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EVOLUTION OF SOCIALITY: USING WILLIAMS-BEUREN SYNDROME TO IDENTIFY CONSERVED “SOCIAL GENES”

Iris Chin

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The prevalence of sociality and social behaviors in diverse animal genera hints toward the existence of a conserved “genetic node” which plays a role in the biological networks that drive interactions between animals and their social environments. Williams-Beuren Syndrome (WBS) is a human neurodevelopmental disorder linked to the hemizygous deletion of 26-28 genes on chromosome 7 (the ‘WBS region’). Along with an array of physiological and developmental symptoms, individuals with WBS display stereotypically hyper-social profiles. In addition, 7q11.23 duplication disorder, characterized by chromosomal duplication of the WBS region, is associated with Autism-spectrum phenotypes. This ostensible negative correlation between gene dosage of the WBS region and human sociability makes the affected genes prime candidates for investigation while studying the processes that drive animal sociality. Remarkably, a majority of the genes in the mammalian WBS region are conserved in the *Drosophila melanogaster* genome. In this project, I systematically downregulated the expression of *Drosophila* WBS homologs in the nervous system using a transgenic RNAi approach, and tested the effects of gene knockdown on fly sociability by employing a “social-space displacement” assay. My studies revealed that knockdown of at least two WBS-related genes, *frizzled* (*fz*) and *eukaryotic translation initiation factor 4H1* (*eIF4H1*), produced social displacement phenotypes significantly different from that of wild type control animals. However, *fz*-knockdown flies also displayed generally abnormal locomotion, which may explain, at least in part, the observed “social space” phenotype. Regardless, these data suggest that at least one of these genes may have a conserved function in the biological network responsible for social behavior.