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GENETIC RESOURCES OF *Hordeum spontaneum* FOR BARLEY IMPROVEMENT

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The vast genetic resources of wild barley, *Hordeum spontaneum* (HS), the progenitor of cultivated barley, is the best, largely unexploited, resource for improving the narrowing genetic base of the cultivar.HS is widely distributed in the East Mediterranean basin and West Asia. Its center of origin, and diversity is the Fertile Crescent, particulary Israel, where it displays the highest genetic diversity. HS is a generalist colonizer, very variable genetically at the protein and DNA levels. Genetic diversity of HS is largely nonrandom, nonneutral, variable spatially and significantly correlated with the environment, at micro- and macroscales.It displays significant associations of general genetic diversity, allele frequencies, unique alleles, extensive linkage disequilibria and genome organization with abiotic and biotic variables. HS harbours extensive genetic resources for barley improvement. These include development, biomass, yield, earliness, quality and quantity of storage proteins (hordeins), amylases, nitrogen economy, malt quality, drought and salt tolerance, sodium content, C-13 and N-15 diversities, adaptive traits to adverse ecological stresses and temperature extremes, heat productivity, biorhythmicity, disease resistances (e.g. powdery mildew, leaf rust, scald, viruses). Pioneering breeding success transferred alien genes and traits to the cultivar (e.g., higher grain yield, straw, total biomass, high harvest index and volume weight, earliness and disease resistances). Detailed genetic maps and QTL mapping by marker analysis could expose the rich, yet untapped, genetic potential for barley improvement.