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IDENTIFICATION OF *HELIANTHUS* HYBRIDS THROUGH DNA BARCODES

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The nuclear internal transcribed spacer (ITS) sequence, bi-parentally inherited, is proposed as barcoding locus in plant kingdom. We evaluated the feasibility of ITS for following paternal and maternal genome lineages in interspecific hybrids in the *Helianthus* genus.

Seedlings of *Helianthus annuus*, *H. argophyllus*, *H. debilis* subsp. *cucumerifolius* and interspecific hybrids were cultivated at the experimental farm of Udine University (I). The interspecific hybrids were between *H. argophyllus* and *H. debilis* subsp. *cucumerifolius*, *H. debilis* subsp. *cucumerifolius* x *H. annuus* and *H. annuus* x *H. tuberosus*. Artificial hybrids were obtained by rubbing together the heads of parental species during the time of anthesis. The heads were bagged before anthesis and after pollination in order to prevent pollen contamination from other plants. Young leaves from each plant were collected for total genomic DNA extraction.

The species and hybrids were characterized at the molecular level through ITS. The nuclear 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.

In interspecific crosses, double peaks were clearly visible in those positions where the parental species were distinguishable enabling the correct identification of both parental species.

According to our results it is possible to discriminate the putative nature of hybrids between self- and cross-fertilization within *Helianthus* genus using ITS.