A fruit fly model of cervical cancer, a platform for unraveling the disease mechanism and discovery of novel therapeutics

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High-risk human Papillomavirus (HPV) is the leading cause of cervical cancer and has been implicated in several other cancer types including, vaginal, vulvar, anal, penile and oropharyngeal cancers. Among all high-risk HPVs, HPV 16 and 18 are the most prominent types, causing more than 70% of all invasive cervical cancers and majority of other HPV-induced cancers. Despite the recent availability of a vaccine, there are still over 310,000 deaths each year worldwide. Current treatments for HPV-mediated cancers show limited efficacy, and would benefit from improved understanding of disease mechanisms. Drosophila has proven a strongly useful platform for modeling human diseases including cancer, owing in part to high conservation of genes and signaling pathways and availability of a broad array of genetic tools including large-scale drug and functional genetic screens. In my talk I plan to introduce the Drosophila model of HPV18-induced cancer that we developed recently and further demonstrate how we have used this model to identify genes and pathways that play a role in HPV-induced defects and that how these genes can serve as potential therapeutic targets for the disease. I will further share with you some of our other current projects, collaborations as well as future plans.