Carlos Prada Words:

Evolutionary novelty, the acquisition of genes with new functions, among others can be through horizontal transfer mediated by the interaction of the host and its symbionts/parasites. Rumpho et al (2008) and Piskurek and Okada (2008) provide examples of horizontal gene transfer. The former is mediated by genomic interactions of multicellular organisms, maximizing mutualistic interactions. The latter present a case of retrotransposon transfer mediated by a generalist virus vector of both reptiles and mammals.

Rumpho et al (2008) suggests that the acquisition of energy via photosynthetic process is due to a complex interactions between proteins encoded by genes in the algae-plastid genome and the horizontally transfer nuclear encoding counterparts in the sea slug

Species interactions between host and associated microflora. Often for microorganisms (<1mm) the species interactions are mainly achieved within a host, which also substantially interact with its micro flora. However, not until recently the nature of this interactions were thought to be individualistic, in which each partner provide the mutualistic product without the The nature of this interactions are complex and vaguely resolve at the macroscopic level, prey-predator, mutualistic

In an attempt to identify genomic areas under selection, Swanson and colleagues (2005) and Makinen *et al.* (2008) used unparallel approaches to analyze current patterns of population polymorphism and/or divergence among species. Swanson *et al.* (SE) used a method, where the polymorphism/divergence signature of diversifying selection was use as a proxy to identify female genes responsible for female-male interaction in *Drosophila*. Previously, SE reported selection in male reproductive proteins and a likely a co-evolution of male-female reproductive genes. Thus they assumed higher non-synonymous substitutions rates in female reproductive genes compare to genes under neutrality. Conversely, Makinen *et al*. (ME) compared *Fst* values, using previously developed microsatellites (and two indels) linked to morphological QTL’s. They assumed that deviations from neutrality in *Fst* values would identify areas of selection. ME confirmed candidates for directional selection during *Fst* analysis by measuring diversity levels, assuming that selective sweeps decrease polymorphism. Unlike the SE approach, this method provides candidates genes for either diversifying or balancing selection. Nonetheless, SE method is designed to directly identify the gene(s) responsible for the trait under study. SE also make a thorough search of genes being expressed in the reproductive tracts of females, after pulling out genes common to male and females and thus unlikely to be female-specific. It is plausible that the five genes reported by SE under selection are involved in the sperm-egg interaction. SE work is exhaustive as it compares population polymorphism and species divergence, capturing recent and past selective signatures; unlike fast evolving markers (as used by ME) unable to retain polymorphism patters left by natural selection over many generations. Furthermore, SE provide detail evidence of specific codons under selection (through a “beta distribution”) in at least two of the five genes and more surprisingly show that some of the codons are subjected to adaptative pressure in various species.

Interestingly, ME introduce their work as a preliminary survey to locate genomic areas under selection. Yet, their markers were obtained from previous studies, where researchers had reported adaptative evolution and the connection with QTL’s responsible for plate formation (Colosimo *et al*., 2005; Cano *et al.*, 2006; Shapiro *et al.*, 2004). Thus, the genotype-phenotype-ecology interaction had been previously recognized. Thus it is not surprising that the loci under directional selection, reported by ME, are link to the *Eda* region, responsible for plate formation in Stickleback. ME study however highlights the prevalence of balancing selection in agreement with other studies (Bustamante *et al.* 2005) and recapitulates Fisher’s suggestions of the high polymorphism present in natural populations to cope with environmental heterogeneity (Fisher 1930, See Gillespie 2004). On the other hand, SE work is comprehensive as it uses bioinformatics and molecular biology to address the question and find the genetics basis of the trait under study. Importantly, SE had to decrease their discovery cut off to 0.5 in their dn/ds ratios to avoid underestimation of genes under selection. In silent to replacement comparisons genes may show low dn/ds ratios but specific codons can be under selection and careful analysis of the regions is advisable. However, the dn/ds approach used by SE and widely employ in the literature can be compromised as GC rich areas of the genome are more likely to highly recombine (by gene distortion) and generate dn/ds neutral deviations (Galtier *et al.*, 2009).

Both studies provide avenues to find signatures of selection in natural populations. ME approach is more affordable as scoring microsats -AFLPs is relatively cheap for a several number of individuals. The trade off is the inconclusiveness of the result as locating the area of selection is the first step towards finding the gene responsible for the trait. Also, highly dense marker maps are needed to achieve power and it is unavailable for many species and unfeasible to construct in long-lived organisms. SE work is costly; as it requires sequences from clones of bacterial libraries and the need for previous genome sequences to compare the results, but can potentially locate specific genes and codons within genes under selection. Future approaches will use the ever-increasing accessibility and economy of high-throughput sequence methods to construct robust datasets with the advantage of having more information to infer selection patterns and thus more efficiently use of *Fst* based comparisons, maximum likelihood dn/ds ratio tests for species, populations and codon comparisons.

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