



Sequence Transpositions Restore Genes on the Highly Degenerated W Chromosomes of Songbirds

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Abstract

The female-specific W chromosomes of most Neognathae birds are highly degenerated and gene-poor. Previous studies have demonstrated that the gene repertoires of the Neognathae bird W chromosomes, despite being in small numbers, are conserved across bird species, likely due to purifying selection maintaining the regulatory and dosage-sensitive genes. Here we report the discovery of DNA-based sequence

duplications from the Z to the W chromosome in birds-of-paradise (Paradisaeidae, Passeriformes), through sequence transposition. The original transposition involved nine genes, but only two of them (*ANXA1* and *ALDH1A1*) survived on the W chromosomes. Both *ANXA1* and *ALDH1A1* are predicted to be dosage-sensitive, and the expression of *ANXA1* is restricted to ovaries in all the investigated birds. These analyses suggest the newly transposed gene onto the W chromosomes can be favored for their role in restoring dosage imbalance or through female-specific selection. After examining seven additional songbird genomes, we further identified five other transposed genes on the W chromosomes of Darwin’s finches and one in the great tit, expanding the observation of the Z-to-W transpositions to a larger range of bird species, but not all transposed genes exhibit dosage-sensitivity or ovary-biased expression We demonstrate a new mechanism by which the highly degenerated W chromosomes of songbirds can acquire genes from the homologous Z chromosomes, but further functional investigations are needed to validate the evolutionary forces underlying the transpositions.

Keywords: avian genomics, sex chromosomes, transpositions, sex-specific selection

1. Introduction

Unlike mammals, birds have a female heterogametic (ZW) sex

