

## TAXONOMIC RESOLUTION OF *CONYZA* WEEDS IN BRAZIL THROUGH MORPHOLOGICAL AND MOLECULAR CHARACTERS

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**Destaque:** The combination of (DNA) barcoding loci and specific morphological characters efficiently discriminated the majority of the *Conyza* accessions.

**Resumo:** The genus *Conyza* includes numerous species of weeds that are a threat to the soybean cropping systems worldwide. Among them, *C. bonariensis*, *C. canadensis* and *C. sumatrensis* are reported as the most prevalent species in Brazil. They can exhibit different herbicide resistance patterns and the specie identification is key to plan the control strategy. But, the existence of species varieties, overlap of phenotypic traits and suspicion of hybrids have challenged this task. We characterized 314 *Conyza* accessions in 2020-2021 from 20 different soybean production areas across Brazil by comparing 33 quali-quantitative morphological characters and by sequencing five proposed genome (DNA) barcoding loci. The accessions were grouped in two species and two specie varieties according to the taxonomic keys: *C. bonariensis* var. *angustifolia*, *C. bonariensis* var. *bonariensis*, *C. sumatrensis* var. *leiotheca* and *C. sumatrensis* var. *sumatrensis*. Morphological characterization revealed phenotypic morphotypes by specie even with some polymorphic characters, and 13 characters were useful to distinguish the species, mainly the involucre, phyllaries and inflorescence parameters. *ITS* (nuclear) and *rps16-trnQ* (chloroplast) gene regions showed potential to distinguish *Conyza* at the species level, and their combination was a suitable multi-loci barcode, except in six cases that did not match the morphological data. Although no morphological differences were observed between these accessions and their respective morphotypes, these cases reinforce the possibility of interspecific hybridization between *Conyza* species under field conditions. In conclusion, a combination of *ITS* and *rps16-trnQ* barcoding loci together with specific morphological characters efficiently discriminated the majority of the *Conyza* accessions from different soybean production areas across Brazil.

**Palavras-chave:** DNA barcode; DNA sequencing; matK; rbcL; trnL-trnF

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