**Deep time to modern species, the evolution of genomic diversity in ferns**

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Evolution is fundamental to all living organisms. During the past 150 years, scientific breakthroughs have revolutionized our understanding of evolutionary processes, shedding light on the source of hereditary material and the forces that influence its organization on all levels—from single chromosomes to whole genomes, within individuals, across generations, and spanning entire species. Unfortunately, the bulk of knowledge regarding these fundamental biological and evolutionary processes is almost exclusively restricted to studies of model organisms (e.g., yeast, *Arabidopsis*, and humans). Gaps in our understanding of evolutionary processes in non-model lineages are truly chasms, representing a world of untapped biological and genomic resources with the potential to massively benefit engineering, medicine, and agriculture. In the Grusz lab, we are dedicated to exploring these many levels of evolution in non-model systems (plants in particular), through the lenses of both recent and deep evolutionary time. Here, I present a series of vignettes to illustrate how we in the Grusz lab leverage non-model species (ferns) to better understand evolutionary processes; furthermore, highlighting our commitment to the documentation and study of biological diversity, regionally and globally.

Relevant literature:

Grusz, A. L., E. M. Sigel, C. Witherup. *In press*. Homoeologous chromosome pairing across the eukaryote phylogeny. *Molecular Phylogenetics and Evolution* doi: 10.1016/j.ympev.2017.05.025

Wolf, P. G., E. B. Sessa, D. B. Marchant, F.-W. Li, C. J. Rothfels, et al. 2015. An exploration into fern genome space. *Genome Biology and Evolution* 7, 2533–2544.