

Genome scan of landrace populations of the self-fertilizing crop species rice, collected across time, revealed climate changes' selective footprints in the genes network regulating flowering time.

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Abstract

Analysis of the genetic bases of adaptation to climate changes are often conducted on natural populations. We report here on a study based on diachronic sampling (1980 & 2010) of the self-fertilising crop species, *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice), in the tropical forest and the Sudanian savannah of West Africa. First, using historical meteorological data we confirmed changes in temperatures (+1°C on average) and rainfall regime (less predictable and reduced amount) in the target area. Second, phenotyping the populations for phenology, we observed significantly earlier heading time (up to 10 days) in the 2010 samples. Third, we implemented two genome-scan methods, one of which specially developed for selfing species, and detected 31 independent selection footprints. These loci showed significant enrichment in genes involved in reproductive processes and bore known heading time QTLs and genes, including *OsGI*, *Hd1* and *OsphyB*. This rapid adaptive evolution, originated from subtle changes in the standing variation in genetic network regulating heading time, did not translate into predominance of multilocus genotypes, as it is often the case in selfing plants, and into notable selective sweeps. We argue that this high adaptive potential results from the multiline genetic structure of the rice landraces, and the rather large and imbricated genetic diversity of the rice meta-population at the farm, the village and the region levels, that hosted the adaptive variants in multiple genetic backgrounds well before the advent of the environmental selective pressure. The complex selection footprints observed in this empirical study calls for further model development on genetic bases of plant adaptation to environmental changes.

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