

Chromosomal deletions drove parallel domestication of plant architecture in Asian and African rice

With the support by the National Key Research and Development Program of China and National Natural Science Foundation of China, the research group led by Prof. Tan LuBin (谭禄宾) at the Department of Plant Genetics and Breeding, China Agricultural University, reported that the chromosomal deletions closely linked to *PROSTRATE GROWTH 1* (*PROG1*) gene are involved in the parallel domestication of plant architecture in Asian and African rice, which was published in *Nature Communications* (2018, 9: 4157).

Human ancestors domesticated wild plants through selecting favorable genetic variations, thereby meeting human needs and promoting the development of human society. Rice was one of the earliest domesticated crop species and is now a primary staple for millions of people around the world. In general, cultivated rice has an erect growth habit and less tillers, whereas the wild ancestor of cultivated rice tends to have a prostrate or semi-prostrate growth habit and more tillers. The transition of plant architecture in rice domestication has potential advantages for denser plantings and higher yield. Hence, identification of genetic factors associated with the key transition of plant architecture will untie the history of rice domestication.

Previous reports published in *Nature Genetics* (2008, 40: 1360—1364 and 2008, 40: 1365—1369) revealed that the variations of the zinc-finger transcription factor *PROG1* were fixed in Asian cultivated rice, leading to erect growth and improved grain yield. To identify new genetic factors controlling the transition of plant architecture during rice domestication, Tan's group developed a set of introgression lines using an accession of wild rice (*Oryza rufipogon* Griff.) with semi-prostrate growth habit from Dongxiang County, Jiangxi Province, China. Through the positional cloning approach, a novel quantitative trait locus (QTL) responsible for the transition of plant architecture was fine mapped into an 8.9-kb interval, which is closely linked with the previous identified *PROG1* gene. Therefore, this locus was named *RICE PLANT ARCHITECTURE DOMESTICATION* (*RPAD*). Comparison of genome sequences showed that Asian cultivated rice had a 110-kb chromosomal deletion at the *RPAD* locus, eliminating a tandem repeat of seven zinc-finger genes. Further genetic transformation experiments demonstrated that three of these zinc-finger genes regulate tiller angle and tiller number and affect grain yield. Sequence analysis showed that 136 Asian rice varieties contain an identical deletion at the *RPAD* locus, indicating that the deletion may have been a single evolutionary event that has been strongly selected in the domestication process. This finding provides new evidence in support of the “multiple origins, single domestication” hypothesis regarding the origin of Asian cultivated rice.

Interestingly, Tan's group analyzed the *RPAD* syntenic region in the genomes of African cultivated rice (*O. glaberrima*) and its wild ancestor *O. barthii* and found that a similar but independent 113-kb deletion occurred at the *RPAD* locus in African cultivated rice, implying that the convergent evolution of crop plant architecture shares a common underlying mechanism. Notably, foxtail millet (*Setaria italic*) and its presumed progenitor green foxtail (*S. viridis*) also had a similar tandem repeat of zinc-finger genes in the *RPAD* syntenic region, suggesting that the *RPAD* locus might have a conserved function in plant architecture development in the grass family. Thus, the *RPAD* syntenic region could be a target for designing novel plant architecture and accelerating the domestication of the semi-domesticated or wild grass plants to meet the future challenges of global food security.



Figure Plant architecture of wild rice (*O. rufipogon*) and cultivated rice (*O. sativa*).