Variation in the Abundance of TaiI-1 Repetitive Sequence in Four Psathyrostachys Species. (C07-wang110159-Poster)

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Abstract:

The Ns genome of Psathyrostachys species is a component of the polyploid genome in the genus Leymus. There are two existing hypotheses on the genome constitution in Leymus species; one holds that tetraploid species of Leymus have the genome formula NsNsNsNs and the other states that they have NsNsXmXm with the Xm coming from an unknown source. The occurrence and abundance of two tandem repetitive sequences, TaiI-1 and PstI-1 that were isolated from Leymus racemosus (Lam.) Tzvelev by Kishii et al. (1999), were assayed in four species of the genus Psathyrostachys using fluorescence in-situ hybridization (FISH). The PstI-1 sequence was absent in all four Psathyrostachys species. While P. fragilis and P. huashanica do not have the TaiI-1 sequence, P. juncea and P. lanuginosa are highly variable for the abundance of this sequence. Fifteen accessions of P. juncea have TaiI-1 FISH sites ranging from 7 to 16 in different plants, whereas two accessions of P. lanuginosa have FISH sites ranging from 2 to 21. This information is useful in determining sources of the Ns genome in various Psathyrostachys species. It may also shed light on the nature of polyploidy in different Leymus species when they are assayed for the two repetitive sequences.

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