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HELIANTHUS BARCODING DATABASE

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To make a database of the genus *Helianthus* we used the approach of barcoding which is becoming an increasingly accepted method to distinguish different species. The genus *Helianthus* comprises more than 50 sunflower species, some of them have become important as models for the study of the genetics of adaptation and speciation. Moreover wild species are interesting sources of many useful characters (drought and salinity resistance, source of CMS, disease resistance) for cultivated species. In this study we characterized at the molecular level using two DNA sequences, the nuclear internal transcribed spacer region (*ITS*) and the plastid *trnH-psbA* intergenic spacer, *H. annuus, H. argophyllus, H. tuberosus* and three *H. debilis* ssp. The nuclear and plastid regions were PCR amplified with specific primers and sequenced with an ABI Prism 3730 Automated DNA sequencer. Intraspecific and interspecific sequence variation was evaluated to assess the technique resolution. After sequence editing with specific software (Phred, Phrap and Consed) we was able to distinguish unambiguously each species looking for SNP, InDel and SSR. According to our results both *ITS* and *trnH-psbA* could be the sequences of choice to develop a database of reference sequences to serve as a *Helianthus* library in providing a practical, standardized, species-level identification tool that can be used for biodiversity assessment, ecological studies and analysis of interspecific hybridization.