کارگاه‌های آموزشی مرکز اطلاعات علمی

آموزش نرم‌افزار Word برای پژوهشگران

روش تحقیق کمی

آموزش مهارت‌های کاربردی در تدوین و چاپ مقالات ISI

CHROMOSOME DATA

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داده های کروموزوم

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با مروری بر تاریخچه شمارش کروموزوم ها در گیاهان، اهمیت و ارزش این مطالعات در سیستماتیک و فیلوژنتیک مورد تاکید قرار می گیرد. یکی از مهمترین کار برد های سنتی شمارش های کروموزومی تشخیص پلی پلوئیدی در گیاهان به خصوص تفسیر پلی پلوئید های باستانی است. بررسی این داد ه ها به عنوان اطلاعات پایه ای زمینه را برای بسیاری از آنالیز های ژنومیک مقایسه ای در دهه های اخیر فراهم نموده‌اند.

Chromosome cytology has a rich history in plant systematics and evolutionary biology. The central importance of chromosome numbers was long recognized with a long history of nearly a century. Classic compilations of chromosome numbers include those of Löve and Löve (1948); Darlington and Wylie (1955); Fedorov (1969). Excellent reviews are provided by Goldblatt and Lowry (2011); Cusimano et al. (2012) and most recently by Rice et al. (in press.).

One of the more important traditional uses of chromosome numbers has been the investigation of polyploidy, including inferences of ancient polyploidy, with a rich tradition that includes the work of Stebbins (1950) and Grant (1981), reviewed in Soltis et al. (2014). These foundational studies set the stage for many of the comparative genomic analyses conducted in the past decade.

Genomic insights are now common, but for decades basic cytological research was the major source of information that provided a view of the genome. The chromosome number of a plant species remains one of the most foundational pieces of information a researcher can garner for an organism. Nothing is more fundamentally important than a chromosome number (or numbers—it is crucial to acknowledge the variability of chromosome numbers in a species) for a plant species. For decades a standard part of botanical training was instruction in making chromosome counts, both mitotic and meiotic as well as instruction regarding the detection and interpretation of chromosome pairing abnormalities at meiosis, particularly in hybrids and polyploids. Traditional chromosome squashes permits the detection of chromosome changes-- inversions and translocations, aneuploidy.

The DNA revolution has brought many important and beneficial changes to systematics and evolutionary biology, but one downside has been the loss of a fundamental skill—chromosome cytology. Systematists and evolutionary biologists strayed a bit from this foundational mantra during the first decades of the molecular systematic era, focusing instead primarily on DNA-based phylogenies (Soltis et al. 2004). As a result, students are often not instructed in chromosome methodology today and the fundamental importance of a chromosome number is not always appreciated. Talks at major scientific meetings as well as published papers now abound that present beautiful well-supported phylogenies that clarify relationships within genera. This is of course important work, but the underlying chromosome numbers of these species often remain unknown—are some of these species polyploids? Does a given species have more than one chromosome number? This remains essential information, which is even more valuable when placed in a phylogenetic context.

Importantly, here has been a resurgence in chromosome research due to the application of new methods such as the modern cytogenetic methods fluorescence and genomic *in situ* hybridization (FISH and GISH). These approaches have been shown to be powerful tools, particularly in the study of hybridization and polyploidy (reviewed in Chester et al. 2010). Another important modern tool in the study of chromosomes has been flow cytometry. Flow cytometry has greatly accelerated the process of surveying natural populations and species so as to better understand the great diversity of chromosome

numbers (e.g. Arumuganathan and Earle 1991; Suda and Trávnícek 2006). This approach has shown the extent of variability of chromosome numbers within species. But flow still requires initial groundwork using traditional cytogenetic methods of chromosome squashing and counting.

One of the more exciting recent developments in the study of chromosome numbers is the work of Rice et al. (in press) to build a global Chromosome Counts DataBase (CCDB). This powerful resource provides a searchable format for most known plant chromosome counts (8751 genera from 539 families). Most of the sources of chromosomes counts encompassed by the CCDB had not previously been available in a digitized searchable format.

The vast amount of chromosome number data that is now assembled and available via the CCDB permitted Rice et al. to examine the distribution of chromosome numbers in the major clades of plants. The results are exciting, but also indicate how much more work is needed in terms of gathering chromosome counts. For example, Rice et al. (in press) found for angiosperms that counts are available for about 20% of the accepted plant species names. Significantly, they also found that 23% of the species in their data base exhibited infraspecific chromosome number variation.

Several observations stem from the important work of Rice et al. (in press). First, the analyses of Rice et al. (in press) reveal just how important additional chromosome counting is in plant biology. A staggering number of species still have no known chromosome counts; furthermore, we now know that chromosome number variation is high and that multiple counts per species are required. Much of the chromosome number variation detected is polyploidy within named species. The findings of Rice et al. (in press) further support the suggestion that we have grossly underestimated the amount of polyploidy (particularly autopolyploidy) in nature (see Soltis et al. 2007).

These observations underscore the importance of the continued need for more chromosome research in plants. The value of the compilation of chromosome numbers for plants of Iran is therefore of crucial value to the field of systematics. I applaud these efforts in Iran and similar studies are encouraged in all areas of the globe.

In addition, we are also reminded that it is imperative that we contribute to these chromosomal data to new data basing efforts. New counts should be submitted to the CCDB and data bases not currently included in the CCDB are encouraged to do so.

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