Identifying Regulators of Rho Family GTPases Required for Collective Cell Migration in Drosophila Testis Nascent Myotubes

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Abstract

Collective cell migration is a biological process in which groups of cells migrate together to form new tissues during embryonic development and tissue repair. Collective cell migration has been studied *in vivo* in both vertebrate and invertebrate models, such a *D. melanogaster* border cells, the Zebrafish lateral line, and *Xenopus* neural crest and mesoderm, revealing diverse ways by which cells collectively migrate inside the complex environment of a living organism. We used a novel system to study *in vivo* cell migration, the *Drosophila* nascent testis myotubes. The adult testes of *Drosophila* are ensheathed in muscle, and testis muscle development occurs during the pupal stage. One goal is to identify which receptors and ligands are important for cell migration of nascent testis myotubes and to define downstream pathways. We used a myotube-specific RNAi screen to identify potential receptors important for cell migration, and then used RNAi-mediated knockdown to assess which receptors and ligands cause morphological defects. We found that PlexA, a known transmembrane receptor protein in the Plexin family causes an interesting migration defect. Our earlier work and the literature suggest that Rho-family GTPases act downstream. I am using an enhancer-suppressor screen to identify GEFs and GAPs regulators that act downstream of PlexA, or which act in parallel pathway. The approach involves comparing single RNAi of PlexA, single RNAi of a Rho-family GEF or GAP, and simultaneous double RNAi of both. Our logic is as follows: A knockdown of GEFs or GAPs that act downstream of PlexA will not enhance migration defects as the PlexA part of the pathway is already knocked out. An enhanced migration phenotype will suggest that the respective GEFs or GAPs regulators act in parallel to *PlexA* in different pathways that regulate migration. Double knockdown of Plex A and two of the GEFs, Sponge and RhoGEF2, led to enhanced phenotypes. This suggests both Sponge and RhoGEF2 are GEFs that act in parallel to the PlexA pathway.