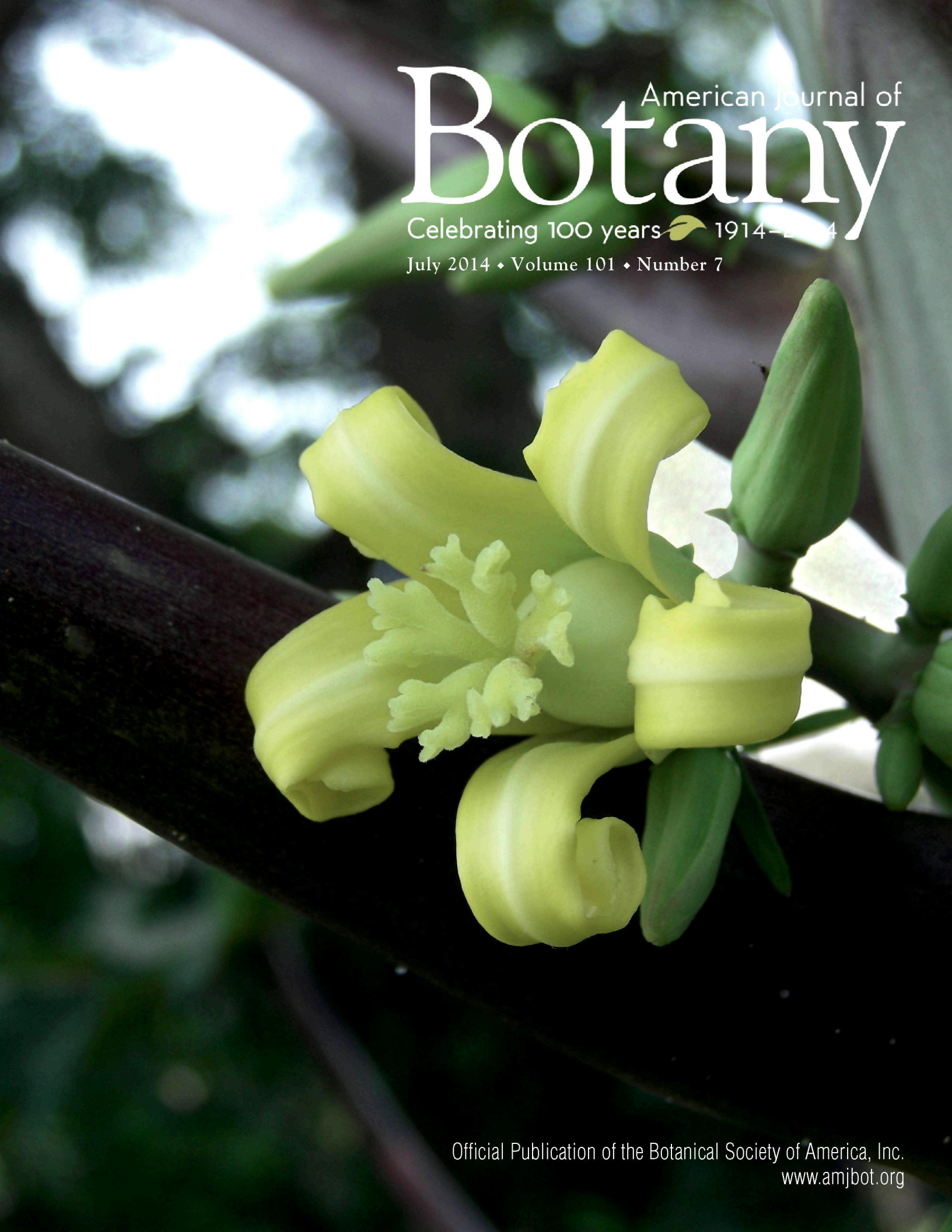

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Cover Illustration: Female flower of a wild papaya tree (*Carica papaya;* Caricaceae) from the Los Tuxtlas rainforest, southeastern Mexico. Floral morphology represents one of the main differences between wild and cultivated papaya; natural populations of *C. papaya* are strictly dioecious, whereas cultivated plants can also be hermaphroditic. Wild papayas are mainly pollinated by hawk moths, and their fruits are dispersed by birds and small mammals. Natural populations of *C. papaya* are rare and persist naturally in tropical rainforests from Mexico to North Central America by colonizing large, newly created light gaps. The conservation of the natural habitats of wild populations of important crop plant species such as papaya is of the utmost importance to assure sufficient levels of genetic diversity to maintain the evolutionary potential of these species. In Mexico, the natural habitat of wild papaya has become extensively fragmented over the last 50 years. Due to the dioecy, rareness, and short life of the wild papaya, disturbances in its natural habitat could constrain the reproductive success of populations by altering gene flow and modifiying sex ratios. In this issue in "Habitat fragmentation threatens wild populations of *Carica papaya* (Caricaceae) in a lowland rainforest" on pp. 1092–1101, Chávez-Pesqueira et al. found that genetic variation and high population differentiation in the wild populations of papaya that inhabit forest fragments was lower than in populations in the continuous primeval forest. Moreover, sex-biased populations had reduced effective population sizes. Because agricultural lands and cattle pastures represent important barriers to gene flow of wild papaya in Los Tuxtlas, its mating system, rarity, and short life cycle exacerbate the effects of rainforest fragmentation on the genetic diversity and structure of wild populations, threatening the genetic reservoir and their persistence in papaya's proposed place of origin. *Photo credit*: Juan Núñez-Farfán.

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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_2O, 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_{IS}, 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; Nm, 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