

POPULATION GENOMICS

Resolve barley domestication

New Phytol. <http://doi.org/cmmz> (2018)

The domestication history of barley remains largely mysterious, though it has been recognized that the Fertile Crescent area is probably the location. The double origins of the non-brittle spike trait of cultivated barley, and the fact that the domesticated barley genome consists of sequences from multiple wild barley populations, suggests that barley was domesticated in a slow and polyphyletic process. However, it remains elusive how the domestication process shaped the mosaic ancestry patterns of the genome. Through population genomic analysis based on targeted resequencing of 433 barley lines, Artem Pankin, from the Heinrich-Heine-University and Max Planck Institute for Plant Breeding Research, and colleagues now provide a clearer answer to this question.

The researchers conducted Illumina enrichment resequencing for 344 wild and 89 domesticated lines representing worldwide barley diversity. More than 500,000 high-quality SNPs were identified. Population structure analysis based on the SNP markers, classified these lines into wild, cultivated and admixture genotypes. 137 signatures of selective sweeps were then identified through genome scans, covering all chromosomes. These putative selected regions contained candidate domestication genes implicated in different biological processes, such as light signalling regulation, circadian clock and carbohydrate metabolism pathways.

Ancestral analyses for the neutral and selected regions showed that the ancestry of neutral loci can be traced to wild barley populations all over the Fertile Crescent, while the ancestral genotypes of candidate domestication loci originated specifically from the eastern and western parts of the Fertile Crescent — that is, the Levantine and Zagros regions. These data supported a scenario where domestication was initiated in the Levantine and Zagros regions but multiple wild or protodomesticated lineages were involved through continued gene flow, resulting in the current mosaic ancestry patterns of the barley genome.

Jun Lyu

Published online: 26 March 2018
<https://doi.org/10.1038/s41477-018-0135-8>