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Diversity of seed storage protein patterns of Slovak accessions in jointed goatgrass (*Aegilops cylindrica* Host.)

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Abstract

Variations in seed storage protein patterns were investigated for six accessions of jointed goatgrass (*Aegilops cylindrica)* populations collected from Slovakia within the framework of the bilateral Co-operation in Science and Technology between the Slovak Republic and Hungary. The study covered populations collected from the southwestern (localities: Sered and Dunajská Streda), southern (localities: Chlaba and Kamenica nad Hronom) and southeastern (localities: Cierna nad Tisou and Dobra) parts of Slovakia. Analysis of profiles of seed storage proteins – glutenins and gliadins – was carried out using acid polyacrylamide gel electrophoresis and sodium dodecyl sulphate polyacrylamide gel electrophoresis. All accessions have a uniform three-band high molecular weight glutenin pattern with CxCyDy subunit composition. The highest variations in gliadin bands among the populations were observed from Cierna nad Tisou. There were small differences among the populations from Chlaba and Dobra. The lowest variations were in populations from Sered, Dunajska Streda and Kamenica nad Hronom. The present investigation showed that these jointed goatgrass populations are valuable genetic resources for wheat crop improvement programmes.

Keywords: *Aegilops cylindrica* Host.; diversity; gliadins; glutenins

Introduction

The *Aegilops* genus contains species closely related to wheat. Electrophoretic analyses of seed storage proteins – glutenins and gliadins – have proven very useful in evaluating and characterizing of jointed goatgrass (*Aegilops cylindrica* Host.) accessions. Jointed goatgrass has C and D genomes. High molecular weight-glutenin subunits (HMW-GS) are controlled by genes at two complex loci – *Glu-1C* and *Glu-1D* – located on the long arm of the group 1 chromosome. Different allelic subunits at each *Glu-1* locus have been identified by sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE). Each *Glu-1* complex locus consists of two tightly linked but not always expressed genes (Payne *et al*., 1981). Within the loci, recombination is rare. In diploid species, both subunits are expressed, whereas in polyploid species such as wheat and jointed goatgrass, there is silencing of one or more subunits (Payne *et al*., 1981; Galili and Feldman, 1983). Jointed goatgrass has a three-band pattern due to non-expression of the *Glu-1Dx* subunit (Johnson, 1967).

Materials and methods

We analysed six accessions of *A. cylindrica* populations collected from the Slovak Republic. HMW-GS were extracted from randomly selected single seeds, and protein was extracted from the non-embryo half of the seed. Extractions, electrophoretic separation of glutenin and detection procedures used were in accordance to

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International Seed Testing Association (ISTA) standard procedure for SDS-PAGE, and glutenin subunits were identified following the catalogue of HMW-GS alleles (Payne and Lawrence, 1983). Gliadin in the genotypes was examined using acid PAGE according to the standard ISTA reference method (Bushuk and Zillman, 1978).

Results and discussion

The x- and y-type subunits of the respective C and D genome band contributions to the HMW glutenin pattern for jointed goatgrass were identified by comparison with the band pattern of *Triticum aestivum* cv. Chinese Spring. The *Glu-1* subunit assignment system developed by Payne and Lawrence (1983) was used to identify the relative band positions for the *Glu-1A, Glu-1B* and *Glu-1D* subunits. *Glu-1C* alleles are not encompassed in this assignment system. Jointed goatgrass has a three-band HMW glutenin pattern with a CxCyDy subunit composition and is in agreement with the assignments determined by Wan *et al.* (2000). *Glu-1Dx* subunit was not expressed in all tested material. This low variation for the *Glu-1* genetic marker was consistent with other findings of low genetic diversity in jointed goatgrass (Okuno *et al.*, 1998). Gliadin electrophoresis (Fig. 1) showed a higher level of polymorphism than glutenin and therefore should be better for use in population identification. Gliadins are a highly polymorphic and biochemically unusual class of proteins characterized by very complex electrophoretograms when separated under acid conditions. Traditionally, the electrophoretograms of gliadins are divided into α, β, γ and ω zones, with proteins found in each zone being grouped into separate subclasses. The ω gliadins have a low cysteine content, differing from the other groups of gliadins, which are cysteine-rich (Shewry and Tatham, 1990). We identified γ, δ and ω zones of gliadins in the jointed goatgrass populations, but not α. The highest variation in gliadin bands among the populations was from Cierna nad Tisou, with five different compositions. There were small differences among the populations from Chlaba and Dobra, with three different gliadin compositions. The lowest variations were from Sered and Dunajska Streda populations, with only two different compositions. The present investigation showed that the jointed goatgrass populations collected from Slovakia were valuable genetic resources for wheat crop improvement programmes.

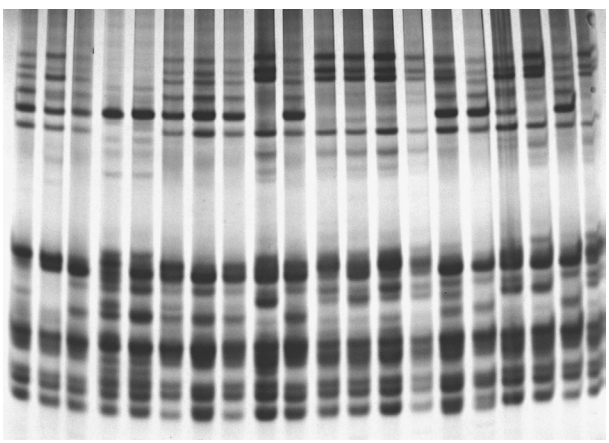

Fig. 1. Gliadin pattern of Slovak accessions in jointed goatgrass (*A. cylindrica* Host.): lanes 1–3, populations from Chlaba; lanes 4, 5, populations from Sered; lanes 6, 7, populations from Dunajska Streda; lines 8–10, populations from Kamenica nad Hronom; lanes 11–17, populations from Cierna nad Tisou; lanes 19–20, populations from Dobra.

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