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Nucleotide Diversity and Molecular Evolution of the *ALK* Gene in Cultivated Rice and its Wild Relatives

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Abstract Gelatinization temperature (GT), an important parameter for rice cooking quality, is mainly regulated by the *ALK* gene encoding starch synthase IIa. Here, we reported the nucleotide diversity of the *ALK* gene in 122 cultivated accessions and 199 wild rice accessions that were collected around the Pearl River Basin in China. A total of 93 single nucleotide ploymorphisms (SNPs) were identified, with an average of one SNP per 40 bp. Tajima D statistics revealed that the DNA sequences covering the last exon have probably evolved under balancing selection. Based on two functional SNPs (an A to G substitution at 4198 bp and a GC to TT dinucleotide substitution at 4330/4331 bp), three haplotypes, G/GC, G/TT, and A/GC, were identified in both wild and cultivated accessions, with the G/GC haplotype being predominant. Interest-

ingly, the A/GC haplotype was exclusively found in the wild accessions from Guangdong province, while the G/TT haplotype was only present in the wild accessions from Jiangxi province and Hainan Island. This suggests that the G/TT and A/GC variants may have arisen independently and undergone balancing selection on separate haplotypes in multiple populations. Our result supports earlier hypothesis that cultivated rice was independently domesticated from multiple domestication events in China. Our study aids in the understanding of the domestication process that led to the improvement of rice grain quality.

Keywords Rice \cdot Gelatinization temperature $\cdot ALK \cdot$ Single nucleotide polymorphism \cdot Balancing selection

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