Computational and functional genomics approaches toward improving abiotic stress resistance in rice

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Rice is the dietary staple for more than half of the world's population. Genomic and geo-environmental Information derived from rice landraces (cultivars adapted to the local climate) can be used to develop improved varieties and promote food security and sustainability. To contribute to this approach, we developed Oryza CLIMtools, the first resource for pan-genome prediction of climate-associated genetic variants in a crop species [1]. Oryza CLIMtools allows investigation of the environment by genome associations for 658 Indica and 283 Japonica rice landrace varieties that have been collected from geo-referenced locations and sequenced as part of the 3K Rice Genomes Project. Through association analyses we identified the sole canonical rice Gα subunit, *OsRGA1*,as a candidate gene in the regulation of plant height and local adaptation to the prevailing potential evapotranspiration gradient [1]. Heterotrimeric G proteins, composed of Gα, Gβ, and Gγ subunits, are ubiquitous second messengers in eukaryotes. We confirmed a role of *OsRGA1* variants in the control of plant architecture and drought tolerance in both greenhouse studies and field trials [2].

[1] Ferrero-Serrano Á, Chakravorty D, Kirven KJ, Assmann SM. Oryza CLIMtools: A genome-environment association resource reveals adaptive roles for heterotrimeric G proteins in the regulation of rice agronomic traits. (2024) Plant Commun. 5:100813. doi: 10.1016/j.xplc.2024.100813.

[2] Ferrero-Serrano Á, Assmann SM. The α-subunit of the rice heterotrimeric G protein, RGA1, regulates drought tolerance during the vegetative phase in the dwarf rice mutant d1. (2016) J Exp Bot. 67:3433-3443. doi: 10.1093/jxb/erw183.