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Wide Hybridization to Develop Perennial Wheat Line with *L. mollis* in Korean Wheat Breeding Program

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[Introduction]

Wild rye is very important as a future-oriented research material to overcome the genetic limitations of cultivars. This is because wild rye not only has adaptability to harsher environments than cultivar, but also has resistance to biological and abiotic stress.

[Materials and Methods]

Leymus mollis (Trin.) Piler (2n = 4x = 28, NsNsXmXm, allotetraploid) and Chinese Spring (*Triticum aestivum* L. 2n = 6x = 42, AABBDD, hexaploid) were used to perform wide hybridization for Korean wheat breeding program. Metaphase chromosomes were observed by squash method with 2% acetocarmine. Genomic *in situ* hybridization was performed to identify chromosome number and behavior.

[Results and Discussion]

The objective of this study is to develop perennial wheat lines by wide-hybridization. We produced wheat-*L. mollis* F_1 hybrids. Five of F_1 seeds(10 seeds) germinated with two shoots and one thicker root than major three roots. That F_1 hybrids showed perennial characteristics, after growth stage new shoot appeared. New shoot was from rhizome like *L.mollis* with perennial nature. We observed chromosome of F_1 hybrids, Chinese Spring and *L. mollis*. It was expected to have 35 chromosomes(21 form CS and 14 from *L. mollis*), but F_1 hybrids has 35~44 chromosomes. By genomic *in situ* hybridization, we observed CS and *L. mollis* choromosomes were disticgiushed. Seeds of F_1 hybrids showed unique traits. The seed were thicker than seed of *L. mollis* and color was brighter but darker than seed of CS. One of F_1 hybrids seeds were shorter than CS and *L. mollis*. Two of Spikes of F_1 hybrids has longer length and rachis than spikes of CS, but size of grain was similar. The density of seed in F_1 hybrids spikes were lower than CS. One of F1 hybrids spikes has similar spike length and grain size of CS. Seeds were formed despite of wide-hybridization, and It seems to be produced by B chromosome(abnormal chromosome) of *L. mollis*, which is different from A chromosome(normal chromosome) of *L. mollis*. It is necessary to study about F_1 hybrids lines in chromosome level.

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