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High transferability and polymorphism of barley EST-SSR markers for the analysis of gene biodiversity in *Hordeum chilense*

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Recently, EST derived microsatellite markers have become a useful tool to complement existing genomic SSR markers. In the present work, barley EST-derived SSR markers (Varshney *et al.* 2005) were tested to determine their usefulness for mapping, introgression and variability studies in *Hordeum chilense*.

100% of the 74 barley EST-derived SSR-markers primer pairs tested for the transferability to *H. chilense*, amplified products of correct size from this species. 24 of the primers (32%) were polymorphic between H1 and H7, producing markers that will be mapped to the species existing linkage groups. The confirmation of their chromosomal localization is being carried out by using the available wheat/*H. chilense* chromosome addition lines.

Sets of barley genomic SSR markers (Liu *et al.* 1996, Li *et al.* 2003) have been previously tested in *H. chilense* (Hernández *et al.* 2002, Castillo *et al.* 2005 respectively). The transferability levels found in this work (100%) are higher, and, overall, EST-SSRs have shown higher polymorphism levels than neutral SSRs. Nevertheless, it should be stated that, considering only the SSRs transferred to the *H. chilense* species, instead of the total numbers of available barley SSRs, the rates of polymorphism within the species are similar or slightly smaller for EST-SSRs, as described for other species (Varshney *et al.* 2005).

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