Glossar OC III

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Agarose: a polysaccharide isolated from seaweed used as a matrix in gel electrophoresis.

Allele: one of two alterate forms of a gene occupying a given locus on the chromosome.

Allosteric control: the ability of an interaction at one site of a protein to influence (positively or negatively) the acitivity at another site.

Alu family: a set of short (ca. 300 bp) related sequences dispersed throughout the human genome. Refers to the property of these sequences to be cleaved once by the restriction enzyme Alu I. Genomes of other mammals contain similar families. Their role is unknown.

Amplification: the production of extra copies of a chromosomal sequence found either as intra- or extrachromosomal DNA. With respect to plasmids it refers to the increase in the number of plasmid copies per cell induced by certain treatments of transformed cells.

Anneal (re-anneal): the (re)establishment of base pairing between complementary strands of DNA or a DNA and an RNA strand.

Antibody: a protein that specifically recognizes and binds to an antigen.

Anticodon: a triplet of nucleotides in a constant position in the structure of tRNA that is complementary to the codon(s) in mRNA to which the tRNA responds.

Antigen: any molecule which, upon entry into the organism, causes the production of antibodies (immunoglobulins).

Antisense: a strand of DNA that has the same sequence as mRNA (also coding strand).

Antisense Oligonucleotide: a synthetic, usually modified oligonucleotide of around 20 nucleotides length which is complementary to the mRNA coding region and thus suppreses translation.

Apoptosis: is the programmed death of a cell within a multicellular organism and follows an ordered process.

Aptamer: DNA or RNA molecules that have been selected from random pools based on their ability to bind other molecules.

Array: a spatial arrangement of e.g. oligonucleotides or peptides which can be at high density (≥10000 individual sequences)

Autoradiography: the detection of radioactively labeled molecules present for example in a gel or on a filter by exposing an X ray film to it.

Auxotrophy: inability of microorganisms to live on minimal medium without supplemented (auxiliary) nutrients.

Back mutation : reverses the effect of a mutation that had inactivated a gene.

Bacteriophages: viruses that infect bacteria; often abbreviated as phages.

Base pair (bp): a duplex of A with T or of C with G in a DNA double helix; other pairs are possible in RNA under some circumstances.

Blotting: transfer of DNA, RNA or protein from a gel to nitrocellulose or other „paper".

Cap: the structure at the 5´-end of eukaryotic mRNA introduced after transcription by linking the 5´-end of a guanine nucleotide to the terminal base of the mRNA and methylating at least the additional G; the structure is $7Me_G{}^{5'}ppp^{5'}Np...$

cDNA: a single-stranded DNA complementary to an RNA, synthesized from it by *in vitro* reverse transcription.

Chain termination sequencing: see Sanger-Coulson sequencing.

Chip: usually a silicon wafer or simply glass plate presenting sets of oligonucleotides for hybridisation with RNA or DNA.

Chromosome: a discrete unit of the genome carrying many genes, consisting of a very long molecule of DNA, complexed with a large number of different proteins (mostly histones). Chromosomes are visible as a morphological entity only during the act of cell division.

Cis-acting: the ability of a DNA (or RNA) sequence to affect its influence only on the molecule from which it forms a part. Usually implies that the sequence does not code for a protein. When applied to a protein it means that the protein acts only on the DNA (or RNA) molecule from which it was expressed.

Cistron: the genetic unit defined by the cis/trans test; equivalent to gene in comprising a unit of DNA representing a protein.

Clone: a large number of cells or molecules genetically identical with a single ancestral cell or molecule.

Codon: a triplet of nucleotides that represents an amino acid or a termination signal.

Competent: a culture of bacteria or yeast cells treated in such a way that their ability to take up DNA molecules without transduction or conjugation has been enhanced.

Complementation: the ability of independent (nonallelic) genes to provide diffusible products that produce wild phenotype when two mutants are tested in trans configuration in a heterozygote.

Conjugation: directional transfer of DNA between two bacteria.

Consensus sequence: an idealized sequence in which each position represents the base most often found when many actual sequences are compared.

Copy number: the average number of copies of a particular (recombinant) plasmid present in a single host cell. Also used for individual genes.

Cosmids: plasmids into which phage lambda cos sites have been inserted; as a result, the plasmid DNA can be packaged *in vitro* into the phage coat.

Cotransformation: introduction of two or more genes carried on separate DNA molecules into a cell.

Cross-linking: introduction of covalent intra- or intermolecular bonds between groups that are normally not covalently linked. Used to detect proximity of (parts of) (macro) molecules.

Cut: a double-strand scission in the duplex polynucleotide in distinction to the single-strand “nick“.

Deletions: constitute the removal of a sequence of DNA, the regions on either side being joined together.

Denaturation (of protein): conversion from the physiological conformation to some other (inactive) conformation.

DICER: a double stranded RNA (dsRNA) cleaving endoribonuclease which cuts dsRNA into 21-23nt long pieces.

Direct repeats: identical (or closely related) sequences present in two or more copies in the same orientation on the same DNA (orRNA) molecule; they are not necessarily adjacent.

DNAzyme: short catalytic single-stranded DNA molecules.

Domain (of a chromosome): may refer either to a discrete structural entity defined as a region within which supercoiling is independent of other domains; or to an extensive region including an expressed gene that has heightened sensitivity to degration by the enzyme DNase I.

Domain (of a protein): a discrete continuous part of the amino acid sequence that can be equated with a particular function or a particular substructure of the tertiary structure.

Dominant (allele): the phenotype displayed in a heterozygote with another (recessive) allele.

Downstream: identifies sequences proceeding further in the direction of expression for example, the coding region is downstream from the initation codon.

End labeling: the addition of a radioactively labeled group or a fluorescent dye to one end (5´- or 3´-end) of a DNA or RNA strand.

Endonucleases: cleave bonds within a nucleic acid chain; they may be specific for RNA or for single-stranded or doublestranded DNA.

Enhancer element: DNA sequence that increases the utilization of (some) eukaryotic promoters in cis configuration, but can function in any location, upstream or downstream, relative to the promoter.

Epitope: any part of a molecule that acts as an antigenic determinant. A macromolecule can contain many different epitopes each giving rise to a different specific antibody.

Eukaryotic: organisms containing a nucleus.

Excision-repair: systems that remove a single-stranded sequence of DNA containing damaged or mispaired bases and replace it in the duplex by synthesizing a sequence complementary to the remaining strand.

Exon: any segment of an interrupted gene that is represented in the mature RNA product.

Exonucleases: cleave nucleotides one at a time from the end of a polynucleotide chain; they may be specific for either the 5´- or 3´-end of DNA or RNA.

Expression vector: a cloning vector designed in such a way that a foreign gene inserted into the vector will be expressed in the host organism.

Fingerprint: the characteristic array of oligopeptides or oligonucleotides obtained upon two-dimensional electrophoresis of a protein digested with a specific endopeptidase or an RNA digested with a specific endonuclease.

Footprinting: in this context it is a technique for identifying the site of DNA bound by some protein by virtue of the protection of bonds in this region against attack by nucleases.

FRET: Fluorescence **R**esonance **E**nergy **T**ransfer, a fluorescence detection method where a fluorophor donor-acceptor pair is observed in energy transfer, usually Förster Transfer and where the result gives distance information.

Functional genomics: studying the functions of genes in a given genome.

Fusion gene: recombinant gene constructed from parts of two different genes.

Fusion protein: the protein expressed by a fusion gene containing parts of the coding sequence of two different genes.

Gel electrophoresis: electrophoresis performed in a gel matrix (usually agarose or polyacrylamide) which allows separation of molecules of similar electric charge density on the basis of their difference in molecular weight.

Gene: a DNA sequence involved in the production of an RNA or protein molecule as the final product. Includes both the transcribed region and any sequences upstream and/or downstream responsible for its correct and regulated expression (e.g. promotor and operator sequences).

Genectic code: the complete set of codons specifying the various amino acids, including the nonsense codons. The code is usually written in the form in which it occurs in mRNA.

Genome: the entire genetic material of a cell.

Genomics: methods to analyse a given genome.

G-tetrad: four nucleotide strands are involved in a G-tetrad, with participation from one Guanine in each strand.

Hairpin: the double-stranded region formed by base pairing of adjacent complementary sequences in the same DNA or RNA strand.

Hapten: a small molecule that acts as an antigen if it is part of a high-molecular structure.

Heteroduplex (hybrid) DNA: DNA, generated by base pairing between partly non-complementary single strands derived from the different parental duplex molecules; it occurs during genetic recombination.

Hoogsteen Base pairing: hydrogen bonds of purines at the N-7 site (major groove).

Homology: the degree of identity existing between the nucleotide sequences of two related but not complementary DNA or RNA molecules. 70% homology means that on

average 70 out of every 100 nucleotides are identical. the same term is used in comparing the amino acid sequences of related proteins.

Hybridization: the pairing of complementary RNA and DNA strands to give an RNA-DNA hybrid, and is also used to describe the pairing of two single stranded DNA molecules.

Hybridoma: the cell line produced by fusing a myeloma cell with a lymphocyte; it continues indefinitely to express the immunoglobulins of both parents.

Hyperchromicity: the increase on optical density that occurs when DNA is denatured.

Incompatibility: the inability of certain bacterial plamids to coexist in the same cell.

Inducer: a small molecule that triggers gene transcription by binding to a regulator protein.

Initation codon: AUG; sometimes GUG, codes for the first amino acid in protein sequences, which is formylmethionine in prokaryotes fMet is often removed posttranslationally.

In situ hybridization: is performed by denaturing the DNA of cells squashed on a microscope slide so that reaction is possible with an added single-stranded RNA or DNA; the added preparation is radioactively labeled and ist hybridization is followed by autoradiography.

Intron: a segment of DNA that is transcribed, but is removed from within the transcript by splicing together the sequences (exons) on either side of it. The occurrence of introns is almost exclusively limited to eukaryotic cells.

***In vitro* (lit. „in glass"):** refers to any (biological) process occurring outside the living cell.

***In vivo*:** refers to any biological process occurring within the living cell.

IPTG: isopropyl-β-D-thiogalactoside; an artificial inducer of the lac operon (physiological inducer: allolactose).

kb: abbreviation for 1000 base pairs of DNA or 1000 bases of RNA.

Klenow fragment: a piece obtained from DNA polymerase I by proteolytic cleavage; it lacks the 5´ to 3´ exonuclease.

Lac operon: an inducible operon in *E. coli* that codes for three genes involved in the metabolism of lactose.

Leader sequence: N-terminal presequence of trans or secreted peptides and proteins.

Library: a set of cloned fragments together representing the entire genome.

Ligase (DNA ligase): catalyzes the formation of a phosphodiester bond at the site of a single-strand break in duplex DNA. Some DNA ligases can also ligate blunt-end DNA molecules. RNA ligase covalently links separate DNA molecules.

Ligation: the formation of a phosphodiester bond to link two adjacent bases separated by a nick in one strand of a double helix of DNA. (The term can also be applied to blunt end ligation and to joining of RNA).

Linker (fragment): a short synthetic duplex oligonucleotide containing the target site for some restriction enzyme; may be added to ends of a DNA fragment prepared by cleavage with some oher enzyme during reconstructions of recombinant DNA.

LTR: an abbreviation for **l**ong-**t**erminal **r**epeat, a sequence directly repeated at both ends of a retroviral DNA.

Lysis: the death of bacteria at the end of a phage infective cycle when they burst open to release the progeny of an infecting phage.

M 13: an *E. coli* phage containing single-stranded circular DNA which forms the basis for a series of cloning vectors.

Maxam-Gilbert sequencing: a DNA sequencing technique based on specific chemical modification of each of the four bases.

Melting temperature (T_m): the temperature where hyperchromicity is half-maximal.

Metabolone: the total set of secondary metabolites in a cell at a given time.

Minimal medium: a chemically fully defined medium containing only inorganic sources of the essential elements as well as an organic carbon source.

Modified bases: all those except the usual four (T,C,A,G) from which DNA is synthesized; in the cell they result from postsynthetic changes in the nucleic acid.

Monoclonal antibody: a single type of antibody produced by a cultured clone of a hybridoma cell. The antibody is directed against a single epitope of the antigenic substance used to raise the antibody.

Multicopy plasmids: present in bacteria at amounts greater than one per chromosome.

Mutagens: increase the rate of mutation by causing changes in DNA.

Mutation: any change in the sequence of genomic DNA.

Nick translation: the ability of *E. coli* DNA polmerase I to use a nick as a starting point from which one strand of a duplex DNA can be degraded and replaced by resynthesis of new material; this is used to introduce radioactively labeled nucleotides into DNA *in vitro*.

Nonsense codon: any one of three triplets (UAG, UAA, UGA) that cause termination of protein synthesis. UAG is known as amber; UAA as ochre, UGA as opal.

Northern blotting: a technique for transferring RNA from an agarose gel to a nitrocellulose filter on which it can be hybridized to a complementary DNA.

Nucleolus: the region in the nucleus where rRNA synthesis takes place.

Oncogene: a retroviral gene that causes transformation of the mammalian infected cell. Oncogenes are slightly changed equivalents of normal cellular genes called proto-oncogenes. The viral version is designated by the prefix v, the cellular version by the prefix c.

Open reading frame (orf): a series of triplets coding for amino acids terminated by a termination codon; sequence is (potentially) translatable into protein.

Operator: the site on DNA at which a repressor protein binds to prevent transcription from initating at the adjacent promoter.

Operon: a complete unit of bacterial gene expression and regulation, including structural genes, regulator gene(s), and control elements in DNA recognized by regulator gene product(s).

Origin (ori): a sequence of DNA at which replication is initiated.

Palindrome: a sequence of DNA that is the same when one strand is read left to right or the other is read right to left; consists of adjacent inverted repeats.

pBR322: one of the standard plasmid cloning vectors.

PCR: polymerase **c**hain **r**eaction, an *in vitro* amplification of DNA based on primer, template and a thermostable DNA-polymerase.

Phage (bacteriophage): a bacterial virus.

Plasmid: an autonomous self-replicating extrachromosomal circular DNA.

Polyadenylation: the posttranscriptional attachment of up to 200 AMP residues to the 3´-terminus of most eukaryotic mRNA´s.

Polylinker: a synthetic double-stranded DNA oligonucleotide containing a number of different restriction sites.

Polymerase: an enzyme that catalyzes the assembly of nucleotides into RNA or of deoxynucleotides into DNA, usually the enzyme requires single-stranded DNA (sometimes RNA) as a template.

Polymorphism: refers to the simultaneous occurrence in the population of genomes showing allelic variations (as seen either on alleles producing different phenotypes or - for example - in changes in DNA affecting the restriction pattern).

Phosphatase: a class of enzymes that hydrolyses phosphoryl groups from nucleotides as well as from proteins.

Primer: a short sequence (often of RNA) that is paired with one strand of DNA and provides a free 3´-OH end at which a DNA polymerase starts synthesis of a deoxyribonucleotide chain.

Probe (hybridization): a labelled DNA or RNA molecule used to detect a complementary sequence by molecular hybridization.

Prokaryotic: organisms lack membrane enclosed nuclei.

Promoter: in bacteria: the region of the gene involved in binding of the RNA polymerase. In eukaryotes: usually all regions of the gene required for maximum expression (excluding enhancer sequences).

Protein A: a protein from Staphylococcus aureus that binds specifically to immunoglobulin G molecules. Used for detection of proteins by immunological techniques.

Proteinase K: a protease used to remove contaminating protein from preparations of nucleic acids. The enzyme also degrades itself.

Proteome: the entire protein material of a cell.

Proteomics: methods to analyse the given proteome.

Protein kinase: a class of enzymes that phosphorylates a protein with the help of ATP, the phosphorylation takes place preferentially at tyrosines.

Protoplast: cell without cell wall but with intact cell membrane; gram-pos. bacterium after removal of the cell wall.

Pseudoknot: a RNA secondary structure that is minimally composed of two helical segments connected by single-stranded regions or loops.

Recombinant DNA: any DNA molecule created by ligating pieces of DNA that normally are not contiguous.

Renaturation: of DNA or RNA: the reestablishment of the DNA duplex or intrastrand hairpin structures in an RNA molecule after denaturation. Of a protein: the conversion from an inactive into a biologically active conformation.

Replicon: the regulatory unit of an origin and proteins necessary for initiation of replication (specific for this origin).

Repression: the blocking of the synthesis of certain enzymes when their products are present; more generally, refers to inhibition of transcription (or translation) by binding of repressor protein to specific site on DNA (or mRNA).

Restriction enzymes: recognize specific short sequences of (usually) unmethylated DNA and cleave the respecitve DNA molecule (sometimes at target site, sometimes elsewhere, depending on type).

Restriction fragment: a duplex DNA fragment obtained by cutting a larger fragment with either a single or two different restiction enzymes.

Retrovirus: a virus containing a single-stranded RNA genome that propagates via conversion into double-stranded DNA by reverse transcription.

Reverse transcriptase: RNA-dependent DNA polymerase. Originally detected in retroviruses. It is, however, also present in normal eukaryotic cells and even in *E. coli.*

Reversion (of mutation): a change in DNA that either reverses the original alteration (true reversion) or compensates for it (second site reversion in the same gene).

Ribosomes: subcellular particles consisting of several RNA and numerous protein molecules. Involved in translating the genetic code on mRNA into the amino acid sequence of the corresponding protein.

Riboswitch: a part of an mRNA molecule that can directly bind a small target molecule, and whose binding of the target affects the gene´s activity.

Ribozyme: naturally occuring RNA-fold (structure) which cuts cognate RNA by intramolecular transesterification.

RISC: RNA **i**nduced **s**ilencing **c**omplex, part of the RNAi machinery which cuts the siRNA / mRNA hybrid.

RNAi (Inhibitory RNA): double stranded RNA which can silence mRNA by antisense recognition and cleavage by RISC.

Sanger-Coulson sequencing: DNA sequencing technique based on transcription of single-stranded DNA by a polymerase in the presence of dideoxynucleotides. The same technique can also be used for sequencing of RNA.

SDS: sodium **d**odecyl **s**ulphate, a detergent.

SDS gel electrophoresis: gel electrophoresis of proteins in polyacrylamide gels in the presence of SDS. Molecules of SDS associate with the protein molecules giving them all a similar electric charge density and thus allowing separation on the basis of differences in molecular weight.

SELEX: is a technique that allows the simultaneous screening of highly diverse pools of different RNA or DNA molecules for a particular feature.

Selection: the use of particular conditions to allow survival only of cells with a particular phenotype.

Sequencing gel: very thin (0.1-1 mm) high-resolution polyacrylamide gel used.

Shine-Dalgarno sequence: part or all of the polypurine sequence AGGAGG located on bacterial mRNA just prior to an AUG initiation condon; is complementary to the sequence at the 3´-end of 16S rRNA; involved in binding of ribosome to mRNA.

Shuttle vector: a vector which is able to replicate in different host organisms e.g. *E. coli,* COS cells.

Sigma factor: a subunit of bacterial RNA polymerase needed for initiation; is the major influence on selection of binding sites (promoters).

Signal hypothesis: describes the process by which proteins synthesized in the cytoplasm are exported either out of the cell or into one of the cellular organelles. The signal peptide of the protein plays an important role in this process.

Signal peptide: the region (usually N-terminal) of a protein that ensures its export out of the cell or its import into one of the cellular organelles. (s. leader)

Signal transduction: molecular mechanism of transferring the information from the outside of a cell, a receptor, to the nucleus. The stimulus may be e.g. a hormone or cytokine, the tranferring molecules are second messengers, protein kinases and phosphatases and finally transcription factors.

Single nucleotide polymorphisms (SNPs): are common DNA sequence variations among individuals.

Site-directed mutagenesis: introduction in the test tube of (a) specific mutation(s) into a DNA molecule at a predetermined site.

Southern blotting: a procedure for transferring denatured DNA from an agarose gel to a nitrocellulose filter where it can be hybridized with a complementary nucleic acid.

Spliceosome: is a complex of several RNA´s and proteins that remove the non coding parts of RNA (introns) from unprocessed mRNA.

Splicing: describes the removal of introns and joining of exons in RNA; thus introns are spliced out, while exons are spliced together.

Stem: the base-paired segment of a hairpin.

Stop codon: same as termination codon.

Structural gene: gene coding for any RNA or protein product other than a regulator.

Subcloning: the cloning of fragments of an already cloned DNA sequence.

Tac-promotor: a chimaeric bacterial promotor of high strength constructed from parts of the Trp and lac promotors of *E. coli.*

TATA(Hogeness)box: a conserved A-T-rich septamer found about 25 bp before the startpoint of each eukaryotic RNA polymerase II transcription unit; involved in positioning the enzyme for correct initiation.

Template: portion of single-stranded DNA or RNA used to direct the synthesis of a complementary polynucleotide.

Telomere: is a region of highly repetitive DNA at the end of a chromosome.

Termination codon: one of three triplet sequences, UAG (amber), UAA (ochre), or UGA (opal) that cause termination of protein synthesis; they are also called nonsense codons.

Transacting: the ability of a DNA (or RNA) sequence to affect molecules other than the one from which it forms a part. Usually that implies that the sequence codes for a diffusible product.

Transcription: usually the synthesis of RNA on a DNA template. Also used to describe the synthesis of DNA on an RNA template by reverse transcriptase, the copying of a (primed) single-stranded DNA by DNA polymerase and the copying of RNA by (viral) RNA polymerase.

Transduction: the transfer of a bacterial gene from one bacterium to another by a phage; phage carring host as well as its own genes is called transducing phage.

Transfection: the acquisition of native protein-free DNA of a phage by bacteria.

Transformation: the acquisition by a cell of new genetic markers by incorporation of added DNA. In eukaryotic cells it also refers to conversion to a state of unrestrained growth in culture resembling or identical to the tumorigenic condition.

Transcriptome: the total message (mRNA) of the given transcribed DNA at a given time in a given cell.

Transversion: a mutation in which a purine is replaced by a pyrimidine or vice versa.

Triplet: a sequence of three nucleotides in DNA or RNA. Usually means the same as codon.

Toll-like receptor: in vertebrates, they are able to stimulate activation of the adaptive immune system, linking innate and acquired immune responses.

Topoisomerase: a class of enzymes that alter the supercoiling of double-stranded DNA.

Triplex: Triple stranded structure of either 3 polypeptide or three nucleic acid strands. The latter is oriented in the major groove by Hoogsteen base pairing.

Two-dimensional gel electrophoresis: a technique in which a second electrophoretic separation is carried out at right angles to the first. The two separations are based on different criteria (e.g. electric charge and mulecular weight).

Upstream: identifies sequences proceeding in the opposite direction from expression; for example, the bacterial promoter is upstream from the transcription unit, the initiation codon is upstream from the coding region.

Universal Bases: nucleobase substitutes which bind to all four naturally occuring bases with equal strength.

Watson-Crick rules: the base pairing rules that underly gene structure and expression. G pairs with C and A with T (U in RNA).

Western blotting: transfer of proteins from a gel to a nitrocellulose filter on which they can subsequently be detected by immunological screening.

Wild type: the genotype or phenotype commonly encountered in the natural population or laboratory stock of a given organism.

Wobble hypothesis: accounts for the ability of a tRNA to recognize more than one codon by unusual (non-G-C, A-T) pairing with the third base of a codon.

Für Korrekturen, Ergänzungen und Bemerkungen wäre ich Ihnen dankbar!

Notizen:

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