**Not all centromeres are equal, or are they?**

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**Abstract**

Despite a century of research, many fundamental aspects of chromosome number evolution remain a mystery. One example is the dynamics of fissions and fusions in clades with holocentric or monocentric chromosomes. Holocentric chromosomes have centromeres that are diffuse and spindle fibers attach along the entire length of the chromosome, while monocentric chromosomes have a single, localized centromere. This difference in the arrangement has led to the hypothesis that species with holocentric chromosomes may tolerate fissions with less impact on fitness as compared to species with monocentric chromosomes. This is based on the idea that fissions may lead to chromosomal fragments that contain important genes but lack centromeres and thus cannot segregate properly monocentric species. Insects exhibit a wide range of chromosome number and several large clades with monocentric or holocentric chromosomes. To test for differences in the rates of fissions we analyzed data from 12,412 species of insects in both a taxonomic and phylogenetic framework. We found insect orders exhibit striking differences in rates of fissions as well as fusion and polyploidy. Lepidoptera (a holocentric clade) exhibits some of the highest rates. However, looking across all insects we found no evidence that holocentric clades have higher rates of fission, fusion, or polyploidy than do monocentric clades.

**Introduction**

Chromosome number stability is expected among lineages as shifts in chromosome number can lead to a decrease in fitness (Rieseberg 2001). This stability in chromosome number is driven by the underdominance of chromosomal rearrangements (Escudero *et al.* 2016). Chromosome number has even been proposed as a possible driver of speciation (White 1969). However, theoretical work has suggested that a stasipatric model of speciation may be unlikely (Lande 1984). Furthermore, empirical evidence suggests that many chromosomal rearrangements may have little or no fitness effect (Sites Jr and Moritz 1987; Coyne *et al.* 1993). More recently structural rearrangements have been proposed as a mechanism of speciation without the requirement for underdominance (Rieseberg 2001; Faria and Navarro 2010; Guerrero and Kirkpatrick 2014). In light of the possible role of chromosomal change in speciation, identifying traits associated with increased rates of chromosomal rearrangements may explain patterns of extant diversity.

Unfortunately, the evolution of chromosome number has been recalcitrant to the formation of rules or generalizations that can explain variation in patterns and rates across large clades. However, within clades, fusions and fissions are two of the dominant forces in reshaping karyotypes (Lucek 2018). We use these terms (fusion and fission) for simplicity to describe chromosome number changes of plus or minus one. However, in reality, fusions decreasing chromosome number capture two different processes at the molecular level. First, Robertsonian translocations followed by the loss of the short arms can decrease chromosome number (Garagna *et al.* 1995). Second, the fusion of telomeres from two chromosomes followed by inactivation of one of the ancestral centromeres can occur as evidenced by the evolutionary history of human chromosome 2 (Miga 2017). In contrast, changes increasing chromosome number can occur through simple fissioning in the centromere region and the gaining of new telomeric sequences (Moretti and Sabato 1984; Garagna *et al.* 1995). Increases in chromosome number can also occur through polyploidy or aneuploidy. In the case of polyploidy, an offspring can be produced from an unreduced gamete increasing by one the number of copies of the genome (Torres *et al.* 2008). Likewise, aneuploidy can lead to the duplication of single chromosomes (Torres *et al.* 2008).

Because chromosomal rearrangements are thought to often be deleterious or underdominant they should be more likely to fix in populations with low effective population size or meiotic drive (Blackmon *et al.* 2019). However, centromeric structure may modulate the fitness effects of fusions and fissions. In species with monocentric chromosomes fusions and fissions can lead to multiple or no centromeres along the length of a chromosome which leads to failed segregation (Mola and Papeschi 2006; Melters *et al.* 2012). In contrast in holocentric species, the centromeres are diffuse and spindle fibers attach along the entire length of the chromosome. In these species, fusions and fissions do not appear to disrupt proper segregation (Malheiros-Garde and Gardé 1950; Faulkner 1972; Cope 1985; Luceño and Guerra 1996). Therefore, holocentricity has the potential to reduce or eliminate selective pressure against chromosomal rearrangements. This should lead to higher rates of chromosome number evolution in clades with holocentric chromosomes relative to clades with monocentric chromosomes (Escudero *et al.* 2012).

If holocentric clades have higher rates of chromosome evolution, we might expect holocentric species to exhibit higher chromosome number. Anecdotal evidence does seem to suggest that some of the highest chromosome numbers observed are in clades with holocentric chromosomes. For instance, in insects, the highest chromosome numbers are observed in the holocentric order, Lepidoptera (Blackman 1980). However, initial analyses have found no significant difference in chromosome number among holocentric and monocentric clades of insects (Blackmon *et al.* 2017). This previous study was limited to an order level analysis and looked only for an absolute difference in chromosome number between monocentric and holocentric clades. A stronger test of the impact of holocentricity would be to investigate the rates of fusions, fissions, and polyploidy in clades with holocentric and monocentric chromosomes.

In this study, we used chromosome number and centromere type for 599 insects to test whether clades with holocentric chromosomes have a higher rate of fusions and fissions than clades with monocentric chromosomes (Figure 1). We chose to use insects because they have multiple clades with monocentric and holocentric chromosomes, are incredibly speciose, and exhibit striking diversity in chromosome number (Cook 2000; Mora *et al.* 2011; Ross *et al.* 2015; Blackmon *et al.* 2017; Vershinina and Lukhtanov 2017). We hypothesized that clades with holocentric chromosomes should exhibit higher rates of fusions and fissions since these mutations should be less costly in these clades.

**Methods**

*Data collection:* We downloaded all available chromosome data for insects from a prior study (Blackmon *et al.* 2017). This dataset is composed of 12,412 species comprising 376 families and 3,872 genera. The minimum haploid chromosome number is 2 while the maximum haploid chromosome number is 141. There are 3,465 species with holocentric chromosomes and 8,946 species with monocentric chromosomes. This paper also included classification for each order into either monocentric or holocentric. From this dataset, we extracted the homogametic haploid chromosome number for each of the species. We used genus level phylogenies from a previous study that contained 1,726 tips (Church *et al.* 2019). These trees were built using one of two backbones trees from previous studies (CITE THOSE TWO STUDIES). We downloaded two posterior distributions based on these backbone trees. These trees were used for all downstream comparative analyses. Our trait data set had an overlap of 599 genera with the phylogenetic data (Figure 1). In cases where we had multiple chromosome number records for genus, we retained all values and sampled from them as described below. As a first test of the differences between holocentric and monocentric clades we fit an ANOVA and a phylogenetic ANOVA to determine whether there were any differences in mean chromosome number among holocentric and monocentric clades (CITE R PACKAGE)

*Comparative analyses:* We fit a model of chromosome evolution on each tree from the posterior distribution. This model can accommodate up to eight rates: rate of chromosome number increase (fissions γ), rate of chromosome number decrease (fusions δ), rate of whole genome duplication (polyploidy ρ), each of these is estimated separately for clades with holocentric and monocentric chromosomes leading to six chromosomal rate parameters. The final two parameters describe the transition to and from monocentric and holocentric (qMH and qHM). This model was specified using the R package chromePlus (Blackmon *et al.* 2019) and was fit using a Bayesian approach in the R package diversitree (FitzJohn 2012).

For each of the 100 trees in a posterior distribution we randomly sampled tip states for genera with more than one record in our chromosome data set. By sampling across both datasets and trees from the posterior we are able to account for both phylogenetic and tips state uncertainty. For purposes of model fitting trees were rescaled to unit length; however, all rates reported in the paper have been back transformed to be in units of millions of years. The MCMC was initialized with parameter values drawn from a uniform distribution from 0 to 1. Preliminary analyses were conducted with a uniform prior and while most MCMC chains reached convergence quickly, a small fraction of runs would begin to sample very high rates that are biologically unrealistic. Given sufficient time we might expect these runs to eventually converge on the posterior distribution but this length of time can be large due to the relative flatness of the likelihood surface when rates are unrealistically high. To fix this problem, we added an exponential prior with a shape parameter of 0.5. This is a relatively uninformative prior but does favor lower rates avoiding the problem described above. With application of this prior we found that the vast majority of MCMC chains reach convergence in less than 10 generations. We repeated the MCMC with all 100 trees at 50 generations each. We removed the first twenty-five samples as our burnin for each run and combined the postburnin portion of the MCMC from each of the 100 trees. Because our central question is whether holocentric clades have higher rates than monocentric clades, we report our results in terms of a mean rate difference statistic, where the subscript x indicates the rate parameter. For example, for the rate fissions (γ), for each post-burnin sample we calculated as

In addition to estimating the magnitude of this statistic, we also reduced it to a simple test of the motivating hypothesis by comparing the 95% credible interval of (i.e. the 95% highest posterior density) with zero. If the entire 95% credible interval of is positive, we interpret it as support for a higher rate of chromosome evolution in holocentric clades. If the entire 95% credible interval of is negative, we interpret it as support for a higher rate of chromosome evolution in monocentric clades. Otherwise, we conclude there is not support for a significant rate difference in monocentric and holocentric clades. This approach also allows us to compare across all trees in the posterior distribution even if some trees exhibit on average higher or lower rates.

We repeated similar MCMC analyses as above for the analysis of orders, however, we ran the data under two different models. One with polyploidy and one without polyploidy included in the model and because each order is fixed for either holo- or monocentricity we only estimate one set of rate parameters in each clade. We only included orders with more than 20 tips in our phylogeny to insure a sufficient sample size for rate inference. This led to 10 orders level analyses; three of the included orders (Hemiptera, Lepidoptera, and Odonata) have holocentric chromosomes, and seven that have monocentric chromosomes. To compare rates among orders we compared the credible interval for each parameter among orders.

**Results**

*Absolute difference in holocentric and monocentric clades:* We fit a standard ANOVA and a phylogenetic ANOVA to determine whether there was an absolute difference in chromosome number among holocentric and monocentric clades.

*Monocentric and Holocentric Rates:* Rates of chromosome evolution were estimated from the two insect trees with 599 genera. The eight parameters discussed in the methods were included in our model. These parameters included fusion, fission, polyploidy, and the transitions between monocentric and holocentric chromosomes. Overall, the data had a low variability in the posterior distribution generated by the MCMC (Figure 2). The rates were subtracted from one another to create the differences in rate parameters and graphed in Figure 2. The differences in rates of fusions (descending), fissions(ascending), and polyploidy did not show a difference between monocentric and holocentric chromosomes because all differences in the rates overlapped with zero (Figure 2). This indicates that there are no significant differences among rates of chromosome number evolution based on the type of chromosome.

*Orders Rates:* Rates of chromosome number were tested for each of the 10 orders. Three orders have holocentric chromosomes (Hemiptera, Lepidoptera, Odonata), while the other 7 have monocentric chromosomes (Blattodea, Coleoptera, Diptera, Hymenoptera, Isoptera, Neuroptera, and Phasmatodea). Our analysis of the data described with ascending (fissions) and descending (fusions) rates of chromosome number evolution alone showed a large variability between orders, with Phasmatodea and Lepidoptera having the largest variance (Figure 3a). Despite this variability, there is no pattern in chromosome number evolution associated with monocentric or holocentric orders. This indicates differences among orders, but no relationship between holocentricity and rates of chromosome number evolution.

With the addition of polyploidy into the model, the variance among rates of chromosome number evolution is reduced among the orders (Figure 3b). Despite this, the descending rate was higher in Blattodea, Isoptera, and Phasmatodea. This increase in rates is representative of some, but not all monocentric orders. The order Lepidoptera shows a decrease in ascending and descending rates of chromosome number evolution with the addition of polyploidy into the model. This is most likely driven by a large variation in chromosome number associated with the order.

**Discussion**

The hypothesis that holocentric chromosomes are more tolerant of fusions and fissions and therefore have a higher rate of chromosome number evolution was not supported by our data. Overall, the rates of chromosome number evolution were similar among monocentric and holocentric species. When our data was separated based on orders, the rates showed differences among orders, however, this is not due to differences in chromosome type. This is most likely due to differences amongst orders based on different selective pressures experienced by the clades rather than the type of chromosome. Holocentric chromosomes may be more tolerant of fusions and fissions. However, chromosome number is constrained by external factors that have not caused a difference in the rate of chromosome evolution due to holocentricity alone.

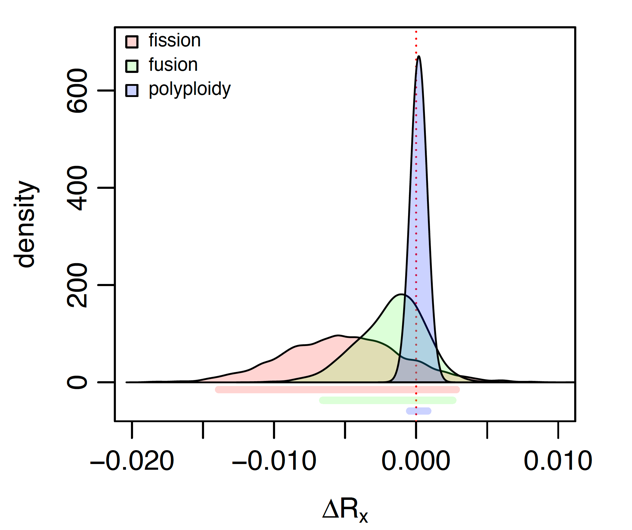
Work in mice has shown that meiotic drive is based on the strength of centromeres, where strength is characterized by the ability to express kinetochore proteins and interact with spindle fibers (Chmátal *et al.* 2014). In this system, a fusion with the same centromere strength was shown to be either favored or disfavored depending on the genetic background that it was segregating within. This indicates that although fissions and fusions occur, they may be selected for and can increase their rates of chromosome number evolution. In holocentric chromosomes, since they have a diffuse centromere, meiotic drive is thought to be more difficult to bias segregation since multiple sequences must be favored to have the chromosome be preferentially segregated (Gassmann *et al.* 2012). However, meiotic drive has been shown in *Caenorhabditis,* which has holocentric chromosomes, to some extent (Zedek and Bureš 2012). This indicates that meiotic drive may constrain fusions and fissions and potentially increase rates in monocentric chromosomes comparable to rates in holocentric chromosomes.

In conclusion, monocentric and holocentric chromosome species do not show differences in rates of fissions, fusions, or polyploidy in chromosome number evolution. When our data was separated by orders, we failed to find a pattern between rates of chromosome number evolution and monocentric and holocentric orders. We did find a difference between orders in that each order had different rates of chromosome number evolution. This is most likely caused by different selective pressures between the orders as well as differences in meiotic drive that can modulate rates of chromosome number evolution.

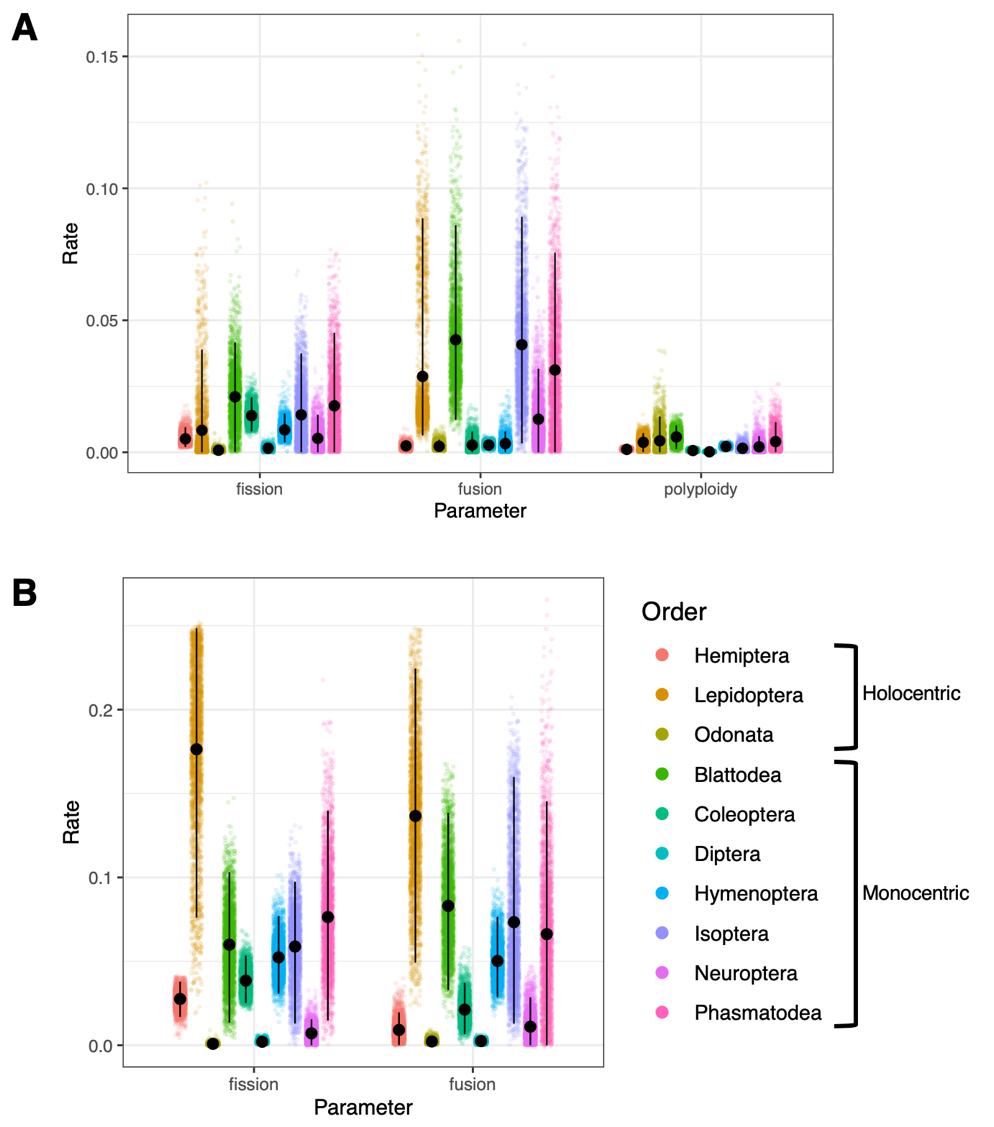
**Figures:**



**Figure 1: Phylogeny of type of centromeres and chromosome number.** The black branches represent orders with monocentric chromosomes and the gray branches represent orders with holocentric chromosomes. The colored circles at the tips represent the haploid chromosome number. The color scale is log transformed to allow better visualization of variation in species with low chromosome number.



**Figure 2: Rates of chromosome evolution.** Each curve represents the posterior distribution of the statistic. Where is either fission, fusion, or polyploidy which is indicated by the color of the fill. Positive values of this statistic indicate that holocentric clades evolve more quickly while negative values indicate that monocentric clades evolve more quickly. Below the curves the three lines indicate the credible interval of each statistic. Since all overlap zero we infer no significant difference in rates of chromosome evolution in clades with holocentric and monocentric chromosomes.



**Figure 3:** **Rate of chromosome evolution based on order**. Ascending rates represent the rate of fissions, descending rates represent the rate of fusions, and pol rates represent the rate of polyploidy. (A) Modeling for the rates of chromosome evolution without polyploidy. The removal of polyploidy has kept most of the other species at about the same rates of chromosome evolution, expect for Lepidoptera. Lepidoptera has an increase in both fusion and fission rates. (B) Modeling for rates of chromosome evolution with polyploidy. The addition of polyploidy in the model has decreased the variation of all rates of chromosome evolution. There is no trend between holocentric and monocentric chromosome orders.

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