

Supplementary Note 1

Our phylogenomic analyses also have implications for the systematics of the genus. The North American native lineage clustered with *P. japonicus* across the genome rather than with any *P. australis* lineage, suggesting that its current placement within *P. australis* sensu stricto requires reappraisal and that it may be more appropriately treated as a clade within *P. japonicus*. Similarly, the consistent affinity between *P. karka* and *P. mauritanus* across multiple analyses raises the possibility that these taxa are conspecific. Resolving these questions will require denser outgroup sampling and chromosome-scale data from additional taxa, but the present analyses underscore that the boundaries of *P. australis* as currently circumscribed do not reflect a monophyletic grouping.

Supplementary Note 2

The greenyellow module, positively correlated with AU, showed no significantly enriched GO terms. The darkred module, negatively correlated with AU, was enriched for methionyl-tRNA aminoacylation. The lightyellow module in the EU invasive population comprised 82 B-chromosome and 146 co-expressed autosomal genes, enriched for plasma-membrane organization, gamete fusion during double fertilization, and other reproduction-related processes. The black module in the USland lineage was enriched for telomere maintenance via telomerase, RNA-templated DNA biosynthesis, and double-strand break repair via homologous recombination. Within this network, a B-chromosome-encoded ubiquitin-like protease homologous to rice Os10g0388600, a gene with documented temporal induction during salt stress¹, occupied a central hub position.

1. Sue-oh, K. *et al.* Ubiquitin-like SUMO protease expansion in rice (*Oryza sativa* L.). *The plant genome* **19**, e70200 (2026).