Cover Illustration: Coenocytic stage of developing endosperm of maize (Zea mays L.; Poaceae), surrounded by maternal nucellus and pericarp tissues. Nuclei share a common cytoplasm around a large central vacuole and divide in tight synchrony without cytokinesis. As the free nuclei divide, starting at the base near the embryo, they migrate toward the large antipodal cells (top) until they completely line the peripheral wall of the tear-drop-shaped endosperm. Cell walls and cytoplasm were stained with propidium iodide, and nuclei were double-stained with propidium iodide and SYTOX Green. Micrograph is a single optical section collected using standard confocal laser scanning optics; magnification ca. 200x. Free nuclear endosperm development in cereal grains has routinely been described as involving three main cytological stages: coenocyte, cellularization by alveolation, and differentiation. This pathway of development is extended to maize, though it is largely based on comprehensive accounts of development in barley, rice, and wheat, with comparison to analogous observations in Arabidopsis. The recent genome sequencing of maize inbred B73, and its use with 25 genetically diverse inbred founder lines to develop a nested association mapping (NAM) population for future dissection of maize genetics, necessitate a thorough understanding of B73 endosperm development. In Leroux et al.—Maize early endosperm growth and development: From fertilization through cell type differentiation, pp. 1259–1274 in this issue, high resolution light and confocal microscopy is used to detail B73 early endosperm development in tandem with morphometric analysis of B73 and four NAM founder lines. Transition between the coenocyte and the cellularization by alveolation stage was more coincident with relative endosperm size than with the number of nuclei or age as previously suggested for maize. Cytological analysis revealed that maize endosperm initially cellularizes through alveolation for the first 2–4 cell layers, followed by a novel and unique second stage of cellularization whereby the remaining central vacuole is subdivided through random partitioning. This unique cellularization of maize contrasts with the smaller endosperms of other cereals (wheat, barley, rice) and Arabidopsis, which strictly cellularize through repeated alveolation. NAM founder analysis revealed differences in endosperm size during early development, which potentially relates to differences in duration of the coenocytic stage and thus timing of cellularization across diverse lines of maize. A B73-specific model of early endosperm development is presented for future analysis of gene expression and endosperm development in other genotypes.

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Table of Contents

AJB Centennial Review
The role of homoploid hybridization in evolution: A century of studies synthesizing genetics and ecology
SARAH B. YAKIMOWSKI AND LOREN H. RIESEBERG 1247

Anatomy and Morphology
Maize early endosperm growth and development: From fertilization through cell type differentiation
BRIAN M. LEROUX, AUSTIN J. GOODYKE, KATELYN I. SCHUMACHER, CHELSI P. ABBOTT, AMY M. CLORE, RAMIN YADEGARI, BRIAN A. LARKINS, AND JOANNE M. DANNENHOFFER 1259

Root contraction in Cycas and Zamia (Cycadales) determined by gelatinous fibers
P. BARRY TOMLINSON, TRACY M. MAGELLAN, AND M. PATRICK GRIFFITH 1275

Ecology
Drivers of a riparian forest specialist (Carex remota, Cyperaceae): It is not only a matter of soil moisture
JAIME URIA-DIEZ, ANTONIO GAZOL, AND RICARDO IBÁÑEZ 1286

Determining past leaf-out times of New England’s deciduous forests from herbarium specimens
PETER H. EVERILL, RICHARD B. PRIMACK, ELIZABETH R. ELLWOOD, AND ELI K. MELAAS 1293

Adaptive plasticity to heterogeneous environments increases capacity for division of labor in the clonal invader Carpobrotus edulis (Aizoaceae)
SEBASTIÁN R. ROLONA, SUSANA RODRIGUEZ-ECHEVERRIA, AARON LOPEZ-OTERO, RUBEN RETUEVO, AND HELENA FREITAS 1301

Individual variation in size and fecundity is correlated with differences in global DNA cytosine methylation in the perennial herb Helleborus foetidus (Ranunculaceae)
CONCHITA ALONSO, RICARDO PEREZ, PILAR BAZAGA, MONICA MEDRANO, AND CARLOS M. HERRERA 1309

Attracting mutualists and antagonists: Plant trait variation explains the distribution of specialist floral herbivores and pollinators on crops and wild gourds
NINA THEIS, NICHOLAS A. BARBER, SANDRA D. GILLESPIE, RUTH V. HAZZARD, AND LYNN S. ADLER 1314

Changing reproductive effort within a semelparous reproductive episode
P. WILLIAM HUGHES AND ANDREW M. SIMONS 1323

Paleobotany
Evolutionary trends and ecological differentiation in early Cenozoic Fagaceae of western North America
JOHANNES BOUCHAL, REINHARD ZETTER, FRIDGEIR GRÍMSSON, AND THOMAS DENK 1332
Miocene leaves of Elaeagnus (Elaeagnaceae) from the Qinghai-Tibet Plateau, its modern center of diversity and endemism  
**Tao Su, Peter Wilf, He Xu, and Zhe-Kun Zhou**  
1350

**Population Biology**
Genetic variation in horizontally transmitted fungal endophytes of pine needles reveals population structure in cryptic species  
**Ryoko Oono, François Lutzoni, A. Elizabeth Arnold, Laurel Kaye, Jana M. U’Ren, Georgiana May, and Ignazio Carbone**  
1362

**Reproductive Biology**
Effects of apomixis and polyploidy on diversification and geographic distribution in Amelanchier (Rosaceae)  
**Michael B. Burgess, Kevin R. Cushman, Eric T. Doucette, Nadia Talent, Christopher T. Frye, and Christopher S. Campbell**  
1375

**Brief Communication**
Inheritance and reproductive consequences of floral anthocyanin deficiency in Silene dioica (Caryophyllaceae)  
**Joelle Rahme, Lionel Suter, Alex Widmer, and Sophie Karrenberg**  
1388

**Erratum**

The authors regret that the name “Psychotrieae” appears on a wrong node on Fig. 1. Because the tribes Psychotrieae and Palicoureeae are sister groups, the name “Psychotrieae” has been moved to the node subtending the well-supported clade formed by the Pacific Psychotria clade, the Indian–Sri Lankan Psychotria clade, the WIOR Psychotria clade, the Australasian Psychotria clade, the Afro-neotropical Psychotria clade, the Afro-WIOR Psychotria clade, and Afro-Asian–WIOR-neotropical Psychotria clade. The online version of this article has been corrected.

**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, hexadeoxytrimethylammonium bromide; cv., cultivar; ddH2O, 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; FT, total deviation from Hardy–Weinberg expectations; FST, genetic diversity among populations; IN, inbreeding within populations; GST, the proportion of genetic diversity among populations; H, Hardy–Weinberg expected heterozygosity; Ho, observed heterozygosity; MP, most parsimonious tree; n, individual chromosome number; Nm, mean number of migrants per generation; P, percentage of polymorphic loci; R, 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; Pt, level of significance; PCA, principal components analysis; r, coefficient of correlation; SE, standard error; SD, standard deviation