Evolutionary metabolomics

Domestication and breeding have influenced the genetic structure of plant populations due to selection for adaptation from natural habitats to agro-ecosystems. In this article [1], Papa et al. investigate the effects of selection on the contents of 51 primary kernel metabolites and their relationships in three Triticum turgidum L. subspecies (i.e. wild emmer, emmer, durum wheat) that represent the major steps of tetraploid wheat domestication. The authors present a methodological pipeline to identify the signature of selection for molecular phenotypic traits (e.g. metabolites and transcripts). Following the approach, they show that a reduction of unsaturated fatty acids was associated with selection during domestication of emmer (primary domestication). They also show that changes in the amino-acid content due to selection mark the domestication of durum wheat (secondary domestication). These effects were found to be partially independent of the associations that unsaturated fatty acids and amino acids have with other domestication-related kernel traits. Changes in contents of metabolites were also highlighted by alterations in the metabolic correlation networks, indicating wide metabolic restructuring due to domestication. Finally, evidence is provided that wild and exotic germplasm can have a relevant role for improvement of wheat quality and nutritional traits.

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