

VARIATION – SOURCES, TYPES AND ROLE IN EVOLUTION

Summary

Genetic variation among individuals within a population concerns both quantitative and discrete traits and manifests at a variety of organizational levels, from whole organisms down to chemical constituents of cells. The results of DNA sequencing revealed even more variation than was detected by earlier comparisons of proteins by gel electrophoresis. The observation of unexpectedly high levels of genetic variation in both coding and the non-coding regions of DNA led to development of the neutral theory which holds that most variation at the molecular level does not affect fitness and can be accounted for by stochastic processes. A relatively constant rate of molecular evolution – the molecular clock – provided it is properly calibrated, became a useful method of estimating the time of events in evo-

lutionary history. While mutations are the ultimate source of genetic variation, the major source of differences among sexually reproducing individuals in populations results from meiotic crossing over, recombination of chromosomes and random fertilization. Since recently, high throughput sequencing methods provide new insights into the evolution of genomes revealing major contributions from gene and whole genome duplications, large deletions and horizontal transfer of genes. The uncovering of the mechanisms responsible for epigenetic phenomena in plants and animals and the observations of trans-generational epigenetic inheritance (i.e. inheritance not dependent on changes in the sequence of DNA) opens the way to study the importance of multigenerational epigenetics for evolution and adaptation.