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Editorial

Editorial Note on Genetic Polymorphism

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EDITORIAL

Ford defined genetic polymorphism as the coexistence of two or more discontinuous types in such proportions within the same neighborhood that the rarest of them cannot be sustained simply by perennial mutation or immigration. "Genetic polymorphism" is defined as "the presence of two or more alleles at one locus in the same population, each with a significant frequency," with the minimum frequency being one hundred and twenty fifth. Scholarly journals give authors more exposure in the rapidly expanding science sector. If more than one allele resides at the locus of a gene in a population, the gene is said to be polymorphic. To be considered polymorphic, each allele must occur in the population at a rate of at least 1% in addition to having several alleles at a particular locus. Polymorphisms in genes may occur in any part of the genome.

The majority of polymorphisms are silent, which means they have no effect on a gene's function or expression. There is some polymorphism apparent. The E locus in dogs, for example, may have any of five different alleles: E, Em, Eg, Eh, and e. the pigmentation and patterns seen in dog coats are caused by various combinations of these alleles. A polymorphic variant of a gene may trigger irregular protein expression or development, which can cause or be associated with disease. For instance, a polymorphic variant of the CYP4A11 gene in which thymidine replaces cytosine at nucleotide 8590 of the gene encodes a CYP4A11 protein that replaces phenylalanine with serine. The enzyme function of this variant protein in metabolising arachidonic acid to the blood pressure-regulating eicosanoid 20 hydroxyeicosatetraenoic acid was decreased. Humans with this mutation in one or both of their CYP4A11 genes have a higher risk of hypertension, ischemic stroke, and coronary artery disease, according to a study.

Genetic variations of less than 1% allele frequency are often classified as mutations rather than polymorphisms, according to a rule of thumb. This is not a reliable way to distinguish new mutations from polymorphisms, however, since polymorphisms can occur at low allele frequencies. Polymorphisms can be found in a number of ways in the laboratory. To amplify the sequence of a gene, several methods use PCR. DNA sequencing can detect polymorphisms and mutations in the sequence after it has been amplified, either directly or after screening for variation using a tool like single strand conformation polymorphism analysis.

Single nucleotide polymorphisms are single nucleotide variations that occur in a specific position in the genome. The most common form of genetic variation is polymorphism. In small-scale insertions/deletions, bases are inserted or deleted in DNA. Polymorphism can also be caused by active transposable elements inserting themselves in new locations. Microsatellites are DNA sequence repeats of 1-6 base pairs. Microsatellites are frequently used as molecular markers, especially for determining allele-allele relationships. Many XPD exons have been shown to have polymorphisms. XPD stands for "Xeroderma pigmentosum group D" and is involved in a DNA replication repair mechanism. XPD operates by chopping and extracting weakened DNA segments caused by things like cigarette smoking and inhaling other environmental carcinogens.

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