Department of Biochemistry and Molecular Biophysics Seminar

Wednesday, May 6 at 4:00 p.m. in Ackert 120

Coffee and cookies at 3:45 p.m. in Chalmers 168

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Investigating the genetic origins of new body parts in *Drosophila*

The rapidly evolving genitalia of *Drosophila* provide a powerful system for studying the developmental basis of morphological novelty. We investigated how the phallus of *Drosophila eugracilis* evolved over 150 differently sized projections. Developmental tracking of cellular morphology uncovered that these projections are unicellular. Our previous work showed that the main transcription factor for the larval trichome (unicellular hairs) genetic network, Shavenbaby, and 14 of its known downstream targets were co-opted to the *D. eugracilis* phallus to establish this novelty.

Although modulation of the trichome network affects the morphology of unicellular projections, it does not account for the large cellular size seen in some of the *D. eugracilis* projections. We find that large unicellular projections contain large nuclei, indicating that these cells have undergone localized endoreplication to give rise to polyploid trichome nuclei. These large cells also express the polyploidy-inducing gene *fizzy-related* during their development. The activation of the larval trichome genetic network in the phallus of *Drosophila melanogaster*, which naturally lacks these unicellular projections, induces only small unicellular projections. The disruption of *shavenbaby* in *D. eugracilis* reduces unicellular projection height but shows no noticeable effect on overall cellular size. This suggests that a second independent genetic network was recruited to the *D. eugracilis* unicellular projections to induce their large morphs. Our work shows how the co-opted traits may initially evolve as a copy of the co-opted structure and subsequently gain unique attributes through the recruitment of additional genetic networks.