



Pungu Okito

Origins of Y Genome in Elymus

The identification of Y genome is a great success in improving crops in the Poaceae family (wheat, rice, barley and rye)



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The Y genome is recently identified in Elymus. The identification of this genome has contributed significantly in improving research on the Gramineae family. Three out of 43 accessions of Pseudoroegneria tested, were positive for the Y genome marker. Sequence Tagged Site marker (STS) allowed the detection of this genome in Elymus species with at least a 95% confidence level. Seven five sequences were analyzed including the Y-genome RAPD marker, JC51 (GenBank accession BV 679236) which was amplified from Elymus rectisetus (StWY). Twelve clones of plasmid DNA sequence were isolated from Pseudogneria spicata (St), five from Pseudogneria ferganensis (St), and seven from Pseudogneria libanotica. The phylogenetic tree was based on the CLUSTAL W alignment of DNA. Elymus fibrosus previously classified as containing the StH genome was tested positive for the Y genome marker because of the presence of Y genome sequence in the St genome rather than the presence of a true present-day Y genome. The copy number of the Y genome marker in Pseudogneria is higher than in Hordeum. Pseudogneria spicata is the prime candidate as donor of the Y genome to the Elymus species (StY, StPY, STWY or STHY genome

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