

Preview

Unloading potatoes: Potato breeding moves forward with only half the genome

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Potato is one of the most important food crops in the world and, in contrast to other staples, has not seen large improvements in yield. Agha, Shannon, and Morrell preview an article recently published in *Cell*, “Phylogenomic discovery of deleterious mutations facilitates hybrid potato breeding,” which advances potato breeding strategies via a genetic approach.

Potato is the most widely grown vegetable crop in the world, central to cultures, cuisines, and economies across the globe. However, in contrast to other staples, there has been no genetic gain in potato yield over the last 100 years¹ (Figure 1A). This is primarily due to the highly heterozygous autotetraploid genome of commercial potato outside South America² (Figure 1B). Autotetraploidy (where the entire diploid genome has a second very similar copy) complicates the use of breeding technologies essential to other crops, such as the creation of inbred lines or incorporation of favorable traits through introgression. Often, early crop breeding efforts focus on creating self-compatible lines that breed true for crucial traits. This is practically impossible in an autotetraploid. The current potato breeding process generally starts with planting tens of thousands of genetically unique individuals, with only ~1% retained because they meet expectations for market class based on visual criteria. Over the past decade, the potato breeding and research community in the public and private sector has been working to transform potato from an autotetraploid clonal crop to a diploid inbred-hybrid one.³ This audacious project will allow potato breeders to fix favorable traits in breeding populations, introgress desirable biotic and abiotic stress resistance from wild diploid relatives, and nimbly respond to changing environments and market demands.

Developing diploid potato is a complex undertaking, and attempts to develop

inbred lines are complicated by lethal levels of inbreeding depression. Much of inbreeding depression results from exposure of recessive alleles that were benign in the heterozygous state. Targeting large-effect deleterious alleles has been adopted to circumvent this problem,⁴ but these approaches are expensive and depend on selecting starting material with relatively few deleterious alleles. Identification of deleterious alleles within the potato germplasm is crucial to breeding. Recently in *Cell*, Wu et al.⁵ take a phylogenetic approach to identify the extensive deleterious load in a diploid potato diversity panel. Using a wealth of data from potato's unusually large number of wild relatives improves the prediction of evolutionary constraint on variants. Furthermore, they argue that lines with more of the genetic load in the homozygous state have better potential for further inbreeding, regardless of phenotype, because they do not carry homozygous large-effect deleterious or lethal alleles. The extent of deleterious variation in the diploid germplasm is an important consideration for potato breeders balancing the desire to advance diploid potato quickly to address grower, consumer, and industry needs and the need to maintain sufficient variation for diploid potato to succeed as a crop into the future.

Diploid forms of potato were domesticated in the Andes Mountains of South America⁶ but have not been subject to intensive modern breeding efforts. The process of domestication and genetic

improvement of crops increases the frequency of traits that are desirable for human use but also incurs the “cost of domestication” that results from reductions in the effective population size (N_e) or the number of individuals contributing to the domesticated population.⁷ The genetic effects of reduced N_e include an increase in genetic drift and a genome-wide reduction in the efficacy of selection. Linked selection also becomes more important with reduced N_e , potentially pulling harmful variants to higher frequency.⁸ Harmful variants that increase in frequency during domestication or improvement contribute to mutational load in domesticated populations. Harmful variants that completely replace benign nucleotide states become a part of *fixed* load, while those that continue to circulate contribute to *segregating* mutational load.

Many domesticated species were brought into cultivation over millennia of selection⁹ and over a broad geographic range, sometimes with multiple independent origins of the cultigen. Both factors mitigate demographic effects and potentially reduce the genetic impact of crop domestication and subsequent improvement. A danger of modern intensive breeding efforts is a severe reduction in N_e , dramatically limiting the genetic diversity in the improved cultigen. The genetic consequences could be a loss of useful genetic variants and dramatic increases in fixed mutational load. Using an enriched set of genetic variants, including those that annotate as deleterious,



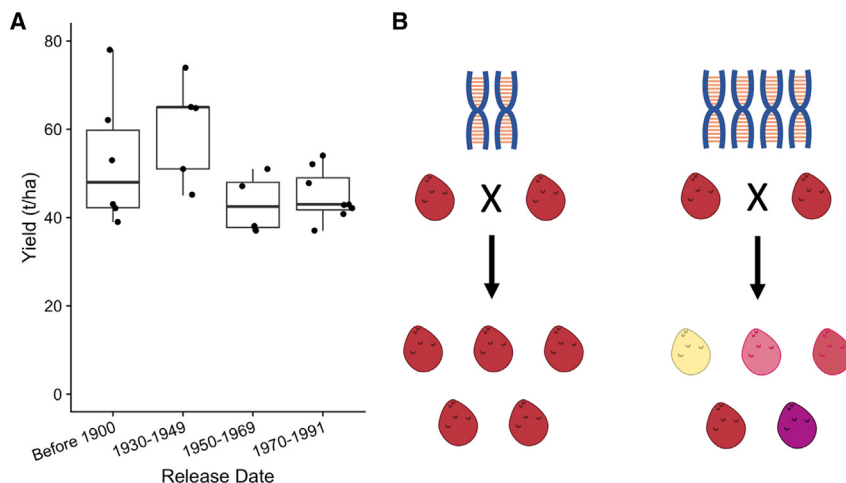


Figure 1. Tetraploid potato in the United States has made little to no genetic gain for yield due to the complexity of the genome

(A) Yield data (in tonnes/hectare) from 23 major US cultivars released between the late 19th and 20th centuries grown in a common field in 1990–1992 in the Montcalm Research Farm, Entrican, MI.¹ No significant increase in yield was observed through the ~100 years of breeding, with the highest yielding cultivar released before 1900.

(B) A comparison of the expectations from crosses in inbred diploid and autotetraploid potato. Here, skin color is fixed in diploid potato while it continues to segregate in tetraploid populations, even after hundreds of years of breeding. This slows breeding progress for other important traits in tetraploids.

can improve “genomic prediction” approaches.¹⁰

Identifying deleterious variants in the diploid potato germplasm will inform the development of inbred-hybrid lines. Mutational load is expected to be one of the major hurdles to establishing elite inbred lines in potato. Once identified, large-effect deleterious variants can be avoided.⁴ Work such as that by Wu et al.⁵ will aid researchers and breeders in developing strategies to minimize fixed load in breeding populations.

Wu et al.⁵ make recommendations regarding the zygosity of deleterious variants when choosing starting material for inbred lines. The authors show that lower heterozygous load, even at the expense of homozygous load, may be a better starting point for inbreeding. When thinking about establishing breeding “populations,” it is also important to consider the difference between fixed and segregating load. Removing fixed load from breeding populations is extremely difficult and requires the use of introgression (or potentially genome editing). Segregating load can be reduced by identification of progeny with less load than their parents. Even deleterious variants in repulsion phase can be removed if a sufficient num-

ber of individuals are generated, though, as the authors point out, this is more difficult. By intentionally selecting materials that minimize fixed load while simultaneously minimizing heterozygous load within individuals, breeders can select individuals that can easily be inbred and establish populations with greater potential to remove segregating load. There is an inherent trade-off between short-term efficiency in inbreeding and long-term, stable improvements in agronomic performance. While Wu et al.⁵ clearly demonstrate that inbreeding efficiency is improved when using individuals with lower heterozygous load, it is important to remember that inbreeding in and of itself is not the end goal.

One strategy under consideration for tackling deleterious variation in diploid potatoes is the development of heterotic groups. The utility of heterotic groups depends on complementation of deleterious alleles, with more distinct sets of deleterious alleles increasing the potential benefits of heterotic groups.¹¹ A deeper understanding of the distribution of fixed and segregating load in specific breeding populations could facilitate the establishment of heterotic groups that maximize fixed load *within* heterotic group while

minimizing segregating load *between* groups. This would result in many recessive deleterious variants masked in hybrid progeny. However, heterotic groups will not compensate for the need for population improvement. N_e within heterotic groups must be sufficient for effective recombination to occur.

An important component of all variants are their fitness and dominance effects. The distribution of fitness effects is notoriously hard to characterize. Wu et al.⁵ perform an analysis of the dominance coefficients of their predicted deleterious variants. Dominance is clearly an important component to heterosis; heterosis only exists because of directional dominance. However, dominance coefficients are not the full story. More research is needed to understand the phenotypic cost of individual deleterious variants to maximize breeding progress.

Wu et al.⁵ help identify a future where intensive plant breeding efforts are informed by an understanding of the nature and effect of variants present in breeding lines.

DECLARATION OF INTERESTS

The authors declare no competing interests.

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