

The genetic basis of inbreeding depression in potato

With the support by the National Natural Science Foundation of China, the research team led by Prof. Huang SanWen (黄三文) at the Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, deciphered the genetic basis of inbreeding depression in potato, which was published in *Nature Genetics* (2019, 51: 374–378).

The adverse effects of inbreeding were first documented by Charles Darwin, through extensive experiments on plants. Inbreeding depression in clonally propagated plants is expected to be more severe than that in seed plants, as more deleterious mutations have accumulated during asexual reproduction while purging of these mutations by recombination is limited. Potato (*Solanum tuberosum* L.) is the most important tuber crop worldwide, but its improvement is slow due to tetrasomic inheritance. Moreover, its clonal propagation bears a considerable carbon footprint. To overcome these drawbacks, Prof. Huang collaborated with the domestic and foreign organizations to initiate “The Upotato Project”, aiming to re-domesticate potato into an inbred line-based diploid crop propagated by seeds. However, severe inbreeding depression has hampered the development of elite inbred lines and therefore there is a need to understand its genetic basis.

Deleterious mutations are considered to be the major cause of inbreeding depression. The authors identified 344,831 predicted deleterious substitutions in 151 diploid potato landraces. These mutations are enriched in the pericentromeric regions, indicating it is impossible to eliminate all of them by genetic recombination. Further analysis showed that only a few (~11.32%) of deleterious substitutions were overlapped between any two diploids. This result indicates that the mutation burden in potato is line-specific, thus breeders can maintain the mutations in the heterozygous state by dedicatedly designed crosses. By contrast, most large-effect deleterious alleles are located in the genomic regions with high recombination rates (Figure), which can be effectively purged by recombination.

Identifying the deleterious mutations that have accumulated during asexual propagation will allow breeders to effectively manage or purge them through sexual hybridization. This study not only provides a basis for the genome design of potato inbred lines, but also contributes to the understanding of the genetic basis of inbreeding depression in clonally propagated plants.

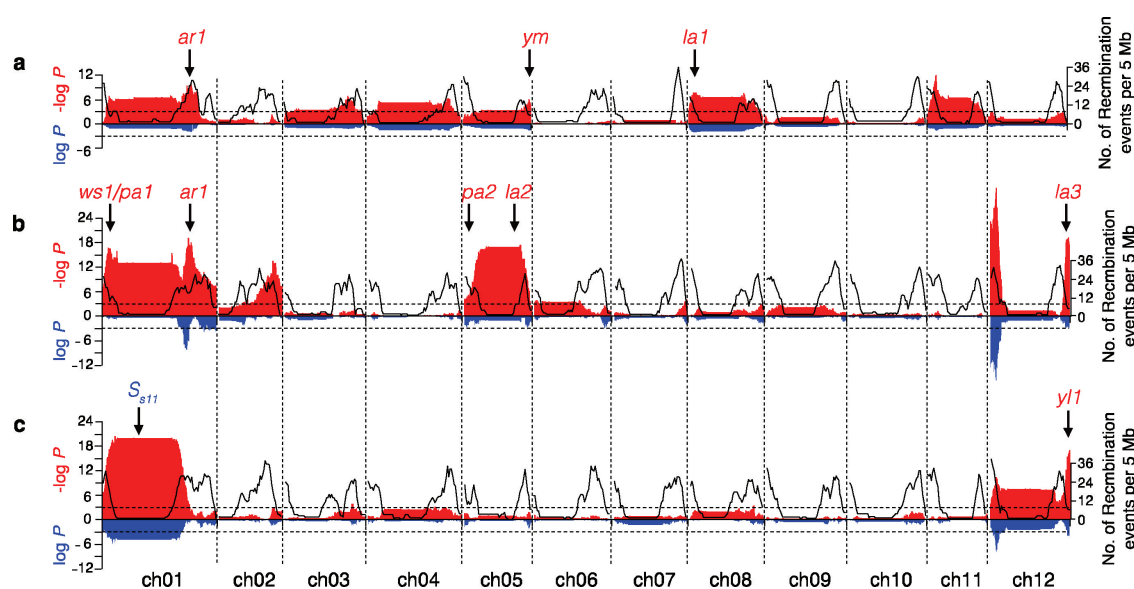


Figure Genome-wide segregation distortions and positions of large-effect deleterious mutations affecting survival and vigor.