



Analyzing genome evolution across mosses

Annals of Botany 125:
543–555, 2020
doi: 10.1093/aob/mcz194

Compared to other plants, mosses (bryophytes) have very small genomes with little variation across species, and high rates of endopolyploid nuclei (that have replicated but not divided generating nuclei with a higher ploidy level in the same individual). **Bainard *et al.*** analyze genome size and endopolyploidy over a broad taxonomic sampling of moss species using phylogenetic comparative methods. Their analyses indicate that genome size evolution in mosses does not appear to be unidirectional. Significant phylogenetic signal was detected for genome size indicating that closely related mosses have more similar genome sizes. Small genome size and high rates of endopolyploidy seem to be under strong selective pressure in mosses.

Authors: Jillian D. Bainard, Steven G. Newmaster, and Jessica M. Budke

For a Commentary on this article see this issue, pp. iv–v.



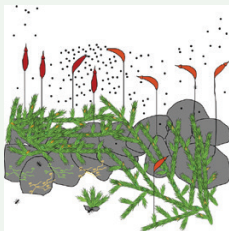
High nitrogen resorption efficiency of forest mosses

Annals of Botany 125:
557–563, 2020
doi: 10.1093/aob/mcz199

To what extent perennial plants recycle nutrients during senescence affects their nutrient use and ecosystems' nutrient cycling. Little is known about the nutrient dynamics of mosses (bryophytes) and their nutrient loss during environmental transitions. **Liu *et al.*** develop a conceptual framework depicting nutrient dynamics of mosses. Using a stable isotope tracer, they assess the dynamics of the nitrogen allocation of two mosses (*Actinotuidium hookeri* and *Hylocomium splendens*). They demonstrate that both mosses recycle the majority of their tissue nitrogen, and that despite a considerable amount of nitrogen being released from live segments, mosses play an important role as nitrogen sinks in ecosystems, though this is dependent upon environmental changes.

Authors: Xin Liu, Zhe Wang, Xiaoming Li, Kathrin Rousk, and Weikai Bao

For a Commentary on this article see this issue, pp. vi–vii

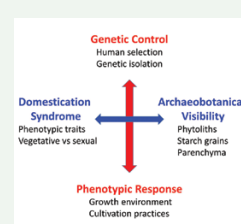


Gene transfer across species and major life cycles in bryophytes

Annals of Botany 125:
565–579, 2020
doi: 10.1093/aob/mcz209

Hybridization and back-crossing is an important evolutionary force because of the transfer of genetic material between species (introgression). **Sawangproh *et al.*** prove that admixed genomes are transferred between generations (i.e., gametophytes, sporophytes, and sporelings) in mixed populations of two related bryophytes. Earlier studies of hybridising bryophytes have not been able to show that recombinant genes are transferred beyond the first generation. The presence of true hybrid zones has strong evolutionary implications because genetic material transferred across species boundaries will be directly exposed to selection in the long-lived haploid generation of the bryophyte life cycle, and may contribute to local adaptation, long-time survival and speciation.

Authors: W. Sawangproh, L. Hedenäs, A. S. Lang, B. Hansson, and N. Cronberg

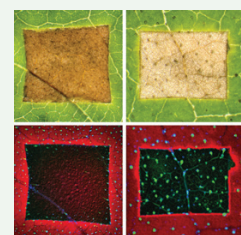


Domestication syndrome in vegetative crops (Research in Context)

Annals of Botany 125:
581–597, 2020
doi: 10.1093/aob/mcz212

Denham *et al.* propose a domestication syndrome of convergent evolutionary traits for vegetatively-propagated field crops that are globally significant for agricultural production today. Domestication traits assessed include mode of reproduction, yield, ease of harvesting, defensive adaptations, timing of production and plant architecture. Although some traits appear to have been 'fixed' during early domestication, others seemingly represent plastic responses to growth environment and practices of cultivation. The proposed domestication syndrome is intended to act as a spur for systematic multidisciplinary (agronomy, archaeology, ecology, genetic and so on) research on the early domestication and geodominestication histories of vegetative field crops.

Authors: Tim Denham, Huw Barton, Cristina Castillo, Alison Crowther, Emilie Dotte-Sarout, Anna Florin, Jenifer Pritchard, Aleese Barron, Yekun Zhang, and Dorian Q. Fuller



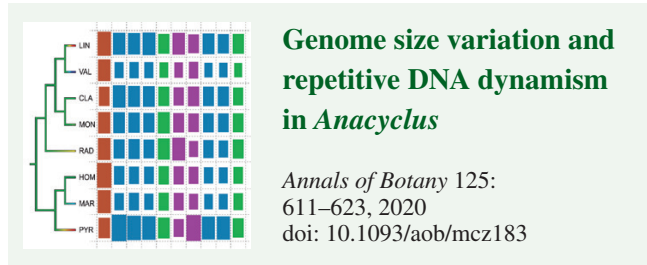
Radiation dose limits for XFM analysis in plants (Technical article)

Annals of Botany 125:
599–610, 2020
doi: 10.1093/aob/mcz195

Accumulated radiation exposure during X-ray fluorescence microscopy (XFM) analysis can lead to significant artefacts. **Jones *et al.*** obtained radiation dose-limits in fresh sunflower (*Helianthus annuus*, Asteraceae) samples that are comparatively low, while frozen-hydrated samples exhibit no apparent damage. Furthermore, living plants subjected to XFM measurement *in vivo*

and grown for a further 9 days, display elemental redistribution at doses as low as 0.9kGy, continuing to develop bleaching and necrosis. The suggested radiation dose limits for studies using XFM to examine plants are important for undertaking multidimensional measurements such as tomography and repeated imaging using XFM.

Authors: Michael W. M. Jones, Peter M. Kopittke, Lachlan Casey, Juliane Reinhardt, F. Pax C. Blamey, and Antony van der Ent



Changes in the amount of repetitive DNA are considered the main contributors to genome size variation across plant species in the absence of polyploidy. **Vitales *et al.*** combine Illumina sequencing data, flow cytometry and bioinformatic analyses to understand the evolution of repetitive DNA in *Anacyclus* (Asteraceae), a genus with a reticulate evolutionary history that displays significant genome size diversity, but a stable chromosome number. They find that proportion and types of different repeats remain about the same throughout the phylogeny, and suggest that genome size differences in *Anacyclus* are more likely related to chromosome rearrangements, possibly associated with homoploid hybridisation.

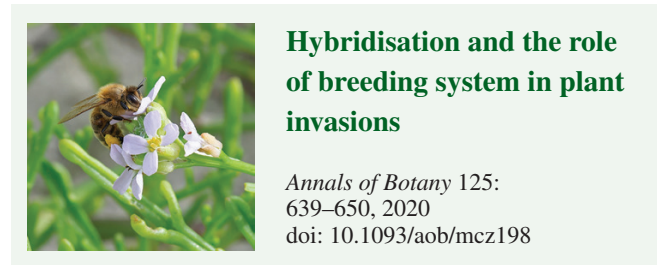
Authors: Daniel Vitales, Inés Álvarez, Sònia Garcia, Oriane Hidalgo, Gonzalo Nieto Feline, Jaume Pellicer, Joan Vallès, and Teresa Garnatje



Contemporary allopolyploid species have originated recurrently, but few are known using multiple natural formations of the same species. **Shiposha *et al.*** investigate the multiple origins, genetic variation, and structure of the allotetraploid model grass *Brachypodium hybridum* and its progenitor diploid species *B. distachyon* (D subgenome) and *B. stacei* (S subgenome) in the Iberian Peninsula evolutionary hotspot. Plastid data detected three different bidirectional allopolyploidization events: two involved distinct *B. distachyon*-like ancestors and one involved a *B. stacei*-like ancestor. Simple Sequence Repeat (SSR) markers showed a close relatedness of current *B. hybridum* D allelic profiles with those of *B. distachyon*, but a lack of similarity with those of *B. stacei*, suggest another *B. stacei* source for the *B. hybridum* S alleles. The genetic and evolutionary

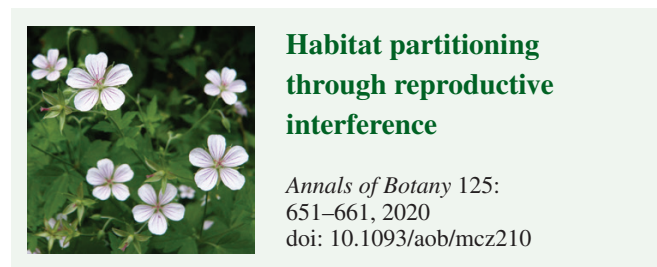
evidence support the plausible *in situ* origin of the SE and northern Iberian Peninsula *B. hybridum* allopolyploids from their respective local *B. distachyon* and unknown *B. stacei* ancestors.

Authors: Valeriia Shiposha, Isabel Marques, Diana López-Alvarez, Antonio J Manzaneda, Pilar Hernandez, Marina Olonova, and Pilar Catalán



A recent prediction is that hybridisation can result in non-adaptive advantages for populations of colonising species that would otherwise be constrained by their breeding system. **Li *et al.*** examined cross-fertilisation success and inheritance of breeding systems in *Cakile maritima* (self-incompatible) and *C. edentula* (self-compatible), two invasive Brassicaceae species that often co-occur. Fertilisation with the self-incompatible species as the pollen recipient was poorer than when it was the pollen donor. Early-generation hybrids were predominantly self-incompatible. Model simulations confirmed that transient hybridisation with a congener could ease early population constraints on an invader, challenging the assumption that hybridisation always assists invasions by aiding adaptation.

Authors: Chengjun Li, Mohsen Mesgaran, Peter Ades, and Roger D. Cousens



Reproductive interference can account for exclusive distributions of closely related species, but how it affects the distributions of wild species at small spatial scale is largely unknown. **Nishida *et al.*** demonstrate reproductive interference between *Geranium thunbergii* and *G. wilfordii* (Geraniaceae), which are apparently sympatric but actually show small-scale partitioning. Using field surveys, hand pollination, genotyping, and fertility measurement results, they reveal that, although neither species reduced the other's seed set, the two species hybridized bidirectionally, producing less fertile offspring. Their results imply that re-evaluation of hybridization may make it possible to recognize reproductive interference between two native species that rapidly leads to exclusion of one or the other species.

Authors: Sachiko Nishida, Koh-Ichi Takakura, Akiyo Naiki, and Takayoshi Nishida



Genetic species assignment and admixture levels in European white oaks

Annals of Botany 125:
663–676, 2020
doi: 10.1093/aob/mcaa001

Hybridization and admixture impact on evolutionary processes like speciation and adaptation. Assessing species admixture requires accurate distinction between parental taxa, ideally using species-discriminatory genetic markers. Blurred species separation and ongoing hybridization have hampered assigning European white oaks to species (*Quercus* spp., Fagaceae) based on leaf morphology or microsatellite markers. **Reutimann et al.** developed a novel set of single-nucleotide polymorphisms (SNPs) to distinguish between the three most common white oak species in Switzerland (*Q. robur*, *Q. petraea*, and *Q. pubescens*) and to assess their admixture levels. The authors found that these white oaks mostly kept their species integrity despite high levels of species admixture.

Authors: Oliver Reutimann, Felix Gugerli, and Christian Rellstab



Population subdivision and hybridization between three *Gentiana* species

Annals of Botany 125:
677–690, 2020
doi: 10.1093/aob/mcaa003

Revealing factors fostering plant divergence and the role of hybridization in the Qinghai-Tibetan Plateau (QTP) and testing

Mountain Geo-biodiversity Hypothesis (MGH), **Fu et al.** assess the evolutionary history of two *Gentiana* (Gentianaceae) species. The population genetic analyses based on plastid DNA sequences and nuclear microsatellite marker datasets, together with species distribution modelling, reveal that geographically distinct clades in the two species were shaped through recolonization from the refugia they shared. Moreover, there is evidence of hybridization between the two gentians that probably occurred in the refugium located on the plateau platform. This study offers insights into plant evolution in the QTP and evidence for in depth testing of the MGH.

Authors: Peng-Cheng Fu, Shan-Shan Sun, Gulzar Khan, Xiao-Xia Dong, Jin-Zhou Tan, Adrien Favre, Fa-Qi Zhang, and Shi-Long Chen



Response of bracken fern to light

Annals of Botany 125:
691–700, 2020
doi: 10.1093/aob/mcaa006

Invasive plants are often more resource-use efficient than natives. **Baer et al.** examine the eco-physiological attributes of sun and shade populations of *Pteridium aquilinum*-- a weedy, cosmopolitan fern -- under a variety of light conditions to determine whether the presence of vessels and other trait factors influence its success. Their results show that shifts in leaf area and xylem content allow *P. aquilinum* to occupy sunny habitats but intrinsic xylem qualities such as cavitation resistance are the same in both sun and shade populations. *P. aquilinum* seems constrained by its fundamental body plan and thus unable to make key xylem modifications.

Authors: Alex Baer, James K. Wheeler, and Jarmila Pittermann