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Evolutionary Analyses of *SSII-1* Gene Provides Insight into Its Domestication Signatures in Collected Rice Accessions

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[Abstract]

Starch synthase proteins (*SSI*, *SSII* and *SSIII*) in rice are mainly involved in amylopectin synthesis mediating its chain elongation, and the functional loss of *SSII* can increase amylose accumulation through decreasing of amylopectin chain proportions. For purposes of identifying functional haplotypes and evolutionary analyses of this gene, *SSII-1*, we investigated 374 rice accessions belonging to different subgroups of origins. We subsequently performed bioinformatic analyses on their variations through haplotyping, resequencing and structuring based on different classified populations. Haplotyping of cultivated rice accessions using genetic variations within *SSII-1* genomic region of chromosome 10 revealed a total of 8 haplotypes, representing 6 functional haplotypes by 4 non-synonymous SNPs of three different exons (1, 4 and 10), which effect on protein structure. Higher nucleotide diversity value was found in wild group (0.0055) compared to any of cultivated subpopulations, of which *aus* showed the most reduction of diversity value (0.0003). Tajima's *D* analysis exhibits the most Tajima's *D* value only in *admixture* group (0.3600) which appears to be the cause of a sudden population contraction by rare alleles scarcity. A clear separation of some wild accessions from the admixed cultivated subpopulations was observed in PCA and phylogenetic analysis. Similar admixed pattern of population structure was estimated with an increased K values of 2 to 8 where genetic components of almost all cultivated subpopulations were shared with the wild which can also be subsequently estimated by very low F_{ST} -values by -0.011 (wild-aromatic) and -0.003 (wild-admixture).

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