（学位第３号様式）

学 位 論 文 要 旨

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題　目	Genetic analysis of segregation distortion caused by abortion during seed development in the interspecific crosses among AA genome *Oryza* species （AA genome *Oryza* 種間交雑で見出された種子発育不全がもたらす分離歪み現象の遺伝解析）

Wild rice relatives having the same AA genome as domesticated rice (*Oryza sativa*) comprise the primary gene pool for rice genetic improvement. Among them, *O. meridionalis* and *O. rufipogon* are found in the northern part of Australia. Three Australian wild rice strains, Jpn1 (*O. rufipogon*), Jpn2, and W1297 (*O. meridionalis*), and one cultivated rice cultivar Taichung 65 (T65) were used in this study. A recurrent backcrossing strategy was adopted to produce chromosomal segment substitution lines (CSSLs) carrying chromosomal segments from wild relatives and used for trait evaluation and genetic analysis.

In the first half of the study, the segregation of the DNA marker RM136 locus on chromosome 6 was found to be highly distorted, and a recessive lethal gene causing abortion at the seed developmental stage was shown to be located between two DNA markers, KGC6_10.09 and KGC6_22.19 on chromosome 6 of W1297. This gene was named as *SEED DEVELOPMENT 1* (gene symbol: *SDV1*). *O. sativa* is thought to share the functional dominant allele *SDV1-s* (*s* for *sativa*), and *O. meridionalis* is thought to share the recessive abortive allele *sdv1-m* (*m* for *meridionalis*). Though carrying the *sdv1-m* allele, the *O. meridionalis* accessions can self-fertilize and bear seeds. We speculate that the *SDV1* gene may have been duplicated before the divergence between *O. meridionalis* and the other AA genome *Oryza* species, and that *O. meridionalis* has lost the function of the *SDV1* gene and has kept the function of another putative gene named *SDV2*.

In the second half of the study, we performed fine mapping of *SDV1*, narrowing down the area of interest to 333kb on chromosome 6. Haplotype analysis around the *SDV1* locus of *O. meridionalis* accessions indicated that they shared the DNA polymorphism, suggesting that they have a common abortive allele at the *SDV1* locus. Linkage analysis of the candidate *SDV2* gene showed that it was located on chromosome 4. The candidate proved to be true *SDV2*, using a population in which both the *SDV1* and *SDV2* genes were segregating. The chromosomal region covering the *SDV1* gene was predicted to contain 30 protein-coding genes in *O. sativa*. Four of these genes have conserved DNA sequences in the chromosomal region of the *SDV2* gene on chromosome 4, and not on chromosome 6, of *O. meridionalis*. These results suggest that these four genes could be candidates for *SDV1*, and that their orthologous genes located on chromosome 4 of *O. meridionalis* could be candidates for *SDV2*.