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SCR-22 of pollen-dominant S haplotype class is recessive to SCR-44 of pollen-recessive S haplotype class in *Brassica rapa*

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Abstract

SCR/SP11 encodes the male determinant of recognition specificity of self-incompatibility (SI) in *Brassica* species and is sporophytically expressed in the anther tapetum. Based on dominance relationships in pollen and nucleotide sequence similarity, the *S* haplotypes in *Brassica* have been classified as class I or class II, with class-I *S* haplotypes being dominant over class-II *S* haplotypes. Here, we revealed that *S*-22 in *B. rapa* belonging to class I is recessive to class-II *S*-44 and class-I *S*-36 in pollen, whereas it is dominant over *S*-60, *S*-40, and *S*-29 based on pollination tests. *SCR/SP11* of *S*-22 (*SCR*-22) was sequenced, revealing that the deduced amino-acid sequence of *SCR*-22 has the longest C-terminal domain among the *SCR/SP11* sequences. The expression of *SCR*-22 was found to be suppressed in *S*-22/*S*-44 and *S*-22/*S*-36 heterozygotes. Normal transcription of *SCR*-44 was considered to be due to the transcription suppression of *Smi* sRNA of the *S*-22 haplotype and a very low methylation state of the *SCR*-44 promoter region in the tapetum of *S*-22/*S*-44 heterozygotes. In *SCR*-22, only the cytosine residue located at the -37 bp position of the promoter region was hypermethylated in the tapetum of *S*-22/*S*-44 heterozygotes, and few methylated cytosines were detected in the promoter and coding regions of *SCR*-22 in *S*-22/*S*-36 heterozygotes. *SCR*-22 was also expressed in microspores in *S*-22 homozygotes but not in *S*-22/*S*-44 and *S*-22/*S*-36 heterozygotes. These results suggest that a mechanism different from class-II *SCR/SP11* suppression may operate for the suppression of recessive class-I *SCR*-22 in *S* heterozygotes.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6355930/>

