Quantitative genetics machinery was extended to between-species evolution in the pioneering work of Russ Lande almost 40 years ago. Only in the past 20 years has the availability of molecular phylogenies made it possible to investigate the effects of genetic drift and natural selection across multiple species. In that period "the comparative method" changed from a vague statement of interest in looking at multiple species, to formal statistical methods using Brownian Motion and Ornstein-Uhlenbeck models to test hypothesis about covariation between characters and heterogeneity of processes in different parts of an evolutionary tree. In effect, this extends the concept of realized heritability to differences among species. This talk will cover phylogenetic uses of morphometrics and of the quantitative-genetic threshold model. It will range from ways of placing fossils on a phylogeny to uses of comparative methods within species. And all the while the speaker will have in the back of his mind the worry that we have extrapolated processes of single-generation change too far.