

CANINE GENOMICS AND THE RAPID GENERATION OF PHENOTYPIC DIVERSITY

Violeta Munoz-Fuentes¹, Carles Vila²

¹*Uppsala University, Evolutionary Biology, Uppsala, Sweden*

²*Estacion Biologica de Donana-CSIC, Sevilla, Spain*

Violeta.Munoz@ebc.uu.se

Rapid generation of morphological change is difficult to reconcile with the low frequency at which point mutations occur. In general, the mechanisms that underlie the genesis of extreme diversity are unknown. In this study, we use the dog (*Canis familiaris*) as a model organism for the study of some of such mechanisms, a system that is specially appropriate for at least two reasons. First, dogs have an extreme phenotypic diversity and have reached the greatest levels of morphological diversity among all vertebrate domestic species. Second, the ancestor of the dog, the wolf (*Canis lupus*), is still extant and, therefore, available for comparison. Third, the genome of the dog has been sequenced, a reasonably well-defined genetic map exists and a large number of markers are available. Here we apply different methods to compare the genomics of these two species in order to shed some light into the molecular mechanisms that may be responsible for the rapid generation of phenotypic diversity. These mechanisms may be acting in natural populations as well.