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Since the discovery of polyploidy in plants just more than a century ago, research on polyploidy is as vigorous as ever. At the Botany 2015 meeting in Edmonton, Alberta, six researchers participated in the symposium “The Evolutionary Importance of Polyploidy” to address recent debates on polyploid speciation. These authors are joined by others in this special issue of the *American Journal of Botany* to highlight recent advances in polyploid research. The 19 articles collected here represent a diverse range of research from established and nascent scientists. Here we provide a guide to the articles in this issue and highlight their major results. Perhaps no topic of study has received a greater boost from the genomics era than polyploidy. Speciation by genome duplication was recognized early in the study of evolutionary genetics and “represented the first major triumph in the genetics of speciation” (Coyne and Orr, 2004, p.322). Plants with sets of doubled chromosomes were encountered in early cytological studies (Lutz, 1907), and Winge (1917) provided one of the most influential hypotheses for the origins of these numbers. He proposed the now familiar concept that these polyploid plants were fertile because genome doubling restored chromosome pairing in otherwise sterile hybrids. The restoration of fertility to sterile hybrids by doubling their genomes was a potent and elegant demonstration of how postzygotic reproductive isolation could be solved (Clausen and Goodspeed, 1925). Further support for Winge’s hypothesis came from Müntzing (1930) who recreated a naturally occurring polyploid species. These studies demonstrated one of the first mechanisms of how new species may arise from genomic changes of existing species. The pioneering polyploidy research of these botanists played a leading role in shaping research on speciation genetics. Their experiments even inspired a young Dobzhansky (1933) to test whether polyploidy restored fertility to sterile fruit flies (it did not). By the time of the modern synthesis, polyploidy was already a relatively well-studied topic and recognized as the biggest difference between plant and animal speciation (Dobzhansky, 1937)—and was the most shocking and important correction to Darwin’s theory of the origin of species (Haldane, 1959). By the latter half of the 20th century, however, polyploidy had been relegated as largely unimportant by many researchers. Many plant species were certainly recognized to have polyploid origins (Stebbins, 1950; Grant, 1981), but the prevalence and persistence of diploids raised questions about the evolutionary contribution of polyploidy (Stebbins, 1971). Although ancient polyploidy was hypothesized and implicitly recognized in many “basic” chromosome number estimates (Stebbins, 1950, 1971; Klekowski and Baker, 1966; Ohno, 1970; Grant, 1981), many biologists came to regard polyploidy as “evolutionary noise” (Wagner, 1970). During his talk at the Botany 2015 symposium on polyploidy, Doug Soltis recounted that as a young researcher he was told to avoid polyploidy because it was a black hole of research! Today such advice would probably not be given. Research beginning with the molecular era revealed that even plants with high chromosome numbers have diploid patterns of gene expression (Gastony and Gottlieb, 1982; Gastony and Darrow, 1983; Barker and Wolf, 2010; Haubler, 2014). One hypothesis proposed to explain these patterns of chromosome number and gene expression was diploidization following ancient polyploidy (

Stebbins, 1985 ; Haufli er andSoltis, 1986 ; Haufli er, 1987 ; Gastony, 1991).

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