Diverse genetic mechanisms underlie worldwide convergent rice feralization

Genome Biolog

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Background

Worldwide feralization of crop species into agricultural weeds threatens global food security. Weedy rice is a feral form of rice that infests paddies worldwide and aggressively outcompetes cultivated varieties. Despite increasing attention in recent years, a comprehensive understanding of the origins of weedy crop relatives and how a universal feralization process acts at the genomic and molecular level to allow the rapid adaptation to weediness are still yet to be explored.

Results & Conclusions

We use whole-genome sequencing to examine the origin and adaptation of 524 global weedy rice samples representing all major regions of rice cultivation. Weed populations have evolved multiple times from cultivated rice, and a strikingly high proportion of contemporary Asian weed strains can be traced to a few Green Revolution cultivars that were widely grown in the late twentieth century. Latin American weedy rice stands out in having originated through extensive hybridization. Selection scans indicate that most genomic regions underlying weedy adaptations do not overlap with domestication targets of selection, suggesting that feralization occurs largely through changes at loci unrelated to domestication.

This is the first investigation to provide detailed genomic characterizations of weedy rice on a global scale, and the results reveal diverse genetic mechanisms underlying worldwide convergent rice feralization.





non-domestication regions. (a) The overlapping rate between de-domestication

Fig. 1 | Geographic locations of global weedy rice sampling. Circle sizes indicate samples zes by country, and colors indicate inferred crop. Overlapping circles indicate geographic regions with more than one type of weedy rice



regions of weedy rice and domestication regions of rice. (b) Differentiation between domestication region and non-domestication region. (c) The distribution for F_{ST} values of each gene between weedy and cultivated. (a' 20 15 (c)

Fig. 2 | Cultivar founders for weedy rice based on Kinship analysis. (a) Rice cultivar founders for multiple Asian weedy rice populations. (b) The pedigree of Nanjing11. (c) Phylogenetic tree for the Nanjing11 pedigree accessions and weedy rice which have the highest kinship with Nanjing11 Fig. 4| Genomic differentiation and parallel selection in global weedy rice. (a) F_{ST} of different groups of weedy rice compare to cultivated rice. (b) A divergent genomic region in weedy rice, (c) Characterization of a seed germination-related gene GD1, which is under parallel selection in japonica weeds.

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GD1

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