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Mobile elements are often found in eukaryotic organisms and as other areas of the genome are subject to selection and drift. Gonzalez et al (2008) and Lockton et al (2008) present examples in which the evolution of transposable elements is driven by natural selection -adaptation to cold- and by population size changes acting both by changing fixation rate and relaxing purifying selection, respectively.

Both studies aim to study the evolution of transposable elements but their systems are different and their findings and approaches are different.

Spady *et al.* (SE) use a cDNA synthesis approach to isolate the opsin genes present in the retina of Tilapia and infer phylogenetic relationships of orthologues across species for each paralogous copy. Also, SE identify the functional difference of each paralogue or optimal length light of each variant, show differential expression patterns at three life stages and make a comparison of cone visual pigments of Tilapia and lake Malawi cichlids. Conversely, Matsuo approach is based on a comparison of the available genomes of *D. melanogaster* and *D. pseudoopscura* to elucidate differences in copy number in opsin genes at the *Obp57d/e* and a follow exhaustive search of duplications in these loci in the melanogaster species complex. Matsuo work is more extensive, taking advantage of the availability of whole genomes, while SE is localized to genes expressed in the retinal tissue or eye (larvae) and largely ignoring duplicates that may not exclusively are expressed in retinal tissue (Suga *et al.* 2008). However, SE work is deeper in testing for functional divergence among paralogues and thus connecting genetic architecture with ecology.

SE suggest that all Tilapia opsin duplicates are functional and sub-fuctionalization models could explain the functional partition of each paralogue to a narrower light length optimum, while differential expression patterns at various life stages could be interpret as neo-fuctionalization. Conversely, Matsuo supports the notion that OBP have likely be the product of sub-fuctionalization follow by neo-fuctionalization shaped by natural selection. For SE sub-fuctionalization is not a necessary step to neo-fuctionalization or at least not notable in their work, while Matsuo see sub-fuctionalization as a transitory process to neo-fuctionalization in OBP but further *in vivo* testing is warranted. Moreover, Matsuo and SE invoke selection as a driver of sub-fuctionalization of paralogous copies. However, only Matsuo highlights the importance of random processes as a force creating new variants and concerted evolution eliminating unnecessary copies. Whether natural selection or random processes induce the duplication remain controversial and their influences uncertain.

A contrasting pattern of both works is that Matsuo find that non-functional copies of the OBP contribute to the total number of gene copies but they do not increase phenotypic variation and are likely to be eliminated of the genome. Conversely, SE report that all opsin copies found by analyzing genes expressed in retinal tissue are functional and have functionally diverged. Yet their approach may have unable to recover opsin copies expressed in other tissues (Briscoe 2001, Suga *et al.* 2008), unexpressed copies or highly degraded products. Additionally, SE highlights the importance of diverging functionality in gene duplications to produce novel combinations and their possible “palette” in which cichlid fish could fine tune light sensitivity and natural selection can act. Yet recent reports suggest that allelic variations at the *LWS* opsin gene is responsible for blue-red differential sensitivity, provoking assortative mating and causing divergence in parapatric populations of cichlids in lake Victoria (Seehausen 2008). Moreover, SE recognize the similarity in the spectral signal in the Rh2a alpha and Rh2a Beta (Figure 5 bottom), suggesting further study to capture the differential functionality of the copies in natural cichlid populations.

Both studies provide avenues to find study gene duplications. Mastsuo approach is preferable in model organisms where whole genomes are available and cross species patterns can be screen. Yet, functional differences among the gene copies would be difficult to asses and experimental work with expressed genes in specific tissues need it to connect gene duplication with function and their importance for natural populations. While, TE approach is exhaustive in testing the functionality of the copies, it is restricted to the copies that are expressed in the study tissues, ignoring other not functional and/or non-eye expressed genes. Once more and in concordance with studies testing for natural selection and/or producing phylogenetic hypothesis (and inferring molecular clocks), future approaches will use the ever-increasing accessibility and economy of high-throughput sequence methods to exhaustively search for gene duplications and provide general patterns of sub-fuctionalization and neo-fuctionalization and their possible ontogenetic connection. Until more data is available the relative role of natural selection and stochasticity as causes or consequences of genetic diversity in copy number and thus phenotypic variation will remain contentious.

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