

Kelly

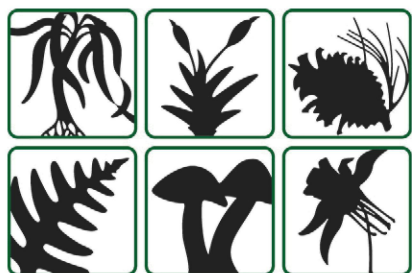
# AMERICAN JOURNAL OF Botany

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**Cover Illustration:** *Conopholis americana*, a root parasite of red oaks in eastern North America, is a representative of one of five major clades of root parasites within Orobanchaceae that are circumscribed using a combined phylogeny of nuclear and plastid data from a broad taxonomic sampling of the family by McNeal et al.—Phylogeny and origins of holoparasitism in Orobanchaceae, pp. 971–983 in this issue. Before the advent of DNA sequencing to infer phylogeny, Orobanchaceae was typically defined to include only holoparasites such as *Conopholis*, which lack photosynthetic activity. DNA evidence reveals that Orobanchaceae include the nonparasitic genus *Lindenbergia* as the basal-branching lineage and suggests a single origin of parasitism followed by three origins of holoparasitism from common ancestors shared with hemiparasites, green leafy parasites that retain photosynthesis. Most of the ca. 2000 species of the family are hemiparasites, attesting to the importance of this way of life. *Orobanchaceae*, the entirely holoparasitic clade which includes *Conopholis*, is the most species-rich of the three holoparasitic lineages, comprising ca. 180 species. Although *Conopholis americana* is an apparently benign parasite, some members of the holoparasitic clades are major threats to crop plants. Photo credit: Sarah Mathews.



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# AMERICAN JOURNAL OF Botany

May 2013 · Volume 100 · Number 5

## TABLE OF CONTENTS

### Anatomy and Morphology

Characteristics of leaf shapes among two parental *Drosera* species and a hybrid examined by canonical discriminant analysis and a hierarchical Bayesian model

YURI HOYO AND SHIRO TSUYUZAKI 817

Impact of spatial constraints during seed germination on the evolution of angiosperm cotyledons: A case study from tropical Hydatellaceae (Nymphaeales)

DMITRY D. SOKOLOFF, MARGARITA V. REMIZOVA, ANTON S. BEER, SHRIRANG R. YADAV,  
TERRY D. MACFARLANE, MARGARET M. RAMSAY, AND PAULA J. RUDALL 824

### Bryology and Morphology

Journey from the West: Did tropical Graphidaceae (lichenized Ascomycota: Ostropales) evolve from a saxicolous ancestor along the American Pacific coast?

ROBERT LÜCKING, ANDERS TEHLER, FRANK BUNGARTZ, EIMY RIVAS PLATA,  
AND H. THORSTEN LUMBSCH 844

### Economic Botany

Geographic differences in patterns of genetic differentiation among bitter and sweet manioc (*Manihot esculenta* subsp. *esculenta*; Euphorbiaceae)

E. JANE BRADBURY, ANNE DUPUTIÉ, MARC DELÈTRE, CAROLINE ROULLIER,  
ALEXANDRA NARVÁEZ-TRUJILLO, JOSEPH A. MANU-ADUENING, EVE EMSHWILLER,  
AND DOYLE McKEY 857

### Evolution and Phylogeny

Reconstructing the evolution and biogeographic history of tribe Cardueae (Compositae)

LAIA BARRES, ISABEL SANMARTÍN, CAJSA LISA ANDERSON, ALFONSO SUSANNA,  
SVEN BUERKI, MERCÈ GALBANY-CASALS, AND ROSER VILATERSANA 867

Phylogeny and fruit evolution in Menispermaceae

KEIR M. WEEFERLING, SARA B. HOOT, AND SUSANA S. NEVES 883

Seed development in *Trimenia* (Trimeniaceae) and its bearing on the evolution of embryo-nourishing strategies in early flowering plant lineages

WILLIAM E. FRIEDMAN AND JULIEN B. BACHELIER 906

Phylogenetic relationships and character evolution analysis of Saxifragales using a supermatrix approach

DOUGLAS E. SOLTIS, MARK E. MORT, MARIBETH LATVIS, EVGENY V. MAVRODIEV,  
BRIAN C. O'MEARA, PAMELA S. SOLTIS, J. GORDON BURLEIGH,  
AND RAFAEL RUBIO DE CASAS 916

Genetic structure and domestication of carrot (*Daucus carota* subsp. *Sativus*) (Apiaceae)

MASSIMO IORIZZO, DOUGLAS A. SENALIK, SHELBY L. ELLISON, DARIUSZ GRZEBELUS,  
PABLO F. CAVAGNARO, CHARLOTTE ALLENDER, JOHANNE BRUNET, DAVID M. SPOONER,  
ALLEN VAN DEYNZE, AND PHILIPP W. SIMON 930

# TABLE OF CONTENTS CONTINUED

## Population Biology

Bioclimatic, ecological, and phenotypic intermediacy and high genetic admixture in a natural hybrid of octoploid strawberries

ISABELLA SALAMONE, RAJANIKANTH GOVINDARAJULU, STACEY FALK, MATTHEW PARKS,  
AARON LISTON, AND TIA-LYNN ASHMAN

939

Microsatellite markers reveal a strong geographical structure in European populations of *Castanea sativa* (Fagaceae): Evidence for multiple glacial refugia

CLAUDIA MATTIONI, M. ANGELA MARTIN, PAOLA POLLEGIONI, MARCELLO CHERUBINI,  
AND FIORELLA VILLANI

951

Cytotype coexistence leads to triploid hybrid production in a diploid-tetraploid contact zone of *Chamerion angustifolium* (Onagraceae)

HOLLY A. SABARA, PAUL KRON, AND BRIAN C. HUSBAND

962

## Systematics and Phylogeny

Phylogeny and origins of holoparasitism in Orobanchaceae

JOEL R. MCNEAL, JONATHAN R. BENNETT, ANDREA D. WOLFE, AND SARAH MATHEWS

971

Geographic distribution and taxonomic circumscription of populations within *Coryphantha* section *Robustispina* (Cactaceae)

MARC A. BAKER AND CHARLES A. BUTTERWORTH

984

## Abbreviations

**Miscellaneous:** AFLP, amplified fragment length polymorphisms; a.s.l., above sea level; bp, base pair; BP, before present; BSA, bovine serum albumin; cpDNA, chloroplast DNA; CTAB, hexadecyltrimethylammonium bromide; cv., cultivar; ddH<sub>2</sub>O, double-distilled water; dNTP, deoxyribonucleotide E.C., Enzyme Commission; EDTA, ethylene diamine tetra-acetic acid; f. sp., forma specialis; indels, insertions and deletions; ITS, internal transcribed spacer; LM, light microscopy; mya, million years ago; PAGE, polyacrylamide gel electrophoresis; PCR, polymerase chain reaction; RAPD, random amplified polymorphic dimorphism; SDS, sodium dodecyl sulfate; SEM, scanning electron microscopy; s.l., sensu lato; s.s., sensu stricto; subsp., subspecies; TEM, transmission electron microscopy

**Genetics:**  $A$ , mean number of alleles per locus;  $D$ , mean genetic distance; CI, consistency index;  $F$ , fixation index;  $F_{IT}$ , total deviation from Hardy-Weinberg expectations;  $F_{ST}$ , genetic diversity among populations;  $F_S$ , inbreeding within populations;  $G_{ST}$ , the proportion of genetic diversity among populations;  $H_e$ , Hardy-Weinberg expected heterozygosity;  $H_o$ , observed heterozygosity; MP, most parsimonious tree;  $n$ , individual chromosome number;  $N_m$ , mean number of migrants per generation;  $P_p$ , percentage of polymorphic loci; RI, retention index;  $x$ , base chromosome number

**Statistics and math:** ANOVA, analysis of variance; CV, coefficient of variation; df, degrees of freedom;  $N$ , number of individuals;  $p$ , probability;  $P$ , level of significance; PCA, principal components analysis;  $r$ , coefficient of correlation; SE, standard error; SD, standard deviation