ALLELE

Allele is the short form of allelomorph, a term used by Bateson to denote alternative characters in Mendelian genetics. The term also refers to different forms of a gene occupying a particular locus on a chromosome. Alleles are symbolised by one or more letters, often with appropriate superscripts. Thus \underline{w}^+ , \underline{w} and \underline{w}^{cho} represent alleles which respectively cause the eye colour of Drosophila to be red, white or chocolate. The allele most commonly found in a species is called the wild type allele. It is designated by the superscript A. A diploid individual may carry two different alleles of a gene. With a combination of a wild type and a mutant allele, the organism usually has a normal appearance. The wild type allele is then. said to be dominant and the mutant allele recessive. Sometimes mutant alleles are dominant or partially dominant. Symbols for dominant alleles begin with capital letters.

Structure. A gene is a segment of mucleic acid, commonly DNA (deoxyribonucleic acid) but in certain viruses, RNA (ribonucleic acid). The sequence of four different nucleotides in DNA determines the arrangement of amino acids in a protein specified by this gene (see genetic code). Mutant alleles differ from wild type in one or more nucleotide residues. New alleles arise by substitution, addition, deletion or rearrangement of base pairs in the wild type sequence. An average gene contains several hundred nucleotides and alleles may carry mutational alterations at different sites (<u>heteroalleles</u>) or the same site (<u>isoalleles</u>). In cells containing allelic mutations at non-identical sites, recombination occasionally gives rise to wild type alleles. Recombination between alleles can be used to analyse the fine-structure of a gene.

<u>Function</u>. The function of an allele may be examined at the level of its primary product or through its effect on the organisms phenotype. Geneticists study interactions between different alleles in order to gain information about gene activity. Alleles that lack gene activity are called <u>amorphic</u> while those with reduced levels of activity are called hypomorphic.

Certain mutations lead to substitution of one amino acid in the polypeptide by enother, making the resulting protein non-functional. The mutant genes, producing inactive polypeptides, are called "missense" alleles. The gene <u>Hb</u> in humans determines the structure of haemoglobin, the protein which carries oxygen in the blood stream. A series of mutant alleles produce haemoglobins with unusual amino acids at particular positions. Persons carrying these alleles suffer from sickle cell anaemia. In the case of "nonsense" alleles the formation of complete polypeptide chain is interrupted.

The functional relationship of two mutant alleles can be studied by examining a hybrid carrying these alleles. Consider two homozygous mutants $\frac{m1}{m1}$ and $\frac{m2}{m2}$ with identical phenotypes. If the alleles belong to different genes, the genotype of the hybrid progeny will be $\frac{m1}{m1^+}$, $\frac{m2}{m2^+}$. The missing functions of genes m1 and m2 will be provided by the wild type alleles m1 and m2 + and the hybrid will be phenotypically normal. The mutant alleles, in this case, are said to complement each other. If the hybrid has a mutant phenotype, the alleles must belong to the same functional unit and the genotype is $\frac{m_1}{m_2}$. Failure of complementation is the standard genetic test of functional allelism. Recently it has been found that a stretch of DNA can specify more than one protein. One would expect to find, in such genes, some alleles which simultaneously fail to complement alleles of different genes. Sometimes a hybrid $\frac{m_1}{m_2}$, carrying mutant alleles of the same gene also exhibits normal function. This is known as intragenic complementation, Some functional proteins are aggregates of more than one sub-unit. Two missense alleles can produce altered polypeptides which polymerise together to form a biologically active protein. The defect in one polypeptide is compensated by the other. Intragenic

complementation is, as a rule, restricted to certain specific pairs of alleles.

The effect of a mutation can be reversed by mutations at other loci called suppressors. A suppressor may act on certain alleles of a gene but not on others. Allele-specific suppressors can often suppress mutations in more than one gene. Genespecific suppressors suppress all alleles of a given locus but do not act on other loci.

<u>Complex loci and pseudoallelism</u>. In microorganisms, functionally related genes are often situated on the chromosome in clusters called operons. Genes of an operon function in a coordinated fashion. Certain mutations of one gene can also block the expression of other genes in the operon. These mutant alleles fail to complement mutations in other genes which must be considered non-allelic. Clustering of functionally related genes also occurs in higher organisms where such loci have been described as complex loci. Lack of complementation between apparently different genes has been called pseudoallelism. The distinction between allelism and pseudoallelism is not always easy to make.

Evolution. Mutant alleles in a population provide the necessary material for variation and natural selection. Altered proteins can be detected by electrophoresis. Electrophoretic variants of enzymes are commonly encountered in natural populations. The enzymes produced by these mutant alleles are functionally normal and may, in fact, confer adaptive advantage on the organism.

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<u>Bibliography</u>: E.A. Carlson, The Gene - A critical history, 1966: J.R.S. Finchem, Genetic complementation, 1966: E.B. Lewis, Genes and gene complexes, in R.A. Brink (ed.) Heritage from Mendal, 1967.