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Downregulation of tobacco ADP-glucose pyrophosphorylase gene *NtAGP* arrests the expansion growth of corolla lobes and leads to phenotypic changes in petal limbs

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ADP-glucose pyrophosphorylase (AGPase) genes have been extensively demonstrated to play a pivotal role in starch biosynthesis in various starch-accumulating tissues. Its role, however, in flower development has never been determined. In this study, we characterized the role of *AGPase* in the growth of floral organ, especially petal. A tobacco *AGPase* cDNA (*NtAGP*) was isolated from a cDNA library constructed with flower bud. *NtAGP* was highly expressed throughout flower bud development, from young bud (<1cm) to open flower. Its expression was high in sepal, moderate in carpel and stamen, and low in petal. Genomic Southern analysis revealed that *NtAGP* is encoded by two independent loci. In vivo targeting experiment with tobacco protoplasts showed that *NtAGP* was localized to chloroplast. To determine the function of *NtAGP* in flower development, we generated antisense transgenic tobacco plants. *NtAGP*-antisense plants produced flowers with abnormal petal limbs in that expansion growth of corolla tips was terminated earlier, resulting in petal limbs of distinctive corolla lobes. Microscopic observation of the limb region identified that cell expansion was limited in *NtAGP*-antisense plants, but cell numbers remained unaltered. In *NtAGP*-antisense plants, mRNA levels of *NtAGP*, AGPase activity and starch content were lowered in sepal tissues, consequently, sucrose, glucose and fructose content was significantly reduced in petal limbs. Sucrose feeding to flower buds of *NtAGP*-antisense plants restored the expansion growth between corolla lobes, leading to petal limbs of wild type. These results suggest that *NtAGP* plays an important role in morphogenesis of petal limbs in tobacco through synthesis of starch in sepal, the main carbohydrate source for expansion growth of petal.

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Mapping of new complementary recessive genes for hybrid breakdown in rice

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Hybrid breakdown (HB), the reduction of viability or fertility in the hybrid progenies which is one of the reproductive barriers occurring in genetically remote crosses, often arise in the progenies of inter-subspecific hybrids between *indica* and *japonica* in rice. HB lines which showed poor growth and fewer spikelets were found in an RI population derived from a cross between an *indica* variety, Milyang 23, and a *japonica*variety, Tong 88-7. Segregation of HB in BC_1F_2 populations from reciprocal backcrosses, HB-RILs/Milyang 23 and HB-RILs/Tong 88-7, revealed that HB was controlled by a complementary action of two recessive genes originated from each of both parents. Using a number of STS and SSR markers and bulked segregant analysis, thetwo recessive genes controlling HB were mapped on chromosomes 11 and 2, respectively. The *japonica* parent Tong 88-7 has a new hybrid breakdown gene, which was located between AC135398A and AC136843C on chromosome 11 with a distance of 0.362 cM and 0.361 cM, respectively, whereas the *indica* parent Milyang 23has another gene on chromosome 2. The locus was mapped between AP004083A and AP004053A with a distance of 0.932 cM and 0.434 cM, respectively.

Keywords: Hybrid breakdown; rice; mapping

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Functional analysis of rice phosphate transporter genes in transgenic rice

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Abstract

Since phosphate ion is essential in development and growth of plants, P (phosphate) fertilizer has been widely used to maximize crop production regardless of serious environmental pollution. In order to develop rice plants with high availability of P ion, we engineered 4 rice transporter genes, *OsPT1*, *OsPT4*, *OsPT7* or *OsPT8* to rice (*Oryza sativa* cv. Dongjin) via *Agrobacterium*-mediated transformation. We were able to obtain T_3 generation of homozygous transgenic lines constitutively expressing each *OsPT* gene. Dongjin (parental)and each transgenic line were grown in a large pot containing normal soil (N P K application plot) and P-limited soil (N K (-P) application plot) with 5 replications. Evident physiological changes were observed in *OsPT* transgenic lines such as height, number of tillers, root formation and heading date. P_2O_5 uptake at harvesting stage increased about 2-fold in the aerial parts from *OsPT1* and