**Investigating Faster-Z in *Gallus Gallus* and Taeniopygia guttata**

The sex chromosomes are significantly different from autosomes and these difference likely have an effect on the rate of divergence of sex linked genes. Sex chromosomes have reduced hemizygosity and recombination. Additionally, they have a unique form of inheritance different from autosome which makes it a good option to study different evolutionary phenomenon. The sex chromosomes usually have reduced effective population size seeing that in a species with a 1:1 sex ratio, the population of X and Z chromosome is ¾ the size of autosomes and the population of W and Y is ¼ the size of autosome population. The reduced population suggests that the effect of selection and drift are more effective in the sex chromosome. Reduced recombination in X and Z can contribute to the degeneration of these region as they become more likely to fix deleterious mutations. The reduced population makes the effect of genetic drift stronger which allows for mildly deleterious to be fixed. Furthermore, the reduced hemizygosity in heterogametic sex opens recessive mutation to the action of selection. Faster rate of divergence of coding sequences have been seen in X and Z chromosomes in many species including Chicken, Zebrafinch, D. melogaster, Mus castaneus and Homo sapiens.

A 2007 paper titled “Fast-X on the Z: rapid evolution of sex-linked genes in birds.” by Mank et. Al discover faster-Z in Gallus Gallus (GGA) and Taeniopygia guttata (TGU). The paper evaluates the divergence of coding sequences in the Z chromosome and compares it to coding sequeces in autosomes. They compared it to CDSs in chromosome 1-10 as they have comparable sizes. The calculated the rate of synonymous and non-synonymous substitution per substitution site. Synonymous changes are the nucleotide substitutions that do not change the amino acid coded by the codon while non-synonymous substitutions change the amino acid. The ratio of rate of non-synonymous substitution per substitution site (dN) and rate of synonymous substitution per substitution site (dS) is referred to as dN/dS or omega(ω). dN/dS can be used as a metric of faster-Z evolution when averaged over a large genomic distance.

The authors used a software called PAML or (phylogenetic analysis by maximum likelihood) to calculate pairwise dn/ds between same gene CDSs in GGA and TGU where they found CDSs in the Z chromosome to have a significantly higher dn/ds compared to the autosomes. This paper established faster-Z in birds and has been the basis for many different publications regarding evolution of sex chromosome.

The pairwise dn/ds calculation is a rudimentary option in the software that offere much advanced and complex analyses. For my project I will be investigating this same phenomenon using PAML employing the more advanced method of calculation omega using maximum likelihood. The advancement in newer versions of PAML allows us to use different branch models according to different hypothesis. The TGA and GGA genome from NCBI are improved compared to what it was in 2007. Additonally, I will include a TSD control for the analysis. TSD or temperature dependent sex determination species are organism whose sex determination do not depend on sex chromosome. The sex of the offspring is determined by the temperature of the nest in species like some turtles, alligator, crocodiles, lizards etc. These species lack sex chromosome and thus all the genes present in their genome are in autosomal condition. This will offer a good contrast. I will be using two TSD species with similar divergence time as TGU and GGA such as two Crocodilian species like Aligator senensis and Gavialis gangeticus. They lack sex chromosome and could be valuable as controls in the analyses. All of these species have genome available in NCBI.



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