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Adaptation of A-to-I RNA editing and the impact on genome evolution

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Adenosine-to-inosine (A-to-I) editing is hypothesized to facilitate adaptive evolution by expanding proteomic diversity through an epigenetic approach. However, it is challenging to provide evidences to support this hypothesis at the whole editome level. In this study, we systematically characterized 2,114 A-to-I RNA editing sites in female and male brains of *D. melanogaster*, and nearly half of these sites had events evolutionarily conserved across *Drosophila* species. We detected strong signatures of positive selection on the nonsynonymous editing sites in *Drosophila* brains, and the beneficial editing sites were significantly enriched in genes related to chemical and electrical neurotransmission in *Drosophila*. By adopting a method originally designed to detect linkage disequilibrium of DNA mutations, we examined the editomes of ten metazoan species and detected extensive linkage of editing in *Drosophila* and cephalopods. The prevalent linkages of editing in these two clades, many of which are conserved between closely related species and might be associated with the adaptive proteomic recoding, are maintained by natural selection at the cost of genome evolution. Nevertheless, in worms and humans, we only detected modest proportions of linked editing events, the majority of which were not conserved. Furthermore, the linkage of editing in coding regions of worms and humans might be overall deleterious, which drives the evolution of DNA sites to escape promiscuous editing. Altogether, our results suggest that the linkage landscape of A-to-I editing has evolved during metazoan evolution. If time permitting, I will also talk about other work related to adaptive evolution at the post-transcriptional level.