**Title:** Holocentric chromosomes show increased rates of fusion and fission as compared to monocentric chromosomes

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**Abstract**

**Introduction**

Chromosome number is a fundamental aspect of genome organization and is available for 10,000s of species (Blackmon *et al.* 2017). Eukaryotes show wide diversity both in the type and number of chromosomes within their genome. 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. What is clear is that within clades fusions and fissions are two of the dominant forces in reshaping karyotypes (Lucek 2018). We use these terms for simplicity to describe single chromosome number changes. However, in reality fusions decreasing chromosome number capture two different processes at the molecular level. First, Robertsonian translocations followed by the loss of nonessential DNA, and second, fusion of telomeres from two chromosomes followed by inactivation of one of the centromeres (Miga 2017). In contrast, fission increasing chromosome number can happen in just the way we might imagine through fissions in the centromere region and gaining of new telomeric sequences (Moretti and Sabato 1984; Garagna *et al.* 1995).

It has often been assumed that fissions and fusions should be deleterious or underdominant and as such they should only fix in a population if there is low effective population size. However, centromeric structure may modulate the fitness effect of fusions and fissions. Because holocentric centromeres are diffuse and spindle fibers attach along the entire length of the chromosome it has been hypothesized that species with this type of centromere should have little difficulty segregating chromosomes that have experienced fusions or fissions (Malheiros-Garde and Gardé 1950; Greilhuber 1995; Luceño and Guerra 1996). In contrast, species with monocentric chromosomes have a single, localized centromere and chromosomal fragments generated from fusions or fissions may lack centromeres. These chromosomal fragments will not be able to segregate normally and will thus be deleterious. Therefore, holocentricity has potential to reduce or eliminate selective pressure against and underdominance of chromosome rearrangements. This could allow for a higher rate of fixation (Escudero *et al.* 2012).

**Methods**

We downloaded all available chromosome data for insects from a prior study (Blackmon *et al.* 2017). This generated a dataset of 12,412 records. For this dataset we collected the haploid chromosome number for each of the species. We additionally have obtained trees from a previous study that can be used for comparative analyses (Church *et al.* 2019). Using the trait data and the posterior distribution trees, we are going to implement a chromosome number evolution model using chromePlus (Blackmon *et al.* 2019). This model will allow us to determine if the rate of chromosome number evolution is significantly different in clades with holocentric and monocentric chromosomes. Our hypothesis is that clades with holocentric chromosomes will tolerate fusions because the centromere is diffuse across the entire length of the chromosome, therefore each chromosome fragment will be more likely to properly segregate during meiosis.

**Results**

For this project, I have all chromosome number and centromere type data. 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 chromosome number is 141. There are 3,465 species with holocentric chromosomes and 8,946 species with monocentric chromosomes. We have downloaded two sets of phylogenetic trees based on different backbone trees that will be used for our comparative analysis. Each phylogeny includes 1,726 genera and contains a sample of 100 trees from a posterior distribution. Both of these distributions of trees are to the genera-level and matching this data to our trait dataset we have an overlap of 602 tips. We are fitting our model on each tree from the posterior distribution and we randomly sample trait data when more than one species is available for a genus. This approach allows us to account for uncertainty in phylogeny and tip states. We have begun initial model fitting for this project and are currently exploring the best choice of priors for the MCMC that we are running.

**Discussion**

Due to the size of the transition rate matrix sampling from the posterior and even simple calculation of the likelihood for a given parameter set is computationally expensive. We are likely going to move our analysis onto a Linux cluster that will allow us to analyze 20 or more trees from the posterior simultaneously to deal with this difficulty.

**References**