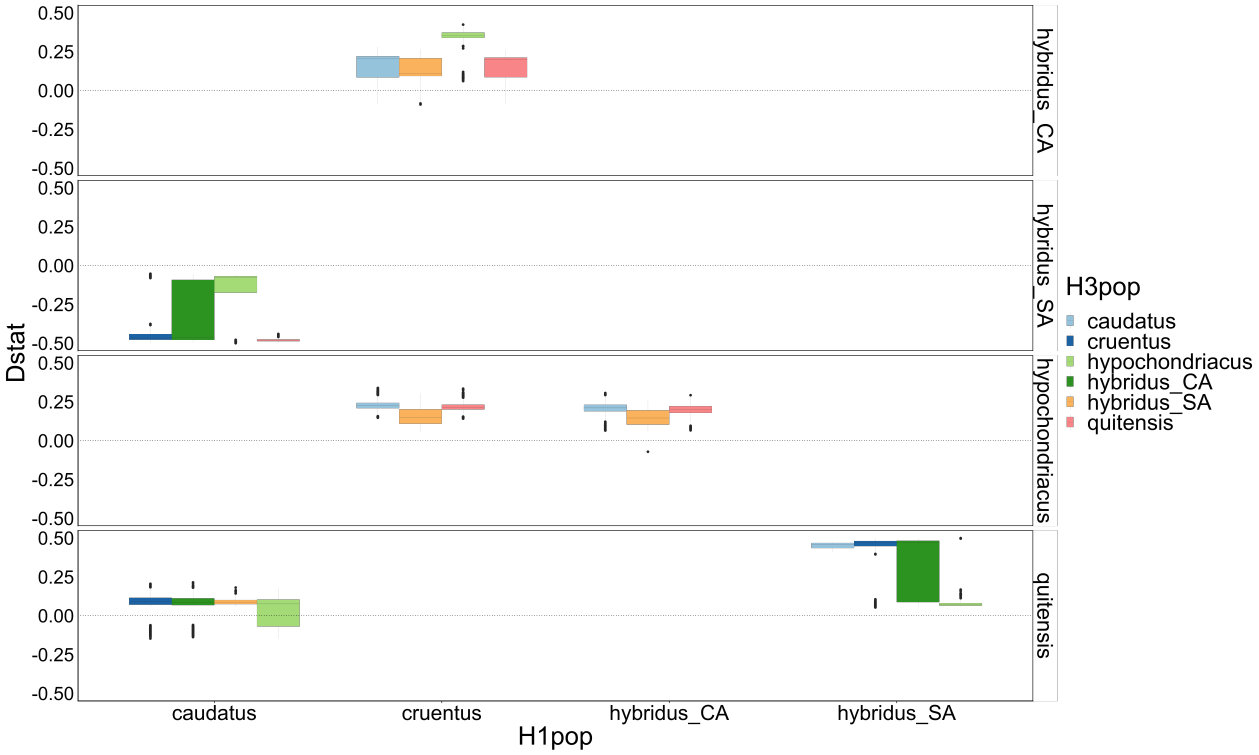

Figure S2 D-statistic value for comparisons between individuals. Each boxplot represents a comparison for a population trios H3 with the inner node H1 and H2. Only significant trees are represented. *A. tuberculatus* was used as outgroup

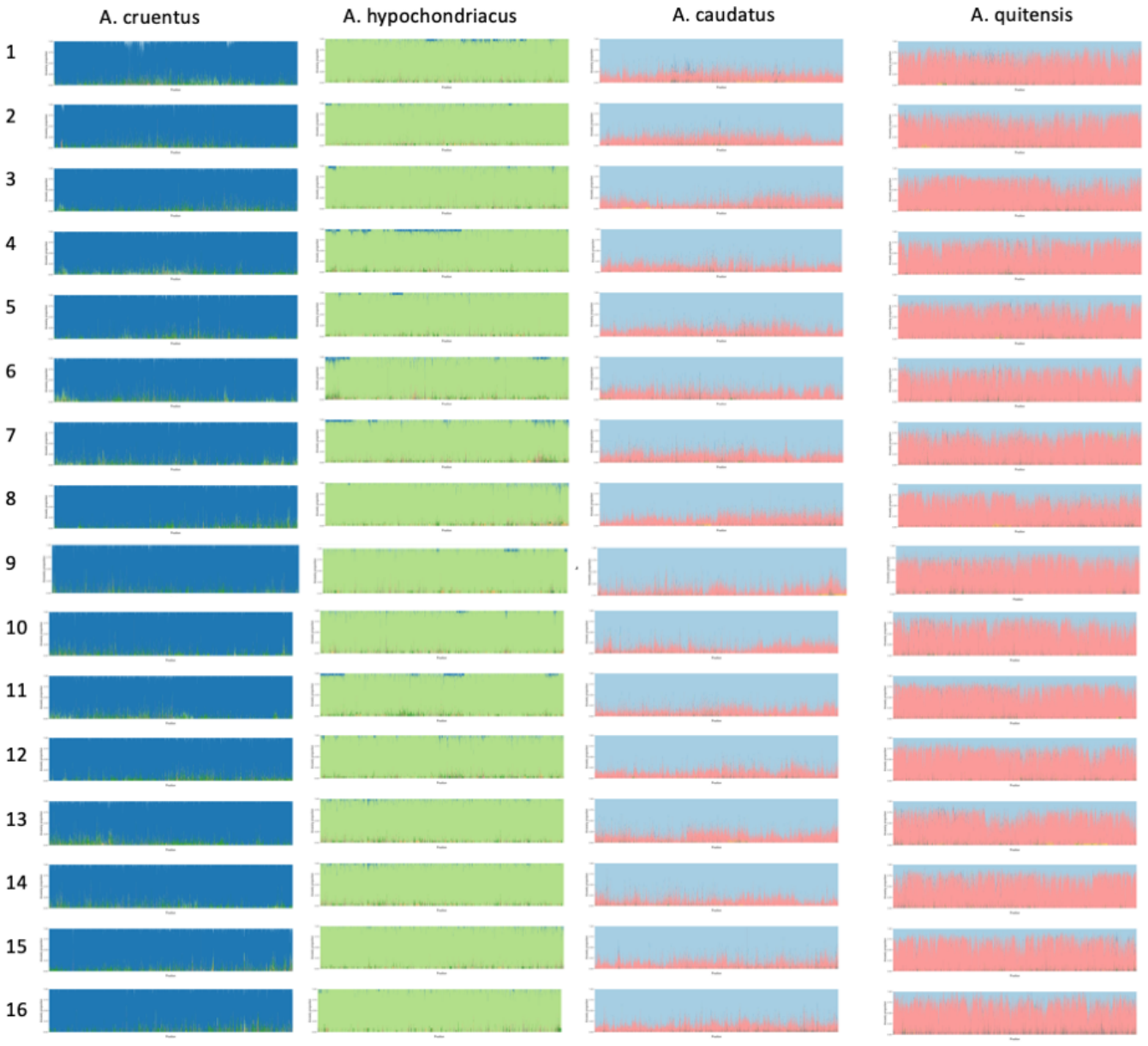

Figure S3 Ancestry proportions summary along the genome, per recipient population, per chromosome. Colors according to Figure 2.

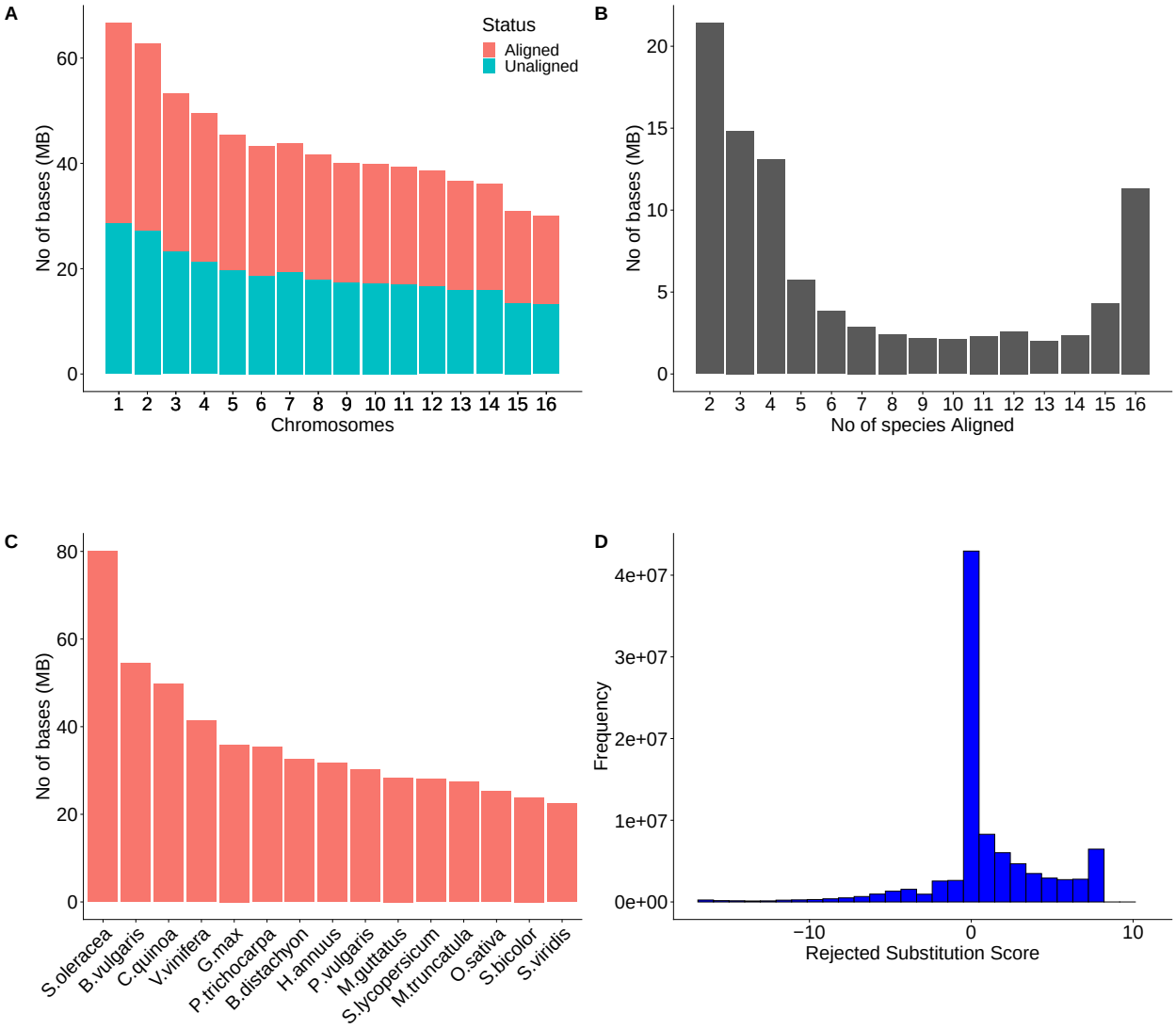

Figure S4 Summary for multiple genome alignment and GERP score. (A) No of bases covered by at least one taxon per chromosome; (B) Per base coverage of the reference genome by aligning taxon (species); (C) No of bases of reference genome (*A. hypochondriacus*) covered by each aligning species; (D) Distribution of GERP score (calculated as rejected substitution score).

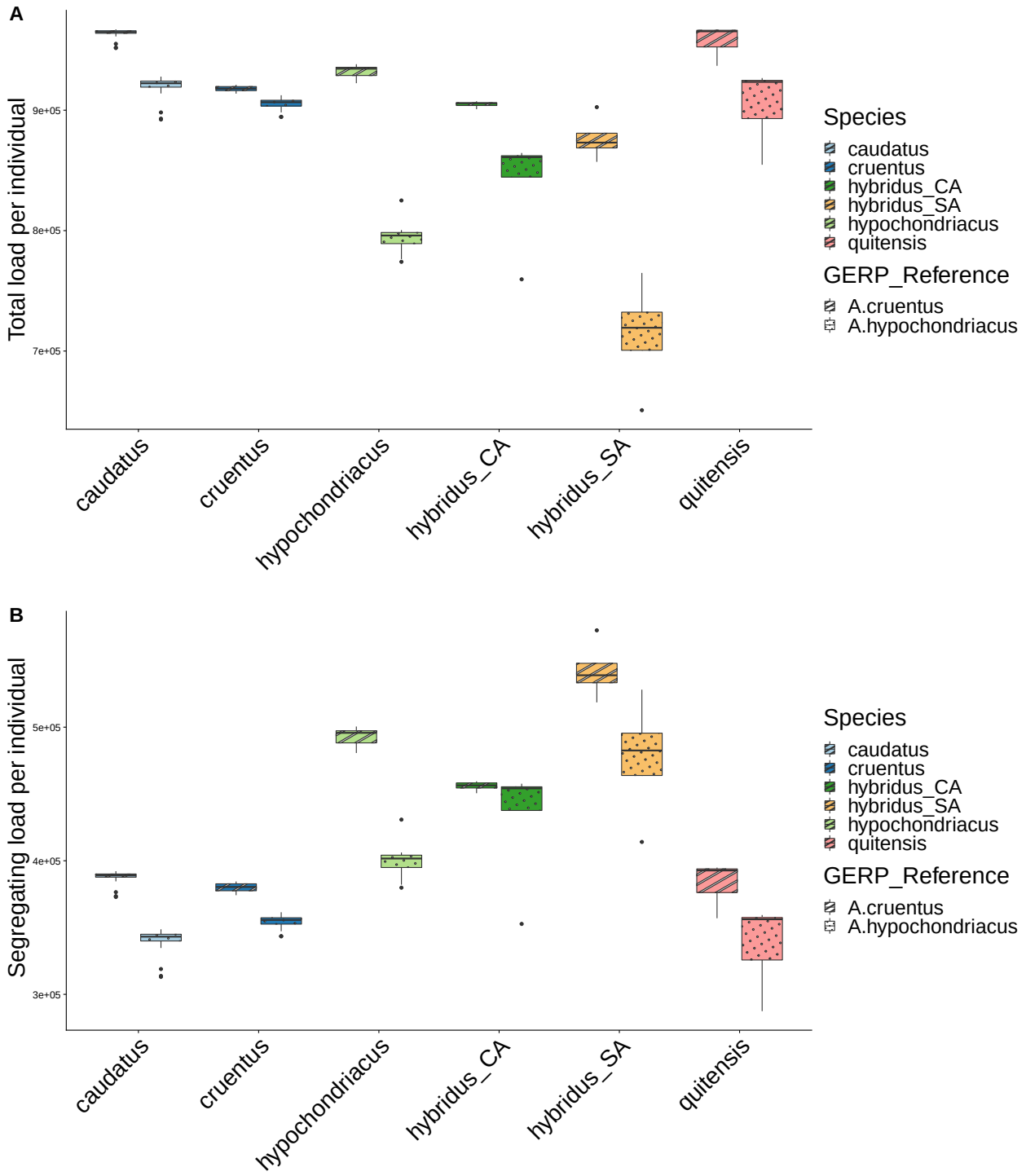

Figure S5 Distribution of genetic load during domestication of grain amaranth using two different genomes to account for reference bias. The genetic load was calculated as sum of GERP scores for derived allele per individual using *A. hypochondriacus* as reference or *A. caudatus* as reference. Distribution of total genetic load per individual in domesticated and wild populations of grain amaranth at (A) all sites (B) segregating sites is depicted using two different reference genomes. The observation of decreased load in hypochondriacus as compared to wild species when using *A. hypochondriacus* genome is not observed when *A. cruentus* is used as reference for calling GERP. However, the overall pattern for load is comparable for both genomes, suggesting for negligible reference bias.

Table S1 Summary of non-redundant trees to which we found significant D-values. Note:Angsd D-Statistic values were updated to positive to and P1 and P2 positions were switched when negative values were present. This was due for easy of comparisons with other tools as they require comparisons only between populations on P2 and P3.

P1	P2	P3 (target)	D (angsd)	D (Dsuite)	D (admixtools)	f4-ratio	f3 (treemx)
hybridus_SA	quitensis	hypochondriacus	0.225016	NA	NA	NA	NA
caudatus	quitensis	hybridus_SA	0.033597	0.0158596	0.0004726645	0.00997218	0.0887609
caudatus	quitensis	hypochondriacus	0.037009	0.0248318	0.0006999955	0.00776116	0.0831595
caudatus	quitensis	cruentus	0.032232	0.0166697	0.0004753609	0.0037502	0.0755036
cruentus	hybridus_CA	caudatus	0.228626	0.192587	0.0097571493	0.108917	0.0723928
hybridus_CA	hypochondriacus	caudatus	0.10076	0.195984	0.0140320691	0.175783	0.0621802
cruentus	hypochondriacus	caudatus	0.228272	0.286137	0.0237892185	0.265554	0.0578926
hybridus_SA	caudatus	hypochondriacus	0.212658	NA	NA	NA	0.028558
hybridus_SA	quitensis	cruentus	0.17963	NA	NA	NA	0.0255764
hybridus_SA	caudatus	cruentus	0.1691	NA	NA	NA	0.0250975
hybridus_SA	quitensis	caudatus	0.728471	NA	0.0894367462	NA	0.00870881
hybridus_SA	caudatus	quitensis	0.70984	NA	0.0889640817	NA	0.00827429

Table S2 Demographic parameters estimated for different demographic scenarios using Fastsimcoal2.

Parameters	Population Split No gene Flow	Population Split- One time Gene Flow	Population Split Continuous Gene Flow		
			Point Estimates	95 % Confidence Interval	
				Lower Limit	Upper Limit
ANCSIZE1	1571884	1713678	1650048	103347	2408236
ANCSIZE2	1564050	446635	496443	240294	2152774
ANCSIZE3	152842	396708	384858	10335	503711
NHCA	15444	17835	20319	11200	27808
NHSA	16529	16548	9637	8736	22814
NHYP	14762	8349	10595	5838	13133
NCAU	15146	12949	8501	7099	14691
THYP	8728	9894	11955	5916	16802
TCAU	9553	9633	5506	5065	12818
TDIV	31036	30952	32832	30405	40153
TMIGSTART	-	9157	-	-	-
TMIGEND	-	9344	-	-	-
MIG23	-	3.38801E-05	3.19288E-05	2.4E-05	4.7E-05
MIG32	-	3.45086E-06	5.39545E-06	2E-06	9E-06
MaxEstLhood	-83545622.13	-82852846.15	-82822883.13	-	-
deltaL	8294205.304	7601429.324	7571466.3	-	-
AIC	384741828.2	381551484.9	381413496.1	-	-
deltaAIC	3328332.113	137988.8248	0	-	-

ANCSIZE1 represents ancestral population size of hypochondriacus and hybridus_CA.
ANCSIZE2 represents ancestral population size of caudatus and hybridus_SA.
ANCSIZE3 represents Ancestral population size.
NHCA represents the population size of hybridus_CA.
NHSA represents the population size of hybridus_SA.
NHYP represents the population size of hypochondriacus.
NCAU represents the population size of caudatus.
THYP represents time of split for hypochondriacus
TCAU represents time of split for caudatus
TDIV represents divergence time between hybridus_CA and hybridus_SA
TMIGSTART represents the start time of the migration
TMIGEND represents the end time of the first migration
MIG23 represents migration rate from hypochondriacus to caudatus
MIG32 represents migration rate from caudatus to hypochondriacus
MaxEstLhood maximum log-likelihood of the best estimate.
deltaL differece between estimated and observed log-likelihood.
AIC Akaike's information criterion, AIC = 2d - 2ln(Lhood), where d is the number of parameters.
deltaAIC AIC - min(AIC).

Table S3 Crosses within and between species. The "intra" represents crosses of plants from the same species (different accessions); "inter" represents crosses between plants of different species.

Crossing type	Maternal species	Paternal species	Maternal accession	Paternal accession	survival rate (%)
inter	*A. caudatus*	*A. cruentus*	PI 490518	PI 511714	0
inter	*A. caudatus*	*A. cruentus*	PI 490518	PI 643058	0
inter	*A. caudatus*	*A. cruentus*	PI 490612	PI 511714	0
inter	*A. caudatus*	*A. cruentus*	PI 490518	PI 643058	0
inter	*A. caudatus*	*A. cruentus*	PI 490518	PI 511717	0
inter	*A. caudatus*	*A. cruentus*	PI 490612	PI 643058	0
inter	*A. caudatus*	*A. hypochondriacus*	PI 490518	PI 558499	100
inter	*A. caudatus*	*A. hypochondriacus*	PI 490518	PI 643070	100
inter	*A. caudatus*	*A. hypochondriacus*	PI 490612	PI 643070	100
inter	*A. caudatus*	*A. hypochondriacus*	PI 490612	PI 558499	100
inter	*A. caudatus*	*A. hypochondriacus*	PI 490518	PI 558499	100
inter	*A. hypochondriacus*	*A. cruentus*	PI 643070	PI 511714	100
inter	*A. hypochondriacus*	*A. cruentus*	PI 558499	PI 643058	100
inter	*A. hypochondriacus*	*A. cruentus*	PI 643070	PI 643058	0
intra	*A. caudatus*	*A. caudatus*	PI 642741	PI 490518	100
intra	*A. caudatus*	*A. caudatus*	PI 490612	PI 490518	100
intra	*A. caudatus*	*A. caudatus*	PI 490612	PI 642741	100
intra	*A. cruentus*	*A. cruentus*	PI 643058	PI 511714	100
intra	*A. cruentus*	*A. cruentus*	PI 511714	PI 643058	100
intra	*A. cruentus*	*A. cruentus*	PI 511717	PI 511714	100
intra	*A. cruentus*	*A. cruentus*	PI 511717	PI 643058	100
intra	*A. hypochondriacus*	*A. hypochondriacus*	PI 558499	PI 604581	100
intra	*A. hypochondriacus*	*A. hypochondriacus*	PI 604581	PI 558499	100
intra	*A. hypochondriacus*	*A. hypochondriacus*	PI 643070	PI 558499	100
intra	*A. hypochondriacus*	*A. hypochondriacus*	PI 604581	PI 643070	100

Table S4 List of accessions used in this the study. Names follow USDA germplasm ID

Name	Country_Origin	Population	ENA_ID
PI 490689	Ecuador	caudatus	ERR3021332
PI 490739	Ecuador	caudatus	ERR3021337
PI 490511	Peru	caudatus	ERR3021351
PI 490491	Argentina	caudatus	ERR3021382
PI 481949	Peru	caudatus	ERR3021403
PI 490459	Bolivia	caudatus	ERR3021366
PI 481957	Peru	caudatus	ERR3021380
PI 511706	Peru	caudatus	ERR3021381
AMA 125	Peru	caudatus	ERR3021385
PI 490561	Peru	caudatus	ERR3021387
PI 642741	Bolivia	caudatus	ERR3021388
PI 511704	Peru	caudatus	ERR3021389
PI 490518	Peru	caudatus	ERR3021390
PI 649227	Peru	caudatus	ERR3021394
PI 481960	Peru	caudatus	ERR3021395
PI 511687	Peru	caudatus	ERR3021397
PI 490612	Peru	caudatus	ERR3021398
PI 649217	Peru	caudatus	ERR3021399
PI 511712	Peru	caudatus	ERR3021400
PI 490431	Peru	caudatus	ERR3021401
PI 490609	Ecuador	caudatus	ERR3021402
PI 511696	Peru	caudatus	ERR3021404
PI 511686	Peru	caudatus	ERR3021405
PI 481965	Peru	caudatus	ERR3021406
PI 511690	Peru	caudatus	ERR3021407
PI 686455	Peru	caudatus	ERR3021408
PI 490604	Bolivia	caudatus	ERR3021409
PI 511679	Argentina	caudatus	ERR3021430
PI 511680	Argentina	caudatus	ERR3021431
PI 511681	Bolivia	caudatus	ERR3021432
PI 608019	Ecuador	caudatus	ERR3021440
PI 649228	Peru	caudatus	ERR3021443
PI 649230	Peru	caudatus	ERR3021444
PI 667165	Brazil	cruentus	ERR3021328

PI 649509	Mexico	cruentus	ERR3021329
PI 643042	Mexico	cruentus	ERR3021422
PI 643039	Mexico	cruentus	ERR3021410
PI 643058	Mexico	cruentus	ERR3021411
PI 511713	Peru	cruentus	ERR3021412
PI 511717	Guatemala	cruentus	ERR3021413
PI 649514	Mexico	cruentus	ERR3021414
PI 606798	Mexico	cruentus	ERR3021415
PI 576482	Mexico	cruentus	ERR3021416
PI 649609	Mexico	cruentus	ERR3021417
PI 451826	Guatemala	cruentus	ERR3021419
Ames5552	Mexico	cruentus	ERR3021421
PI 643049	Mexico	cruentus	ERR3021423
PI 649524	Mexico	cruentus	ERR3021424
PI 433228	Guatemala	cruentus	ERR3021429
PI 511714	Peru	cruentus	ERR3021433
PI 576481	Mexico	cruentus	ERR3021436
PI 643037	Mexico	cruentus	ERR3021442
PI 658728	Mexico	cruentus	ERR3021447
PI 667160	Guatemala	cruentus	ERR3021448
PI 667158	Guatemala	hybridus_CA	ERR3021331
PI 511724	Mexico	hybridus_CA	ERR3021336
PI 604582	Mexico	hybridus_CA	ERR3021340
PI 604574	Mexico	hybridus_CA	ERR3021341
PI 604568	Mexico	hybridus_CA	ERR3021437
PI 490489	Peru	hybridus_SA	ERR3021333
PI 511754	Ecuador	hybridus_SA	ERR3021391
PI 686451	Peru	hybridus_SA	ERR3021426
PI 636180	Colombia	hybridus_SA	ERR3021441
PI 649537	Mexico	hypochondriacus	ERR3021343
PI 643036	Mexico	hypochondriacus	ERR3021344
PI 649575	Mexico	hypochondriacus	ERR3021345
Ames5457	Mexico	hypochondriacus	ERR3021346
PI 633589	Mexico	hypochondriacus	ERR3021347
PI 649565	Mexico	hypochondriacus	ERR3021348
PI 604559	Mexico	hypochondriacus	ERR3021349
PI 643070	Mexico	hypochondriacus	ERR3021350
PI 604581	Mexico	hypochondriacus	ERR3021352

Ames2085	Mexico	hypochondriacus	ERR3021353
PI 643041	Mexico	hypochondriacus	ERR3021354
PI 649602	Mexico	hypochondriacus	ERR3021355
PI 604587	Mexico	hypochondriacus	ERR3021356
PI 649607	Mexico	hypochondriacus	ERR3021357
PI 511731	Mexico	hypochondriacus	ERR3021359
PI 643067	Mexico	hypochondriacus	ERR3021360
PI 649559	Mexico	hypochondriacus	ERR3021361
PI 649595	Mexico	hypochondriacus	ERR3021362
PI 649623	Mexico	hypochondriacus	ERR3021364
PI 604595	Mexico	hypochondriacus	ERR3021439
PI 649529	Mexico	hypochondriacus	ERR3021445
PI 511749	Ecuador	quitensis	ERR3021365
PI 511737	Ecuador	quitensis	ERR3021367
PI 490664	Ecuador	quitensis	ERR3021335
PI 667156	Ecuador	quitensis	ERR3021338
PI 490705	Ecuador	quitensis	ERR3021370
PI 490684	Ecuador	quitensis	ERR3021342
PI 691596	Argentina	quitensis	ERR3021368
PI 649246	Peru	quitensis	ERR3021369
PI 511745	Ecuador	quitensis	ERR3021374
PI 652426	Brazil	quitensis	ERR3021371
PI 490720	Ecuador	quitensis	ERR3021376
PI 511741	Ecuador	quitensis	ERR3021377
PI 669830	Peru	quitensis	ERR3021378
PI 511751	Peru	quitensis	ERR3021372
PI 652428	Brazil	quitensis	ERR3021373
PI 652422	Brazil	quitensis	ERR3021375
PI 490466	Peru	quitensis	ERR3021392
PI 490673	Ecuador	quitensis	ERR3021393
PI 669836	Argentina	quitensis	ERR3021379
PI 490670	Ecuador	quitensis	ERR3021334
PI 490679	Ecuador	quitensis	ERR3021396
PI 669839	Peru	quitensis	ERR3021428
PI 511736	Bolivia	quitensis	ERR3021434
PI 511747	Ecuador	quitensis	ERR3021435
ERR3220318		tuberculatus	ERR3220318