

**P005** Genetic analysis and molecular mapping of a premature senescence gene *Pse1(t)* locus in rice (*Oryza sativa* L.)  
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A premature-senescence rice mutant, named *pse1(t)*, was isolated from T-DNA inserted rice mutant pool. It is apparent that senescence progress severely in the premature-senescence mutant than in the wild-type plant (Zhonghua 11, japonica). Genetic analysis revealed that the premature-senescence phenotype is controlled by a single recessive nuclear gene, tentatively symbolized as *Pse1(t)*. Unfortunately, *pse1(t)* is not induced by T-DNA insertion. To better understand the molecular basis of the premature-senescence occurring in *pse1* mutants, a map-based cloning strategy has been employed to isolate *Pse1(t)*. High-resolution mapping of the *Pse1(t)* gene was carried out using SSR and CAPS markers, furthermore, three new SSR markers and three new CAPS marker were developed. The results of the genetic linkage analysis revealed that the *Pse1(t)* locus was located in chromosome 7, which co-segregated with the SSR marker RM5793, CAPS markers PP4 and PP5, and was mapped between SSR markers SS16 and SS13 at 0.2 cM and 0.25 cM intervals, respectively. Thus, the *Pse1* locus was localized in the 0.45-cM region, and its corresponding physical distance was 200kb. Gene prediction and functional complement with candidate genes are in process.