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Structural and transcriptomic comparisons between soybean reference genomes and soybean's Australian wild relatives

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We will describe an evolutionary analysis of several genome and transcriptome assemblies from species spanning a range of evolutionary distances in the *Glycine* genus. Several groups have collaborated on this research. The Molecular Genetics and Soybean Genomics Laboratory at the University of Missouri and colleagues have generated new reference-quality genome assemblies for *Glycine max* cultivars Lee and Williams82, and for a *Glycine soja* accession. The NSF funded SoyMapII project has generated total RNA transcriptome assemblies from six wild soybean relatives found in Australia (*G. canescens*, *G. cyrtoloba*, *G. dolichocarpa*, *G. stenophita*, *G. syndentika*, *G. tomentella D3*). One of these, *G. syndetika*, was selected for a draft genome assembly by the Doyle lab in Cornell, and SoyMapII collaborators. These Australian species had a common ancestor with *G. soja* and *G. max* around 5 million years ago, while *G. max* and *G. soja* are estimated to have diverged much more recently. We conducted gene sequence and genome structural comparisons for these cultivated soybean accessions and wild soybean relatives. Across a range of evolutionary distances, these *Glycine* genome assemblies show evidence for a short period of rapid genome rearrangement after polyploidy, followed by a period of relative quiescence. The genome assemblies from the two *G. max* cultivars (Williams82 and Lee) and from *G. soja* are, in general, highly similar, but with some local inversions and regions of gene expansion and loss.