



Phylogenetic inheritance of genetic variability produced by neutral models of evolution

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Genet. Mol. Res. 7 (4): 1327-1343 (2008)

Received August 27, 2008

Accepted September 9, 2008

Published November 25, 2008

ABSTRACT. The amount of genetic variability in species and populations has been mainly related to microevolutionary forces operating in natural populations and the influence of phylogenetic processes for the distribution of genetic variability has been neglected. To investigate how the current genetic variability distribution depends on the genetic variability of ancestral species, we simulated the evolution of heterozygosity on a pre-determined phylogeny under three neutral models of evolution: genetic drift, drift vs mutation and drift vs migration. The distribution of genetic variability resulting from the simulations was used to estimate the phylogenetic signal by the phylogenetic comparative method of autocorrelation. Phylogenetic signal in genetic variability was observed for each of the three models, and its intensity was generally higher and persisted longer when forces of drift, mutation and migration were reduced. The prediction of a phylogenetic signal in genetic variability has consequences for: population genetics, which must consider biological processes acting at the species level influencing the amount and distribution of genetic variability; the macroevolutionary

theory, by giving a theoretical basis for species selection by suggesting a heritability of genetic variability between species, and the meta-analyses of genetic variability, which must deal with the non-independence of species. The patterns observed in phylogenetic signal produced by different models of evolution can be used further to compare with data obtained from molecular markers. This is the first study that analyzes the theoretical expectations for the existence of a phylogenetic signal in a population genetic trait.

Key words: Population genetics; Heterozygosity; Neutral evolution; Phylogenetic comparative method; Phylogenetic autocorrelation; Macroevolution