

# ABSTRACTS

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#### Taxonomy of weedy *Cyperus* species (101)

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*Cyperus* is a large (ca. 650 species), taxonomically complex genus widely distributed throughout tropical and warm temperate regions of the world. Many of the species are weedy and four (*C. difformis* L., *C. esculentus* L., *C. iria* L., and *C. rotundus* L.) are ranked among the world's worst 32 weeds. We will present an overview of the traditional morphologically based systematics of *Cyperus*, including a synopsis of infrageneric taxonomy and a discussion of the systematic relationships and geographical origins of selected weedy species. We will explore reasons for inconsistencies in nomenclature and circumscriptions of weedy species and possible solutions and potential problems for new research.

#### Analysis of genetic variation in *Cyperus rotundus* accessions using molecular markers (102)

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DNA-based molecular markers may offer a tool to quantify genetic diversity in native and introduced populations of weed species. The objective of this study was to evaluate *Cyperus rotundus* accessions for genetic variability using random amplified polymorphic DNA (RAPD) markers. A collection of *C. rotundus* accessions was done in Brazil on a countrywide basis. Morphological and physiological studies indicated the presence of distinctive intraspecific biotypes in the Brazilian *C. rotundus* population. Tubers of 66 *C. rotundus* accessions from Brazil, three from Florida, two from Hawaii, one from Mexico and one from Israel were imported into and maintained in a quarantine greenhouse in Gainesville. Based on individual plant analysis, forty-three oligonucleotide primers were used to assess the extent of genetic variation among the accessions. A high level of genetic variability was observed among the accessions tested, suggesting the existence of different clones at different locations. Similarity among accessions was greater for geographically closer clones. The molecular relationships provide new insights into the genetics of Brazilian *C. rotundus* and indicate the possible role of gene flow and/or sexual reproduction in the development of distinctive intraspecific biotypes. Genetic variability of *C. rotundus* should be considered as an important factor in integrated weed management programs.

#### Identification of purple nutsedge (*Cyperus rotundus* L.) biotypes by isoenzymes (103)

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Purple nutsedge (*Cyperus rotundus* L.) is the most widespread weed in the world. The species reduces tremendously the productivity of crops because it is very aggressive and difficult to control. The objective of this study was to identify and map the distribution of the species with isoenzymes. The isoenzyme analysis constitutes a viable technique to identify purple nutsedge biotypes. The enzymes were extracted of leaf tissues and the electrophoresis was based on horizontal starch gel. The morpholine citrate (MC) gel/electrode buffer distinguished different biotypes efficiently. Weed populations were sampled in 66 sites all