

# PATTERNS OF MOLECULAR VARIATION IN PLANT POPULATIONS

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## 1. Introduction

It has recently been argued [8], [9] that rate of evolution at the molecular level is greater than can be accounted for by natural selection and hence that a large part of observed molecular changes must be selectively neutral. This discussion will be concerned with some experimental results, from studies of a number of different species of plants, that bear on this question. These results will be illustrated here in terms of several representative examples taken from studies of various general enzyme systems in two of the plant species under study, cultivated barley (*Hordeum vulgare*), and the Slender Wild Oat (*Avena barbata*).

The electrophoretic procedures followed are standard ones [6], [11] and consequently they need not be described here. In applying the electrophoretic techniques, we have adopted the procedure of working out the formal genetics of all bands that appear at different migrational distances for five or more enzyme systems in each species chosen for study. An example of such a full analysis of banding patterns is given in Figure 1. This figure shows, in schematic form, some banding patterns observed in a worldwide survey of esterases in cultivated barley and its wild ancestor. Bands appear in seven zones, designated *A* through *G*.

Formal genetic studies show that banding patterns for differences in migrational distances are governed by a single locus in each zone, or by seven loci in all. In the *A* and *B* zones homozygotes are single banded and heterozygotes double banded. In the *C* and *D* zones, homozygotes are double banded and heterozygotes are quadruple banded (triple banded when leading and trailing bands for two alleles are in juxtaposition). Null alleles (no band), which are recessive to alleles which produce bands, are found at the *B*, *D*, *E*, *F* and *G* loci. Loci *A*, *B*, and *C* are very tightly linked, as shown in Figure 2. Locus *A* is located between loci *B* and *C*, 0.0023 to the right of *B* and 0.0048 to the left of *C*. Inheritance of banding patterns for five other enzyme systems (phosphatase, leucine aminopeptidase, peroxidase, amylase, and malate dehydrogenase) which have been studied in barley also usually feature codominance.

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