

Theory predicts that sexually antagonistic mutations will be over- or under-represented on the X and Z chromosomes, depending on the average dominance coefficient of the mutations. However, as little is known about the dominance coefficients for new mutations, the effect of sexually antagonistic selection is difficult to predict. To elucidate the role of sexually antagonistic selection in the evolution of Z chromosome gene content in chicken, we analyzed publicly available microarray data from several somatic tissues as well as somatic and germ cells of the ovary.

We found that the Z chromosome is enriched for genes showing preferential expression in ovarian somatic cells, but not for genes with preferential expression in primary oocytes or non-sex-specific somatic tissues. Our results suggest that sexual antagonism leads to higher abundance of female-benefit alleles on the Z chromosome. No bias towards Z-linkage of oocyte-enriched genes can be explained by lower intensity of sexually antagonistic selection in ovarian germ cells compared to ovarian somatic cells. An alternative explanation would be that meiotic Z chromosome inactivation hinders accumulation of oocyte-expressed genes on the Z chromosome. Our results are consistent with findings in mammals and indicate that recessive rather than dominant sexually antagonistic mutations shape the gene content of the X and Z chromosomes.