

Appendix III

A model for socially mediated speciation (Hochberg *et al.* 2003) hypothesizes that reproductive isolation can evolve within a species with a locus for distinct signals, given two other loci: one for mate choice and one mediating social interactions like altruistic donation or social competition. For example, the color trimorphic *Uta stansburiana* exhibits all three loci required for socially mediated speciation, including (1) signal, (2) mate choice, and (3) donation loci (Sinervo *et al.* 2006; Bleay *et al.* 2007). Genes that control such social interactions are referred to as “greenbeards”. The side-blotched lizard system represents the first example of greenbeard dynamics in vertebrates, but insects (Keller *et al.* 1997; Keller & Ross 1998), protists (Queller *et al.* 2003), and prokaryotes like *E. coli* exhibit similar greenbeard and/or RPS dynamics (Kerr *et al.* 2002, 2004). Obvious parallels among the RPS system in *Uta stansburiana*, the RPS in the lizard *Lacerta vivipara* of Europe (Sinervo *et al.* 2007), and those of protists (Queller *et al.* 2003), and prokaryotes (Kerr *et al.* 2002), suggest that many more examples will be uncovered (reviewed in Sinervo *et al.* 2007, 2008).

Based on gene mapping studies in the field pedigree and mate choice studies, the side blotched lizard exhibits all 4 required loci (loci i-iii: color signals that elicit recognition, and social acts of altruism or competition [Sinervo & Clobert 2003, Sinervo *et al.* 2006] and locus iv: females exhibit self-color preferences for these signals [O for O and Y for Y: Bleay & Sinervo 2007; B for B Sinervo *et al.* 2006]. The number of loci that are required for the functioning of the social systems (minimum of 4 loci, above), and their distribution across the genome on separate linkage groups will generate unfitness between hybrids produced from trimorphic lineages crossed to di- or mono-morphic lineages (different socially “coadapted genes” in each lineage), and ensuing evolution of a RIM.

To generate hybrid unfitness, socially mediated speciation (Hochberg *et al.* 2003) requires separate and unlinked loci for: i) a signal locus (e.g., color), ii) recognition

loci for (self) signals, iii) signal recognition elicits social acts of altruism (to self) or competition (to non-self), and iv) females exhibit (loci) preferences for self (color signals). Even though these loci are unlinked, in spatially prescribed neighborhoods, the model reproducibly generates species with differently colored signals eliciting social acts in one species versus the other. Reduced hybrid fitness at junction between evolving species leads to the selection of mating preferences, which then spread to the core areas of the respective species (Hochberg *et al.* 2003). The number of loci that are required for the functioning of the social systems (minimum of 4 loci, above), and their distribution across the genome on separate linkage groups will generate unfitness between hybrids produced from trimorphic lineages crossed to di- or mono-morphic lineages (different socially “coadapted genes” in each lineage), and ensuing evolution of a RIM.

The process of coadapted mate preferences (e.g., preference for the same color morph: Bleay & Sinervo (2007) is amplified by multi-trait preferences involving color and many other loci (Lancaster *et al.* 2009). Therefore, the levels of linkage disequilibrium due to correlation selection (Sinervo & Svensson 2002), mate preference (Bleay & Sinervo 2007; Lancaster *et al.* 2009) within an RPS mating system are extremely high (Sinervo *et al.* 2006), rivaling the linkage disequilibrium found at a contact zone between species. Fixation and loss of color morphs is expected to result in extremely rapid genetic change (Corl *et al.* 2010a, b) because many other alleles at loci besides the master morph locus will be lost as the alternative optima for the now missing color alleles disappear. Thus, the genes present in a reduced mating system with fewer morphs will be dramatically different than the ancestral RPS system, perhaps generating Dobzhansky-Muller incompatibilities. The formation of Dobzhansky-Muller incompatibilities increases with the number of genes that diverge and with the number of associations among genes (Coyne & Orr 2004), so the loss of a morph could potentially generate a large number of incompatibilities (given the number of autosomal strategic loci with which the OBY locus interacts, Sinervo *et al.* 2006).

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