Outline of Genetics
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Note: To look up references, see the Consciousness Bibliography, listing 10,000 books and articles, with full journal and author names, available in text and PDF file formats at http://www.outline-of-knowledge.info/Consciousness_Bibliography/index.html.

BIOL>Genetics

genetics

Genes and traits inherit {heredity} in patterns {genetics}|. Genetics is about genes, alleles, phenotypes, and regulation.

copy number

After DNA breakage, DNA repair can insert duplicated regions or leave out regions, resulting in more or fewer gene copies {copy number}|. Specific DNA locations can be more likely to break. Aging causes more copy-number variations. Different cells can have different gene copy numbers. Approximately 10% of genes have copy-number variations.

epigenetics
Inheritable proteins and RNAs regulate DNA {epigenetics}|. Chromatin has phosphate groups and ubiquitin, which can have reactions that alter gene expression. DNA methylation suppresses DNA transcription. Histones wound around DNA suppresses DNA transcription. Adding acetyl groups to histone tails allows DNA transcription. Removing acetyls suppresses DNA transcription.

eugenics
Hereditary qualities can improve by preventing undesirable-trait reproduction or by encouraging desirable-trait reproduction {eugenics}|.

one gene one enzyme
One gene codes for one polypeptide, which catalyzes one chemical reaction {one gene one enzyme one reaction hypothesis}.

BIOL>Genetics>Allele

allele
Genes can have variations. Alternative sequences {allele}| can be at genetic loci. Bateson and Saunders invented name [1902]. Different alleles make different polypeptides and produce different phenotypes, such as blood types O, A, B, and AB. Haploid organisms have one allele at each locus. For diploid organisms, one allele is from father, and one is from mother.

genotype
For one organism, all cells have the same gene alleles {genotype}|. Johannsen invented the word [1909].

haplotype
For one organism, all genes have the same gene alleles from one parent {haplotype}|. Algorithms {haplotyping} can identify such alleles.

wildtype
Gene alleles can be normal most-common alleles {wildtype}|.

BIOL>Genetics>Allele>Polymorphism

polymorphism DNA
DNA-sequence genetic loci {polymorphic locus} can have sequence variations {polymorphism, DNA}| {polymorphic variation}. For example, genes can have different alleles. Repeated sequences can have different numbers of repeats.

single nucleotide polymorphism
Sequence positions can have different nucleotides {single nucleotide polymorphism} {single-nucleotide polymorphism} (SNP). At genetic loci, alleles can differ by one nucleotide.

Restriction Fragment Length Polymorphism
Restriction endonucleases cut at different positions for different alleles at polymorphic loci, causing variations in DNA-fragment lengths {Restriction Fragment Length Polymorphism} (RFLP) (FLP). Cutting or non-cutting at restriction-endonuclease sites makes two short DNA fragments or one long DNA fragment.

BIOL>Genetics>Allele>Population Genetics

population genetics

Small populations, non-random breeding, and mutations can change allele frequencies in populations {population genetics}|.

balanced polymorphism
In populations, heterozygous and homozygous proportion tends to stay constant {balanced polymorphism}. Balanced polymorphism uses habitat efficiently and preserves variation. In isolated groups, gene ratios stay constant even if environment favors one allele.

gene frequency
For genes, populations have number of one allele divided by number of all alleles {allele frequency} {gene frequency}.

genetic drift
Small populations can have chance allele-frequency changes {genetic drift}|.

genetic gradient
If individuals have extreme genetic traits, general trait is in species {principle of genetic gradients} {genetic gradient principle}.

Hardy-Weinberg law
In geographic areas, allele frequencies are constant for species with stable populations {Hardy-Weinberg law}.

selection pressure
Allele-proportion change rate depends on allele reproductive advantage {selection pressure}| and on whether allele is recessive or dominant.

variation
Population allele ratio changes by heterozygote superiority, environmental heterogeneity, cycles, agonistic or antagonistic gene linkages, and homozygote selection.

balancing
Natural selection can maintain allele ratios {stabilizing selection} {balancing selection} to maintain variation. Balancing selection happens in large, non-isolated populations with alleles that are neither dominant nor recessive.

directional
Natural selection can change allele ratios {directional selection} {purifying selection} to reduce variation. Directional selection can happen by genetic drift or inbreeding in small isolated populations.

BIOL>Genetics>Allele>Segregation

heterozygous alleles
Homologous-chromosome genetic loci can have different alleles {heterozygous alleles}|. Population allele frequencies determine probability that individuals are heterozygous {heterozygosity}.

homozygous alleles
Homologous-chromosome genetic loci can have same allele {homozygous alleles}|.

pangenesis
Inheritance laws can depend on cell factors {pangenesis, cell}. Darwin invented the word [1868]. De Vries invented the word pangen.

BIOL>Genetics>Allele>Segregation>Law

Mendel laws
Trait inheritance uses regular processes {Mendel's laws} {Mendel laws}: law of segregation and law of independent segregation.

segregation of genes

For all genes, sperm and egg cells have one gene allele {segregation law} {law of segregation, Mendel}, from either father or mother.

independent segregation
Most gene segregations are independent {independent segregation law} {law of independent segregation}, because genes typically are not on same chromosome or are far apart on same chromosome.

BIOL>Genetics>Allele>Segregation>Dominant-Recessive

dominant allele
For heterozygosity, phenotypes can mix two allele traits {incomplete dominance}, one allele {dominant allele}| can determine phenotype, or both alleles can cause recessive trait.

recessive allele
For heterozygosity, one allele can be dominant and one allele {recessive allele}| can have no affect on phenotype, or both alleles can cause recessive trait.

BIOL>Genetics>Chromosome

chromosome
DNA, histone-protein, and acidic-nuclear-protein assemblies {chromosome}| contain genes and replicate. Waldeyer invented name [1888].
shapes
Prokaryotes have one circular chromosome. Eukaryotes have linear chromosomes.
pairing
In organisms with sexual reproduction, chromosomes have pairs, one from father and one from mother. Both pair members have same nucleotide sequences, except for natural allele variations or mutation damage.
number
Red blood cells have no nuclei. Germ cells have 23 chromosomes. Other human cells have 46 chromosomes, in 23 pairs. Ape somatic cells have 24 chromosome pairs. Two ape chromosomes fused to make human chromosome 2.
synteny
Different species can have chromosomes with same genes {conserved synteny}.
linkage
Different species can have same chromosome gene order {conserved linkage}.

Barr body
In female cells, one X-chromosome inactivates early in embryonic development and makes a nuclear body {Barr body}|. Xist gene makes active RNA that coats that X chromosome. Coated X also methylates. The other X-chromosome makes antisense RNA that binds Xist RNA.

chromatin
Stained cell-nucleus parts {chromatin}| show nucleic acid-protein complexes. Inactivated X-chromosomes have chromatin {macrochromatin} that differs in structure and appearance.

cytogenic map
Stained chromosomes show distinctive banding patterns {cytogenic map} under light microscopy.

homologous chromosomes
In diploid organisms, somatic chromosomes {homologous chromosomes}| from father and mother contain same gene sequence, except for natural allele variations or mutation damage.

sterility
Offspring from mating two different species cannot produce offspring {sterility}|, because the chromosome sets cannot interact.

telomere

In all mammals, in most animals, in some fungi, and in some protozoa, chromosome ends {telomere}| have TTAGGG repeated 2000 times. In plants, TTTAGGG repeats. In ciliates, TTTTGGGG or TTGGGG repeats. Telomeres are nucleoprotein complexes at chromosome ends and can have caps.

Chromosome copying starts just inside chromosome ends, so copies are shorter than copied chromosome. Telomeres decrease in length with each replication. Over a lifetime, humans make 150 copies and shorten telomeres by half. Telomerase enzyme restores telomere length in sperm and egg cells, and in cancer cells, using RNA as template for reverse transcriptase. Telomerase prevents shortening in human immune system, hemopoietic system, germline cells, embryonic cells, stem cells, skin cells, intestinal-lining cells, hair-follicle cells, and cancer cells.

After telomeres reach threshold length, cells can have senescence. Perhaps, telomere shortening ends at age 40, related to cell-turnover reduction.

Rodent cells do not have telomere shortening, stop dividing after 10 to 15 doublings, have telomerase, and grow indefinitely in culture.

BIOL>Genetics>Chromosome>Kinds

autosome

Chromosomes {autosome}| can be all chromosomes except X and Y.

polytene chromosome

In salivary glands, fruit flies have 1000 aligned chromosome copies {polytene chromosome}|.

BIOL>Genetics>Chromosome>Kinds>Sex

sex chromosome

X-chromosomes and Y-chromosomes {sex chromosome}| determine sexual characteristics.

male

Male cells have one X-chromosome and one Y-chromosome.

female

Female cells have two X-chromosomes.

genes

Sex-chromosome genes determine sex-linked traits and diseases, such as hemophilia and color blindness. Sex hormones influence some autosomal genes, such as baldness gene and horn gene.

crossing over

X-chromosome and Y-chromosome stopped crossing over in birds and mammals.

meiosis

Tips of Y recombine with tips of X, to allow meiosis.

evolution

Reptiles that led to mammals had two X-chromosomes. SRY gene arose 350,000,000 years ago. Between 320,000,000 to 240,000,000 years ago, ancient X-chromosome larger half, containing SRY, inverted or failed to recombine, making monotreme Y-chromosome. Between 170,000,000 and 130,000,000 years ago, a region on other centromere side inverted or failed to recombine, resulting in marsupial Y-chromosome. From -130,000,000 to -80,000,000 years ago, a large region on other centromere side inverted or failed to recombine, resulting in Eutheria Y-chromosome. From -50,000,000 to -30,000,000, a large region on other centromere side inverted or failed to recombine, resulting in human Y-chromosome. During this succession, SRY gene moved to other arm.

evolution: human

Y-chromosome variations track human migrations. M91 is only in south-Africa San people. Yap, M60, M2, MT68, M89M96, M35, M172, and M304 are in Africa. M170, M343, and LLY22 are in Europe. M9, M201, M17, M173, and M69 are in Near East. M20 and M45 are in India. M175, M174, and M122 are in southeast Asia. M130, M4, and M130 are in Pacific islands. M242 and M130 are in northeast Asia and Americas.

X-chromosome

Sex chromosomes {X-chromosome}| can have 2000 to 3000 genes. Mammals inactivate X-chromosome in females, to prevent overproduction from X genes. X-chromosome started to develop 300 million years ago.

Y-chromosome

Sex chromosomes {Y-chromosome}| can have 80 genes. Some genes are only on Y. SRY is for making testes and derived from SOX3 of X-chromosome. TTY2, CDY, PRY, DAZ, and BPY2 are for making sperm. Other genes are TTY1, TSPY, and XKRY.

Some genes are on X and Y. DBY, EIF1AY, RPS4Y, SMCY, TB4Y, USP9Y, UTY, and ZFY are for housekeeping. RBMY and VCY work only in testes. Others are PCDHY and AMELY.

One Y-chromosome end is 95% of Y-chromosome and has no functioning genes. Y-chromosome has palindrome structure.

BIOL>Genetics>Gene

gene

Heredity has fundamental physical and functional units {gene}. Johannsen invented the word gene [1909]. Genes are nucleotide sequences at chromosome positions. Genes code for proteins or RNAs {gene product} for regulation, structure, or transport. Genes controlling behavior are not qualitatively different from those governing other cell functions.

BMAL1 gene

Master genes {BMAL1 gene} can control timing. Superchiasmatic nucleus regulates waking and sleeping. Dorsomedial nucleus controls eating cycles.

CALHM1 gene

Genes {CALHM1 gene} can regulate neuron calcium concentration.

human accelerated region

Human DNA sequences {human accelerated region} (HAR1) (HAR2) can have rapid mutation compared to chimpanzees. HAR1 codes RNA. HAR2 (HACNS1) regulates wrist and thumb development.

IRGM gene

Genes {IRGM gene} can act against bacteria.

Ku70 gene

Genes {Ku70 gene} can make DNA-repair Ku70 transcription factors.

makorin1 gene

Worms, insects, and vertebrates have pseudogene-regulated genes {makorin1 gene}.

MECP2 gene

Gene {MECP2 gene} mutations can cause autism Rett syndrome.

metalloproteinase

Metal-dependent endopeptidases {metalloproteinase} can break down interstitial type I, II, or III collagen, basement-membrane type IV collagen, or type V collagen. Metalloproteinases {matrilysin} {PUMP-1 gene} can split extracellular matrix. Metalloproteinases {gelatinase A} {gelatinase B} split basement membrane. MMP-1 and MMP-13 split interstitial collagen. Metalloproteinase {stromelysin-3} (MMP-3) splits extracellular matrix.

Plasminogen activators and other serine proteinases activate metalloproteinases. Cells have tissue metalloproteinase inhibitors {TIMP gene}, such as TIMP-1, TIMP-2, TIMP-3, and TIMP-4.

multidrug resistance 1 gene

Genes {multidrug resistance 1 gene} {MDR1 gene} can make cell-membrane pumps that can send chemotherapy drugs out tumor cells.

Runx1 gene

Mice without a gene {Runx1 gene} do not sense heat or cold. Runx1 gene can affect neuropathic pain.

TRIM5alpha gene

Genes {TRIM5alpha gene} can stop PtERV1 from replicating.

Yellow gene
Drosophila genes {Yellow gene} can make black pigment. Without yellow genes, color is yellow.

BIOL>Genetics>Gene>Carbohydrate

AMY1 gene
Genes {AMY1 gene} can make salivary amylase to break down starch. Humans have many copies.

LCT gene
Genes {LCT gene} can make lactase to metabolize lactose.

lac repressor
Protein complexes {lac repressor} can block lactase-gene transcription. Lactose metabolites can bind to lac repressor and cause them to leave DNA, allowing gene transcription.

BIOL>Genetics>Gene>Blood

CETP gene
Genes {CETP gene} can control blood cholesterol-particle size.

CSE gene
Genes {CSE gene} can make enzyme that makes hydrogen-sulfide vasodilator.

Duffy gene
Human red-blood-cell surface genes {Duffy gene} can make part of Plasmodium receptor, in brain, spleen, and kidney.

gamma-glutamyl carboxylase
Enzymes {gamma-glutamyl carboxylase} can clot human blood, be in fruit flies, make cone snail venom, and participate in embryonic development. Carboxylase began at least 540 million years ago, when arthropods, mollusks, and chordates diverged, because arthropod, mollusc, and chordate gamma-glutamyl-carboxylase genes have similar introns, which direct protein folding. Therefore, introns began before 540 million years ago.

hypoxia-inducible factor
Transcription factors {hypoxia-inducible factor 1} {HIF-1 gene} can increase after hypoxia and cause increased red-blood-cell mass, blood-vessel growth, and increased ventilation.

selectin gene
Using sugar, proteins {selectin gene} can bind to white blood cells, to allow cells to leave blood and go into tissue.

tryptophan hydroxylase
Genes {tryptophan hydroxylase I gene} can make serotonin for blood.

BIOL>Genetics>Gene>Cell Death

AKT gene
Gene {AKT gene} products can aid cell suicide.

BCL-3 gene
Gene {BCL-3 gene} products can regulate cell death. Mutated gene causes lymphoma.

lethal gene
Gene {lethal gene} mutations can kill organisms, because gene no longer produces necessary enzyme.

p53 factor

Transcription factors {p53 factor} {p53 protein} can start apoptosis in damaged cells. When p53 gene mutates, gene product causes cancer.

SEPS1 gene
Genes {SEPS1 gene} can break down damaged proteins. Damaged proteins can cause inflammation.

BIOL>Genetics>Gene>Cell Cycle

archipelago gene
Gene {archipelago gene} (ago gene) (AGO gene) products {ago protein} can regulate cell cycle, cell-differentiation Notch signaling pathway, and Alzheimer's-disease beta-amyloid precursor protein (APP) processing pathway. Ago protein contains F-box domain and seven WD40 repeat motifs. F-boxes and WD40 repeats are typically in ubiquitin-ligase complexes of ubiquitin/proteasome proteolytic pathway.

F-box
F-box domain interacts with proteins {Skp1 protein} of protein complexes {SCF complex}. Organisms have many F-box proteins, with more than 100 in Caenorhabditis elegans roundworm, for example.

WD40
WD40 repeats interact with cyclin E and cyclin F. WD40 repeats have repeating units of 40 amino acids, with tryptophan, with symbol W, and aspartic acid, with symbol D, at defined positions.

LRR repeats
Leucine-rich repeats {LRR repeat} interact with cyclin E.

cyclin E
Ago protein recognizes cyclin E and catalyzes covalent ubiquitin-to-cyclin-E attachment. Ago protein decreases cell proliferation by this mechanism.

cyclin E gene
In Drosophila cell cycle, regulatory protein {cyclin E} can increase transition from gap-1 phase to S phase, which has DNA synthesis and replication. Cyclin E genes are tumor suppressor genes. Cyclin E problems can cause cancer. Elevated intracellular cyclin E levels increase cell proliferation.

BIOL>Genetics>Gene>Cell Cycle>Ubiquitin

ubiquitin proteasome proteolytic pathway
Protein-complex {ubiquitin ligase complex} substrate-recognition components are in proteolytic pathways {ubiquitin/proteasome proteolytic pathway}. Ubiquitination attaches 76-amino-acid peptides {ubiquitin, complex} to proteins. The 26S proteasome then degrades ubiquitin and protein. Ubiquitin/proteasome proteolytic pathway decreases cell-cycle-regulation, cell-proliferation, differentiation, and development proteins.

E1 gene
Ubiquitin/proteasome proteolytic pathway has ubiquitin-activating enzymes {E1 gene}.

E2 gene
Ubiquitin/proteasome proteolytic pathway has ubiquitin-conjugating enzymes {E2 gene}.

E3 gene
Ubiquitin/proteasome proteolytic pathway has ubiquitin ligases {E3 gene}, such as SCF types. Ubiquitin ligase connects cell-cycle protein to ubiquitin and controls protein level.

BIOL>Genetics>Gene>Cell Surface Receptor

cell surface receptor
Receptors {cell-surface receptor} can use hundreds of genes.

peptides
Cell-surface receptors can bind acetylcholine, glutamate, glycine, and gamma-aminobutyric acid and endorphin and enkephalin peptides. Acetylcholine binds to sodium-ion-channel receptor. Glutamate binds to NMDA receptor. Glycine

and GABA bind to chloride-ion-channel receptors. Receptor proteins using G proteins can couple to ion-channel proteins. Same-type receptors can have variable binding affinity and transport efficacy.

adrenergic receptor

Alpha-adrenergic and beta-adrenergic cell-surface receptors {adrenergic receptor} can bind epinephrine and similar compounds.

membrane

Amino ends are outside membranes, and carboxyl ends are inside membranes. Seven helices pass through membrane.

functions

Adrenergic receptors can couple to G protein. Adrenergic receptors can activate or inhibit adenylate cyclase to make or decrease cAMP.

functions: phosphates

Adrenergic receptors can activate phospholipase to break down inositol phospholipids in membrane into inositol triphosphate and diacylglycerol. Inositol triphosphate makes calcium vesicles release calcium ions, which bind to calmodulin, which regulates enzymes such as protein kinase. Diacylglycerol activates protein-kinase C proteins. Phosphorylation causes conformational changes that expose active sites and activate protein kinases. Protein phosphatases, such as cytoplasmic CD45 membrane protein, remove phosphates.

CD4 protein

Cell-surface receptor proteins {CD4 protein} can bind protein kinase at carboxyl ends inside membranes.

growth factor receptor

Cell-surface receptors {growth factor receptor} can bind growth factors. Growth factors activate 100 immediate early genes, which then make transcription factors.

structure

Growth-factor receptors pass one helix through membrane. Receptor is outside membrane. Kinase or cyclase is inside membrane.

types

Atrial naturietic peptide has protein kinase and guanylate cyclase. Activin receptor protein has serine-threonine kinase. Phosphoprotein phosphatase has tyrosine phosphatase. Growth factor receptor has tyrosine kinase.

hormone binding receptor

Cell-surface receptors {hormone binding receptor} can bind hormones. Hormone-binding receptors affect G proteins inside cell membranes. G proteins use GTP to activate adenylate cyclase and make cAMP. cAMP affects protein kinase A, which then phosphorylates transcription factors, such as CRE-binding protein, that bind to cAMP response elements (CRE).

nicotinic cholinergic receptor

Muscle-synapse cell-surface receptors {nicotinic cholinergic receptor} can bind acetylcholine. Nicotinic receptors have membrane alpha-helix pores. Acetylcholine binds to two alpha helices. Four genes make protein receptors. Gene alleles have different mRNA splicings, making many slightly different nicotinic cholinergic receptors.

steroid receptor

Cell-surface receptors {steroid receptor} can bind steroids. Steroids can cross membranes and bind to steroid-receptor proteins inside cells, allowing them to move to cell nucleus.

BIOL>Genetics>Gene>Cell Surface Receptor>Binding

G protein

Cell-surface receptors can bind hormones and affect GTP-binding proteins {G protein} inside cell membranes. Activated G protein catalyzes its return to unactivated state, thus timing rate of G-protein processes. Immediate-early genes activated in learning use cAMP signal paths.

cyclic AMP

G protein uses GTP to activate adenylate cyclase and make cAMP. cAMP affects protein kinase A, which then phosphorylates CRE-binding protein, which binds to cAMP response elements (CRE).

senses
Olfactory sensors use G-protein transduction.
structure
G protein is similar to proteins for cross-membrane signaling, protein synthesis, cell molecule transport, and cross-membrane transport.

hormone-response element
Steroid-receptor proteins bind to regulatory-region 15-base sequences {hormone-response element}, for activation or repression.

ionophore
Chemicals {ionophore} can artificially raise cell calcium concentration.

plasminogen activator
Serine proteinases {plasminogen activator} can have cell-surface receptors. Urokinase plasminogen activator (uPA) can activate matrix metalloproteinases. Plasminogen-activator inhibitors counteract tissue plasminogen activator (tPA).

rhodopsin
Retina rod-cell proteins {rhodopsin}| can absorb light and bind GTP to transducin, which activates phosphodiesterase, which breaks down cGMP, which closes cGMP-dependent ion channels and so causes hyperpolarization. Rhodopsin is similar to adrenergic receptor. Opsin proteins are similar to rhodopsin, because both use 11-cis-retinal as chromophore. Absorption maximum differs for opsins and rhodopsin.

transducin
GTP-binding proteins {transducin} can transduce signals in eye.

von Willebrand factor type A
ATR protein, matrilins, integrins, and other cell-surface protein-interaction proteins have extra-cellular domains {von Willebrand factor type A}.

BIOL>Genetics>Gene>Development

development genes
Genes {development genes} can control development. Serotonin affects early embryo development, and mother supplies it before fetus can make it.

histone deacetylase
Genes {histone deacetylase 4 gene} (HDAC4) can regulate muscle and bone development and maintain rod and bipolar cells.

immediate early gene
Genes {early-response gene} {immediate early gene} can respond first to stimulation and then trigger later changes.

master control gene
Homeobox and other genes {master control gene} can start gene-expression chains.

Pitx1 gene
Stickleback-fish gene {Pitx1 gene} products can affect pelvic fin and other structures.

BIOL>Genetics>Gene>Development>Signaling

Notch gene
Gene {Notch gene} products can activate signaling pathways and regulate whether neural precursors become neurons or glia. Enzymes cleave Notch and APP transmembrane proteins in membrane plane {regulated intramembrane proteolysis}, to liberate cytosolic fragments, which enter cell nucleus to control gene transcription. Regulated intramembrane proteolysis is similar from bacteria to humans.

Bmi-1 gene
Gene {Bmi-1 gene} products can activate signaling pathways.

Wnt gene
Gene {Wnt gene} products can activate signaling pathways.

BIOL>Genetics>Gene>Development>Homeobox Gene

homeobox gene
Homeodomain binding proteins have one helix in DNA major groove and another helix across DNA that contacts other proteins. Fruitfly homeotic genes {homeobox gene} control head, jaws, teeth, thorax, and abdomen development and contain 180-base control regions {homeobox} that have helix-turn-helix {homeodomain} sequences, which are in many development genes. Regulatory region has 200,000 bases total.

retinoic acid
Extracellular-fluid retinoic acid controls homeotic-gene expression by binding to cell receptors and builds spinal cord, hindbrain, eye, and limbs. Low concentrations start gene expression at forebrain, and then higher concentrations start gene expression in sequence down to tail.

hormone
Thyroid hormone has similar receptors and controls gene expression.

homeotic series
Human Hox gene and other homeobox development genes {homeotic gene} can have sequences {homeotic series} along chromosomes. First gene is for mouth/nose, and last gene is for tail. Earliest homeobox genes were 1, 2/3, 4, 5, 6/7/8, and 9/10/11/12/13, in sequence. Fruit flies have 1, 2/3, 4, 5, 6, 7, 8, and 9/10/11/12/13. Fruit flies have non-homeobox region of DNA between 6 and 7. Chordates have 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, and 13. Vertebrates have chordate-set variants on four different chromosomes.

BF gene
Mammal genes {BF gene} can control gut, liver, and lungs. BF genes are similar to forkhead genes. BF-1 enlarges nasal retina and dorsal forebrain and is where neurons start dividing {germinal zone} before migrating. BF-2 enlarges ventral forebrain and temporal retina.

empty spiracles gene
Mammal Emx-1 and Emx-2 genes {Emx gene} enlarge cerebrum, including corpus callosum. Fruitfly genes {empty spiracles gene} are similar.

engrailed gene
Fruitfly genes {engrailed gene} can have homeoboxes but not be in homeotic gene sequence for body development. In most vertebrates, En-1 and En-2 genes, similar to engrailed gene, control midbrain and cerebellum growth.

forkhead gene
Fruitfly genes {forkhead gene} can develop gut beginning and end.

Hox gene
Vertebrate genes {Hox gene} can be similar to fruitfly homeobox genes. If Hox genes are missing, symptoms are similar to DiGeorge congenital disease. Hox-b1, Hox-b2, Hox-b3, Hox-b4, and Hox-b5 genes enlarge hindbrain from third rhombomere down.

Lim-1 gene
Genes {Lim-1 gene} can enlarge forebrain, midbrain, cerebellum, and first two or three hindbrain rhombomeres.

Otx gene
Genes {Otx gene} can affect brain development. Otx2 protein is for head development in embryo. After birth, it signals eye coordination.

Pax6 gene
Genes {Pax6 gene} can affect halteres balancing-wing development. Pax genes also affect eye and brain development.

tailless gene
Fruitfly genes {tailless gene} can develop gut beginning and end. Tailless gene enlarges forebrain, retina, and olfaction receptors.

BIOL>Genetics>Gene>Development>Polarity

maternal-effect gene
At fertilization, genes {maternal-effect gene} from mother can code for transcription factors that establish front-to-back and top-to-bottom embryo polarity: bicoid protein, nanos protein, and dorsal gene protein transcription factor.

bicoid protein
Proteins {bicoid protein transcription factor}, at only one pole, can make top-to-bottom gradient across embryo {morphogen, bicoid}. Nanos is at one pole, and bicoid is at other pole.

nanos protein
Proteins {nanos protein transcription factor}, at only one pole, can make top-to-bottom gradient across embryo. Nanos is at one pole, and bicoid is at other pole.

dorsal gene protein transcription factor
Maternal-effect follicle-cell genes can code for transcription factors {dorsal gene protein transcription factor} that establish front-to-back embryo polarity. Factor is similar to rel protein and NF-kappaB. Factor concentrates in cell nucleus ventrally, and cytoplasm dorsally, in all embryo cells. Cactus gene and Toll gene can partition dorsal-gene-protein transcription factor to these cell locations.

BIOL>Genetics>Gene>Development>Segmentation

gap gene
After first cell divisions, genes {gap gene} {hunchback gene} {hunchback-maternal gene} {knirps gene} {Kruppel gene} can code zinc-finger transcription factors that make bands along embryo and body regions by working with maternal-effect genes and by repressing each other. Gap genes also regulate genes expressed later. Transcription-factor binding sites are high-affinity or low-affinity, so transcription-factor concentration affects which genes transcribe and how much, leading to gradients and bands. In small regions, same chemicals cause different effects.

segmentation gene
After gap-gene expression, genes {segmentation gene} can code for transcription factors that segment body, pair segments, and make segment polarity. Segmentation genes work with gap-gene products, and interact with each other using autofeedback, to sharpen segment boundaries. Segmentation genes include pair-rule genes, such as fushi tarazu gene, even-skipped gene, hairy gene, runt gene, and eve gene.

pair-rule gene
Segmentation genes {pair-rule gene} {eve gene} {even-skipped gene} {fushi tarazu gene} {hairy gene} {runt gene} can be about splitting body regions. In small regions, same chemicals cause different effects.

segment polarity gene
Genes {segment polarity gene} can be about front and back. In small regions, same chemicals can cause different effects.

BIOL>Genetics>Gene>Eating

FTO gene
Genes {FTO gene} can have alleles related to obesity.

NCoR gene
Gene {NCoR gene} products can regulate fat-metabolism genes.

PTP1B gene
Hypothalamus proteins {PTP1B gene} can affect leptin signaling inside cells.

SOC3 gene
Hypothalamus proteins {SOC3 gene} can block leptin receptors.

BIOL>Genetics>Gene>Growth

ERK factor
Gene products {ERK factor} can be for cell growth.

MEK factor
Gene products {MEK factor} can be for cell growth.

NEGR1 gene
Genes {NEGR1 gene} can affect hypothalamus neuron growth.

NF-kappaB factor
Transcription factors {NF-kappaB} can be for cell growth and cytokine production.

p16INK4a gene
Mice genes {p16INK4a gene} can regulate cell growth and regeneration. With age, protein increases, and cells regenerate less.

RSK factor
Transcription factors {RSK factor} can be for cell growth.

SOS gene
Gene {SOS gene} products can be for cell growth.

BIOL>Genetics>Gene>Immunity

Fox gene
Fox-01, Fox03, and Fox04 transcription factors {fox factor} {Fox gene} are for glucose metabolism and cell defense.

orai 1 gene
Gene products {orai 1 protein} can be in T-cell calcium-ion channels.

siglec proteins
Proteins {siglec proteins} can prevent immune-system cells from activation.

BIOL>Genetics>Gene>Intoxication

intoxication genes
Genes {intoxication genes} can affect intoxication.

ADH2 gene
Genes {ADH2 gene} can prevent alcoholism in some East Asians by affecting alcohol metabolism.

ALDH2 gene
Genes {ALDH2 gene} can prevent alcoholism in some East Asians by affecting alcohol metabolism.

cheap date gene
Alcohol affects fruitfly genes {cheap date gene}.

CHRM2 gene
Genes {CHRM2 gene} can affect alcohol use.

DRD2 gene
Genes {DRD2 gene} can relate to alcoholism.

GABRA2 gene
Genes {GABRA2 gene} can affect alcohol use.

slo-1 gene
C. elegans genes {slo-1 gene} can code for neuron, muscle-cell, and gland-cell BK potassium-ion-channel proteins. Alcohol affects BK-channel.

BIOL>Genetics>Gene>Ion Channel

ATP1A2 gene
Genes {ATP1A2 gene} can code for membrane sodium-pump and potassium-pump proteins.

CACNA1A gene
Genes {CACNA1A gene} can code for P/Q calcium-channel protein.

SCN1A gene
Gene {SCN1A gene} codes for sodium-channel proteins.

BIOL>Genetics>Gene>Muscle

MyoD gene
Transcription factors {MyoD gene} can be for muscle development and repair.

POP3 gene
Genes {POP3 gene} can build striated muscle. POP2 and POP3 are also in plants.

BIOL>Genetics>Gene>Nerve

cFos gene
Immediate-early genes {cFos gene} can make proteins that are neuronal activation markers.

clathrin gene
Trimer proteins {clathrin triskelion} {clathrin gene} can have tetrahedron shapes at corners of presynaptic-nerve-ending icosahedral neurotransmitter-release structures.

Dscam gene
Genes {Dscam gene} can guide axon growth.

Eph gene
Genes {Eph gene} can build brain topographic maps.

neurogenic gene
Notch, split enhancer, big brain, mastermind, and neuralized genes {neurogenic gene} can make cell-adhesion, signal-transduction, membrane-channel, and transcription-factor cell-to-cell signal proteins, to develop cells and inhibit nearby cells.

neurotrophic factor

After making neurons, genes {neurotrophic gene} can code for secreted proteins {neurotrophic factor} that keep neurons alive, differentiate neurons, and make neurotransmitters, such as nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), CNTF, and NT-3. Other genes code for neurotrophic-factor receptor proteins.

proneural gene
After head and tail develop, daughterless and achaete-scute genes {proneural gene} can code for helix-loop-helix transcription factors that make neural precursor cells to start brain development. da enhances achaete-scute, and emc inhibits it.

reelin gene
Vertebrate genes {reelin gene} can affect axon branching and synapse creation.

Robo gene
Genes {Robo gene} can affect axon travel between hemispheres.

selector gene
Cut and other genes {selector gene} can code for homeobox transcription factors that make neuron types.

BIOL>Genetics>Gene>Nerve>Behavior

FOXP2 gene
Chromosome-7 genes {Forkhead box P2 gene} {FOXP2 gene} can have a mutation [-100000] associated with speech and language problems. Neanderthals also have this allele.

Fru gene
Fruitfly genes {Fru gene} can affect courtship rituals.

stathmin gene
Amygdala proteins {stathmin} can affect fear.

BIOL>Genetics>Gene>Nerve>Brain Size

ASPM gene
Genes {ASPM gene} can help control brain size.

MCPH1 gene
Genes {MCPH1 gene} can help control brain size.

CDK5RAP2 gene
Genes {CDK5RAP2 gene} can help control brain size.

CENPJ gene
Genes {CENPJ gene} can help control brain size.

BIOL>Genetics>Gene>Plant

hothead gene
One base change in a recessive gene {hothead gene} can cause fused petals, but Arabidopsis thaliana mustard plant can revert to wild type.

POP gene
Plants have POP2 and POP3 genes {POP gene}.

terminator gene
Genes {terminator gene} can make proteins {ribosome inhibitor protein} that kill seeds.

BIOL>Genetics>Gene>Respiratory Chain

cytochrome b gene
Nuclear genes {cytochrome b gene} can make mitochondrial respiratory-chain proteins.

cybS
Nuclear genes {cybS gene} {SDHD gene, cytochrome} can make small cytochrome-b subunits. cybS protein is in mitochondria protein complexes {mitochondrial complex II} {succinate-ubiquinone oxidoreductase}, which are in electron transport chains.

Perhaps, cybS genes are tumor suppressor genes, because they are typically not in bladder, breast, cervix, stomach, lung, and ovary cancers or in melanomas. Perhaps, cybS protein is in carotid-body oxygen-sensing system. Without cybS protein, chronic hypoxic stimulation causes cell proliferation. Solid tumors are typically hypoxic compared to normal tissues.

PGC-1alpha regulator
Regulators {PGC-1alpha regulator} {PGC gene} can develop muscles by controlling respiration.

SDHD gene
Nuclear genes {SDHD gene, mitochondria} can make mitochondrial respiratory chain proteins, which are small cytochrome-b subunits.

BIOL>Genetics>Gene>RNA

RNA gene
Genes {RNA gene} can make rRNA, tRNA, microRNA, RNA-protein enzyme complexes such as RMRP, and riboswitches.

riboswitch
In bacteria, long RNAs {riboswitch} have aptamer ends that bind to other molecules to act as sensors and other ends {expression platform, riboswitch} that change structurally, by making and unmaking hairpins, to affect protein translation or RNA transcription.

TRAP complex
Protein complexes {TRAP complex} can bind tryptophan mRNA and inhibit tryptophan-gene transcription and mRNA translation.

BIOL>Genetics>Gene>Sex

DAX gene
X-chromosome genes {DAX gene} can tend to suppress SRY gene {sex-chromosome drive}. Y-chromosome is too small to reduce such suppression.

sexually antagonistic gene
Maleness or femaleness genes {sexually antagonistic gene} cluster together and do not work in other sex. Maleness or femaleness genes are in different chromosomes in birds and mammals.

Sry gene
Y-chromosome genes {Sry gene} can control testes development and so testosterone production. Sry gene starts masculinization. Human SRY differs greatly from ape SRY, but has had few mutations.

BIOL>Genetics>Gene>Transcription Factor

ELT gene
Nematodes transcription-factor ELT-3, ELT-5, and ELT-6 genes {ELT gene} are active in youth. ELT genes are more active in old age. ELT genes are similar to human GATA transcription factors.

GATA gene

Human transcription-factor genes {GATA gene} can be active in youth. Nematode ELT genes are similar to GATA transcription factors.

BIOL>Genetics>Gene>Transcription Factor>Pluripotency

c-myc gene
Transcription-factor genes {c-myc gene} can restore pluripotency to cells.

Klf4 gene
Transcription-factor genes {Klf4 gene} can restore pluripotency to cells.

Oct4 gene
Transcription-factor genes {Oct4 gene} can restore pluripotency to cells.

Sox2 gene
Transcription-factor genes {Sox2 gene} can restore pluripotency to cells.

BIOL>Genetics>Generation

geneaology
Individuals have ancestors {pedigree} {family tree} {geneaology}|.

back cross
Children or grandchildren can breed with parents {back cross}|.

inbreeding
In isolated populations, genetically similar individuals can breed {inbreeding, population}|. Continual inbreeding can result in species varieties in which all individuals are essentially genetically identical. 10% gene flow prevents too much inbreeding and keeps human populations from differentiating into new species.

isolating mechanism
Geographic isolation {isolating mechanism}, ecology, and genetic factors can increase interbreeding.

BIOL>Genetics>Generation>Generations

F1 generation
First filial generation {F1 generation} is children of parents.

F2 generation
Second filial generation {F2 generation} {grandchildren} is children of children.

filial generation
Parental generation can have children {filial generation}, grandchildren, and so on.

parental generation
Males and females {parental generation} can start reproductive lines.

BIOL>Genetics>Genome

genome
Organisms have all genetic material in chromosomes {genome, genetics}|. Typical animal cells express 4,000 to 10,000 genes. Humans have more than 30,000 genes. Two unrelated people differ in 100 to 5000 genes. Human genes differ from chimpanzee genes by one percent. Humans have 85,000 different mRNAs.

Transposable elements are 45% of human DNA. Non-coding DNA is 24% of human DNA. Structural DNA is 20% of human DNA. Repeated sequences are 10% of human DNA.

Protein coding genes are 1% of human DNA. 42% of genes have not been characterized. 14% are nuclear transcription factors. 12% are messengers. 10% are enzymes. 5% are miscellaneous. 5% are structural. 5% are for molecular transport. 3% are cell-surface proteins. 3% are tumor-suppressor genes. 1% are immune-system proteins.

People have 5 x 10^9 nucleotides. Unrelated people differ by 5 x 10^5 nucleotides.

genomics

Genes have sequences, functions, regulation, and interactions with themselves and environment {genomics}|. Computational tools can identify genes, inducers, binding sites, structures, and relations between nucleic acid and protein sequences.

proteomics

Protein study can depend on genes {proteomics}|. Proteomics involves post-translational modification, protein folding, and protein-protein interactions. 10 to 20 million different human proteins are possible.

metabolomics

Human bacteria and humans make many chemicals {metabolomics}. Human bacteria and humans make many chemicals in response to stress {metabonomics}.

Human Genome Project

Projects {genome, human} {Human Genome Project} sequenced human DNA.

purposes

From nucleotide sequences, experimenters can determine gene number, types, and relations. They can identify functional regions, coding regions, pseudogenes, and loci. They can identify regulatory regions, such as promoters, enhancers, silencers, trans-activating factors, transcription factors, and transcription-factor receptors. They can identify splicing sites, such as RNA splicing sites and alternative splicing sites. They can identify repeat regions, such as simple repeats like STR, complex repeats like Alu, or coding-triplet repeats. They can identify translocations and DNA-rearrangement signals. They can identify three-dimensional structure sites. They can identify antigen response sites. They can identify sites involved in polymorphism, disease, and development.

evolution

Experimenters can find racial, cultural, geographic, and individual variations. They can identify evolutionary regions, such as orthologues or dot matrices. They can trace human DNA evolution. They can define heredity traits and study questions about environment role {nature vs. nurture debate}.

questions

Should fetal tissues be research tools?

Should society allow changes to germ cells? How much diversity should society maintain and how much should society try for perfection? Which eugenics program is best, if any? Do parents have right to choose children gender?

Who owns information about genes, regions, or proteins, and is it patentable? Who owns genetic materials and data?

Who can access genetic information: relatives, governments, insurance, and/or employers? How can people have privacy?

Should gene therapies modify behavior? Should society screen everyone for genetic diseases or traits? Is it ethical to have disease diagnosis without available treatment? Should society allow children to have genetic defects, and what are defects? Are treatment costs important factors?

Is anyone liable for genetic makeup or behavior consequences? Does or will genetic defects cause social stigma?

How much education about genetic issues is practical and/or useful?

BIOL>Genetics>Genome>Ploidy

ploidy

Genomes have numbers of homologous somatic chromosomes {ploidy}, such as haploid and diploid. Triploid organisms have three. Tetraploid organisms have four. For sex-linked chromosomes, ploidy can differ between males and females.

haploid

Cells {haploid}| can have one chromosome set, rather than two. Sperm and egg cells {germ cell} are haploid. Bacteria have one gene copy, because they are asexual. However, they have as many different traits and trait variations as sexual organisms.

diploid
Somatic cells {diploid}| can have two chromosome sets. Sexual reproduction contributes one chromosome set from each parent.

polyploidy
Many organisms have more than two chromosome sets {polyploidy}|. Haploids and diploids can make extra chromosomes or chromosome parts. Insects typically have more than two chromosome sets.

BIOL>Genetics>Linkage

linkage of genes
Same-chromosome alleles or RFLP markers tend to inherit together {linkage}| {genetic linkage} {linkage group} in meiotic recombination, mitotic replication, and prokaryote binary fission. Closer markers are less likely to separate during DNA recombination and so are more likely to inherit together. Linkage frequency depends on distance between loci.

finding distance from linkage
Known genetic linkages show relative loci distances. Distances are in centimorgans. Markers less than five centimorgans have less than 1 in 20 chance to separate.

allelic association
Alleles at neighboring genetic loci can more frequently associate than expected from allele frequency and genetic linkage {linkage disequilibrium} {allelic association}. Algorithms can identify linkage disequilibrium.

centimorgan
Units {centimorgan} (cM) can measure recombination frequency. One centimorgan is 1% chance that, at one crossing over, marker at one genetic locus separates from marker at second locus. In humans, one centimorgan is one million base pairs.

DNA mapping
Chromosomes have gene locations {DNA mapping}.

chromosome separation
Cell-sorting machines can sort chromosomes. Alternatively, people can separate chromosomes using microscopes and fine instruments. Human cells treated with x-rays can fuse with mouse cells to isolate chromosome pieces, to map with markers {radiation hybrid mapping}. Two-dimensional electrophoresis using variable fields can separate DNA fragments up to three million bases {pulsed field gel electrophoresis} (PFGE), over several days.

protein removal
Proteolytic enzymes remove protein from chromosomes held in gels, leaving DNA.

DNA fragments
NotI, MluI, NruI, and SfiI restriction enzymes have eight-base sites and cut DNA in few places, to make million-base DNA fragments.

methylation
Tissues can have methylated sites, allowing fewer cuts and larger fragments, so researchers must compare different tissues. Large fragments have further processing.

cloning
YACs allow cloning hundred-kilobase DNA fragments. Phages and cosmids allow cloning 40000-base DNA fragments, for genomic libraries.

separation
From clones, electrophoresis separates restriction fragments by size.

markers
Genetic markers can find loci.

hybridization
20-base oligonucleotide probes can hybridize with DNA. Probes can have minor-groove binder to enhance exact hybridization, allowing shorter probes. Probes hybridize with clone DNA fragments. Overlapping DNA fragments hybridize to same probe. Clone-fragment sequence-tagged connector ends hybridize to probes.

sites

Using unique primers, processing identifies unique 200-base to 500-base sequence-tagged sites, which have known locations.

overlapping

DNA fragments overlap to build longer sequences {contig, DNA}, to sequence chromosome DNA.

hitch-hiking natural selection

Neutral or disadvantageous gene mutations can survive if they are adjacent to advantageous genes {hitch-hiking natural selection}.

liability class

Complex genetic diseases divide into different onset ages and/or different disease severities {liability class}. This can increase genetic-linkage information by accounting for phenocopy traits, whose appearances are similar but have different causes. Categories have different phenocopy rates. Phenocopy rates increase as onset age increases and as severity decreases.

locus of gene

Genes and other markers are at relative or absolute chromosome positions {locus, gene}| {loci} {genetic locus}.

LOD score

Individual marker traits have probabilities. Probabilities differ for linkage or no linkage. Values {LOD Score} can measure linkage degrees in families by estimating recombination fraction: base-10 logarithm of ratio between probability assuming linkage and probability assuming no linkage. In LOD-score analysis, disorders can make complex patterns.

Transmission Disequilibrium Test

Testing father, mother, and child to establish genetic linkage and association {Transmission Disequilibrium Test} (TDT) can find linkage disequilibria.

BIOL>Genetics>Mutation

mutation

Chemicals, radiation, and copying and repairing errors can cause chromosomal DNA-sequence damage {mutation}|. People can inherit changed genotypes.

types

Single nucleotides, short regions, genes, and chromosomes {muton} can mutate. Mutations include nucleotide deletions, insertions, and changes {point mutation}. Mutations include chromosome number or structure changes. DNA regions can delete, insert, invert, double, and alter.

rate

Trait mutation rate is 10^-4 to 10^-6 per generation. One to ten percent of cells have mutations.

affects

Mutations are typically bad, but bad mutations can be good in new environments. Mutations degrade good, working genetic code to make it more variable, and this process adds to genetic variability. Higher mutation rates affect organisms with more genes more.

experiments

In animals or plants, to discover if genes {candidate gene} relate to diseases, researchers mutate genes to see if mutation causes disease symptoms.

error catastrophe

Higher mutation rates typically cause poorer adaptation {error catastrophe, mutation}.

maternal inheritance

Modified plant genes can go only to ovules {maternal inheritance}, not to pollen.

silent mutation

Codons, with same first two bases but different third base, can code for the same amino acid. For those codons, third-base mutations {silent mutation} do not make any difference to survival.

However, different codons bind to different t-RNAs, and some t-RNAs are more abundant than others. Times to bind scarcer t-RNA are longer than times for more abundant t-RNA. Time differences can affect protein folding, change protein structure, and affect function.

Silent mutations can accumulate and eventually encode new proteins. For example, mutations can cause body-part replication. Subsequent generations can modify replicated parts to make new structures and functions.

BIOL>Genetics>Mutation>Experiments

in vitro mutagenesis

Gene changes can help identify which genes are performing which functions.

process

Plasmids and other vectors can have genes. Added chemicals or enzymes can mutate genes {in vitro mutagenesis}. Vectors go into hosts, express genes, and make protein.

methods

Gene changes can be at restriction endonuclease sites. If sites have overhanging strands, S1 nuclease can remove overhanging single-strand DNA, or DNA polymerase can extend shorter strands, to make blunt ends. Linkers can attach to blunt ends.

Chemicals can alter gene nucleotides. Sodium bisulfite makes C into U. Hydrazine and formic acid delete nucleotide nitrogenous base, leaving sugar and phosphate. At low nucleotide concentrations or in harsh chemical conditions, DNA polymerase can add wrong nucleotides during DNA synthesis.

site-directed mutagenesis

In vitro mutagenesis {site-directed mutagenesis} can study binding sites and functional regions. Site-directed mutagenesis hybridizes synthetic 10-base to 15-base oligonucleotides to DNA sites. Oligonucleotides differ from original sequences by one nucleotide at end. Oligonucleotides hybridize well to original sequences, because they differ by only one nucleotide. Hybridized sequences replicate to make mutated genes.

enzymes

DNA ligase connects perfectly aligned DNA strands. Mutated ends do not ligate {ligase-mediated}, showing mutation locations. RNase A cuts DNA-RNA complexes where sequences mismatch and can detect mutation locations. Osmium tetroxide and hydroxlamine cut at unmatched C or T bases. Restriction enzymes fragment single-strand DNA. Different DNA fragments have different conformations and so different mobilities {single-stranded conformation polymorphism} (SSCP).

BIOL>Genetics>Nucleic Acid

mRNA storage granule

Near synapses, neurons have granules {mRNA storage granule} to provide mRNA for synapse connections. Animal egg-cell mRNA storage granules provide mRNA for early development.

small nuclear RNA

RNA {small nuclear RNA} (snRNA) can have sequences complementary to intron 5' sequences.

BIOL>Genetics>Nucleic Acid>Silencing

small silencing RNA

RNA interference, microRNA, and piRNA {small silencing RNA} silence genes.

RNA interference

After viral genes or mobile genetic elements express, double-stranded RNA can catabolize their mRNA {RNA interference} {RNAi}. When extra gene copies insert into organisms, double-stranded RNA suppresses expression.

short interfering RNA

Dicer enzyme hydrolyzes double-stranded RNA to make 22-base-pair double-stranded RNA {short interfering RNA} {small interfering RNA} (siRNA). siRNA has unpaired nucleotides at ends. Proteins {Argonaute protein} can bind to siRNA ends. siRNA unlinks its two strands. One strand binds to proteins {RNA-inducing silencing complex} (RISC). RISC tries to bind to mRNA. If binding is good, Slicer enzyme splits mRNA, which leaves RISC. If binding has short mismatched regions, mRNA stays bound to RISC. Both cases have no translation.

evolution
RNAi began in plant, animal, and fungi common ancestor, one billion years ago, to protect against viruses and mobile genetic elements.
experiments
Using RNAi, researchers can destroy gene mRNA and study results.

microRNA
RNAi can regulate growth and development using regulatory double-stranded RNA {microRNA} precursors, which Dicer makes into microRNA. MicroRNA has same metabolism as siRNA. Two hundred microRNA genes include JAW, lin-4, and let-7. Small RNA and protein numbers are approximately the same.

piRNA
RNA {piRNA}, with 25 to 30 nucleotides, binds to Piwi protein in mammal male germ cells, especially at meiosis, making 20000-base to 90000-base clusters {piRNA complex} (piRC). Piwi protein is homologous to Argonaute protein.

BIOL>Genetics>Nucleic Acid>Regions

3' end
DNA-sequence ends {3' end} can have expressed sequence tags. At 3' ends, ESTs accumulate, end within 10 bases of each other, and overlap near polyadenylation consensus sequence, after coding region and before polyA terminus. 3' ends are within last 1500 bases of transcript 3'-UTR.

cap of nucleic acid
Nucleic acids have 5' ends {cap, nucleic acid}.

cistron
DNA sequences {cistron}, typically having several genes, can underlie biochemical functions.

complementary DNA
Messenger RNA can be templates for single-stranded DNA synthesis {complementary DNA} (cDNA). cDNA corresponds to cell-DNA exons.

complementary RNA
RNA {complementary RNA} (cRNA) can transcribe from single-stranded DNA.

exon
Gene regions {exon} transcribe as mRNA sequences. Exons are not introns. Functional mRNAs have spliced exons, with intron regions removed.

intron
Genes have regions {intron} that are not for translation. Introns can affect protein folding.

open reading frame
DNA sequences {open reading frame} can code for one mRNA, because they have no stop codons until end.

polyA tail
Poly(A) polymerase adds 100 to 300 adenosines {polyA tail} to 3' ends. Perhaps, polyA tails block RNAse.

junk DNA
DNA contains repetitive sequences, introns in gene-coding regions, untranslated sequences 5' and 3' to gene-coding regions, pseudogenes, and transposed regions {junk DNA} {selfish DNA}. Almost all DNA is non-coding junk DNA. Over time, species can gain and lose junk DNA.
repeats
Most junk DNA is repetitive. Species have distinctive repetitive sequences. Repetitive regions change in cancer and cell growth.

Satellite DNA has 100 bases. Minisatellite DNA, such as GGGCAGGAXG, has 10 to 20 bases, is at 1000 loci, has 5 to 50 repeats, and initiates gene swapping. Microsatellite DNA has less than 20 bases.

Alu repeats are only in primates, repeat million times in different locations, are 10% of DNA, have internal promoter, and are similar in sequence to ribosome gene.

B1 repeats are in mice.

LINE-1 repeats contain reverse transcriptase, are 15% of DNA, and have a hundred thousand copies.

introns

Humans and other highly evolved species tend to have more, longer, and more-complex introns.

untranslated regions

5' and 3' untranslated regions contain enhancers and suppressors and regulate protein translation. Humans and other highly evolved species tend to have longer and more-complex 5' and 3' untranslated regions.

transposition

Retroviruses and bacteria cause transposition. DNA transposition rate in primates is lower than in mice. Immune responses use transposition.

language

Junk DNA statistically appears to have sequence patterns with characteristics similar to patterns in language. Junk sequences can be codes for processes that control signal transmission, gene expression, protein alteration, or other processes that use information.

pseudogene

Many non-functional DNA regions {pseudogene} are similar in sequence to actual genes, such as ribosome genes. Reverse transcription can incorporate host or foreign mRNA into DNA {processed pseudogene} {retropseudogene}, using RNA-mediated retroposon transposition. Mutations can make pseudogenes. Pseudogenes can have copies and repeats. They can harbor RNA sequences. Pseudogenes can represent information to turn off or turn on. Species have distinctive pseudogene patterns.

BIOL>Genetics>Nucleic Acid>Regions>DNA Repeat

DNA repeat all

In eukaryotes, important genes and satellite DNAs repeat {DNA repeat, genetics}. Eukaryotes have many repeated or duplicated DNA regions. Histone, rRNA, tRNA, and other genes that are fundamental to cell processes repeat many times in same chromosome regions {clustering, chromosome}.

gene duplication

Gene duplication allows variant protein forms to arise. Original gene still provides needed protein. Duplicate gene can mutate and recombine to make variant protein, such as globin chains. Duplication can revert, by gene conversion after sequence break, using normal sequence as template to repair mutant sequence.

satellite DNA

Besides repeated and duplicated genes, eukaryote genomes have many short, often tandemly repeated sequences {single-sequence DNA} {satellite DNA} of 5 bases to 200 bases.

delta element

Yeast has retrotransposon Ty elements, which contain reverse transcriptase, whose direct repeats or long terminal repeats {delta element} have promoters.

microsatellite DNA

Simple tandem repeats {simple tandem repeat} (STR) {microsatellite DNA}, like repeated CA, vary in repeat number. Mononucleotide, dinucleotide, trinucleotide, or tetranucleotide tandem repeats, such as CA dinucleotide repeats, with differing lengths, are in all chromosomes. DNA markers can have mononucleotide, dinucleotide, trinucleotide, or tetranucleotide repeats in tandem arrays, such as CA or GT dinucleotide repeats. Perhaps, they distribute throughout genomes. Microsatellites can aid genetic mapping. Simple tandem repeats can have polymorphism.

variable-number tandem repeat

Minisatellite DNA tandem repeats {variable-number tandem repeat} (VNTR) between restriction sites {hypervariable loci} can vary in repeat length and repeat number and are useful for DNA fingerprinting. Forensics, cell

cultures, and family relationship tracing can identify individuals. Large-enough polymorphism sets can provide high probabilities that identifications are unique. Myoglobin-gene introns, mitochondrial DNA, and class II HLA gene DQalpha test for polymorphisms in forensics.

BIOL>Genetics>Nucleic Acid>Regions>DNA Repeat>Interspersed

short interspersed element
Satellite DNA, found only in vertebrates, can have 130-base to 300-base repeats that are not tandem {short interspersed element} (SINE). RNA polymerase III transcribes SINEs. SINEs include Alu repeats. Human genome has one million Alu repeats. SINE-repeat sequences entered genomes by transposition.

long interspersed element
Satellite DNA, found only in vertebrates, can have long repeats {long interspersed element} (LINE) that are not tandem. LINE repeat sequences entered genomes by transposition.

BIOL>Genetics>Nucleic Acid>Regions>DNA Repeat>Minisatellite

minisatellite DNA
Satellite DNA {minisatellite DNA} can have 10-base to 100-base sequence that tandem repeats 20 to 50 times. In all chromosomes, 10-nucleotide tandem repeats, with differing lengths, often cluster near telomeres. Minisatellite DNAs do not transcribe. At genome locations, repeat number gradually evolves, so individuals have different repeat numbers.
uses
Minisatellite DNA can be for genetic mapping. Minisatellite DNA lengths are unique to individual and can be for identification by DNA fingerprinting.

DNA fingerprinting
Minisatellite DNA lengths are unique to individuals {DNA fingerprinting}, for identification. At genome locations, repeat number gradually evolves, so individuals have different repeat numbers.

BIOL>Genetics>Nucleic Acid>Regions>Regulation

operon
Genes and cistrons have control regions {operon}, where repressors bind to prevent transcription.

repressor gene
Genes {repressor gene} can make repressors, which bind to operator regions.

operator region of gene
Repressors bind to operon regions {operator region} that precede coding regions.

promoter region
RNA polymerase binds to regions {promoter region} just before coding regions. Repressors block RNA polymerase binding. Derepressors can bind to repressors at allosteric sites to release repressors from operators. Corepressors can bind to repressors to aid repression. Inducers can bind to repressors to block repression.

zinc finger
RNA-polymerase-III 50-base internal-control regions have two regions {zinc finger} that bind zinc.

primer DNA
Oligonucleotides {primer DNA} can start polymerization by DNA polymerase.

CpG island
Repeated CGs {CpG island} can be in regulatory DNA.

BIOL>Genetics>Phenotype

phenotype
Organism physical, biochemical, and physiologic traits {phenotype}| result from genotype and environment interactions. Johannsen invented the word [1909]. Organisms can express behavior and structure genes. Some phenotypes confer better fitness and adaptation. Offspring phenotypes are typically intermediate between parent phenotypes.

roles
Phenotypes can have adaptations, be pleiotropes, have neutral fitness, or have exaptations.

expressivity
Gene phenotypes vary in expression {expressivity}.

homeosis
New species come from repeated-body-segment structure and number changes. Modifications are similar to existing parts {homeosis} {homeotic transformation}. Parts can have jumps. For example, upper thoracic vertebrae can have no ribs, or lower cervical vertebrae can have ribs.

penetrance
Gene phenotypes have expression ranges {penetrance}.

phenocopy
Traits {phenocopy} can have appearance similar to other traits but have different causes. Phenocopy rate increases as onset age increases and as severity decreases.

phenotypic variance
Genotypes and environments vary phenotypes {phenotypic variance}.

pleiotropism
One gene can control more than one phenotype {pleiotropism}|.

trait in genetics
Organism functions and behaviors {trait}| have genetic determinants. Tasting phenylthiocarbamide and other traits can depend on only one gene.

BIOL>Genetics>Phenotype>Roles

exaptation
Structures can arise and then later have purposes {exaptation, role}.

spandrel
Phenotypes can be adaptation side effects {spandrel, phenotype}, because they are pleiotropic.

BIOL>Genetics>Phenotype>Gene Interactions

gene interactions
Genetic traits typically interact {gene interaction}, allowing different optimum conditions or gene combinations. Environments and other-gene effects can suppress gene potentials. Most genes act differently depending on other-gene actions. Gene changes can affect individuals, families, troops, groups, demes, populations, and species. Genes that favor adaptability at more than one level are reinforcing. Genes that favor one level but harm another level are counteracting.

polygenetic trait
Most traits {polygenetic trait}, such as intelligence and personality, depend on multiple genes. Learning and environment affect polygenetic phenotypes more.

polygenic inheritance
Independent genes can add {polygenic inheritance} effects to make phenotypes, such as skin color and height.

BIOL>Genetics>Phenotype>Gene Interactions>Complementary

complementary genes
Independent genes can interact to produce phenotypes. Independent dominant genes {complementary genes} can interact to determine phenotype.

supplementary genes
Independent genes can interact so one dominant allele is complementary but other dominant allele is not complementary {supplementary genes}, such as in albinism or skin color.

BIOL>Genetics>Phenotype>Mixtures

atavism
Earlier traits can reappear in modern organisms {atavism}|.

chimera genetics
Animals {chimera}| can have parts or genes from other animals.

mosaicism
In individuals, different phenotypes can express at different body locations {mosaicism}| {mosaic, genetics}. Individuals can have male or female tissues, where one allele prevails.

recidivism
Lower-organism phenotypes can appear in individuals {recidivism}|.

BIOL>Genetics>Phenotype>Phenotypic Laws

idiographic law
individual regularity {idiographic law}.

nomothetic law
species regularity {nomothetic law}.

BIOL>Genetics>Plant

plant genetics
Plants have asexual and sexual reproduction, and plant cells have chromosomes {plant genetics}. Plants make many seeds, so seed generations have many mutations and recombinations. Many plants have polyploidy, allowing more variation.
cloning
Electroporation and tungsten bullets can introduce DNA fragments into plants. The small flowering-plant weed Arabidopsis thaliana can clone genes.
cloning: expression
Plants can express oils and seed proteins. Plants can add drought and frost resistance. Plants can become able to fix nitrogen.
insects
Plants can protect themselves from insects. Bacillus thuringiensis sporulation makes protein crystals that kill many insect larvae. Tomato, potato, and cowpea serine-protease inhibitors inhibit serine protease in insect intestines.
weeds
Weeds grow faster and so use more chemicals than regular plants. Plant-killing chemicals inhibit growth mostly in weeds, but other plants have affects. Herbicide-tolerant plants have enzymes that break down herbicides, increase herbicide-targeted enzymes, or have mutated enzymes that herbicides cannot affect. Bacteria can have enzymes that break down herbicides.

petal gene

Ultrapetala gene {petal gene} controls petal number by modifying meristem cell number.

BIOL>Genetics>Plant>Disease

geminivirus
Double-stranded plant DNA viruses {geminivirus} can hold foreign genes for cloning in plants.

BIOL>Genetics>Plant>Disease>Crown Gall Tumor

crown gall tumor
Agrobacterium-tumefaciens Ti plasmids cause tumors {crown gall tumor} in dicot plant cells. Agrobacteria have genes that make proteins that hold bacteria on plants.

Ti plasmid
Agrobacterium-tumefaciens large, circular, DNA plasmids {Ti plasmid} can cause crown gall tumors. Ti plasmids carry genes and antibiotic marker genes into plant leaf cells, in the leaf-disk technique. Ti-DNA sequences can insert into dicot-plant-cell chromosomes. Ti DNA codes auxin enzyme.

vir gene
Regenerating-plant-cell molecules activate Ti-plasmid genes {vir gene}, which make trans-acting proteins to transform cells to tumors. After vir genes start making proteins, cells release transposable elements with 25-base border ends as single-strand DNAs {T-DNA}.

opine amino acid
T-DNA codes for special amino acids {opine, amino acid} that other Ti enzymes break down for food.

auxin enzyme
Ti DNA codes enzymes and hormones {auxin enzyme} {phytohormone} that together cause tumor-cell division.

BIOL>Genetics>Plant>Regeneration

callus of plant
Plant tissue {callus, plant}| can cover wounds. Callus cells can make new plants. Different callus cells from the same plant callus make different plants {somaclonal variation}, because gene expression differs.

edge cell
After cutting leaves, edges regenerate using special cells {edge cell}.

protoplast
Removing cell walls from plant embryo cells, with fungal cellulase, leaves cells {protoplast}| surrounded only by plasma membrane. Protoplasts can start new plants.

selfed
One plant can make new plants {selfed}|, because plants can self-fertilize.

BIOL>Genetics>Post-Transcription

post-transcription
After transcription {post-transcription}, eukaryotic mRNA can change. For example, poly(A) polymerase adds 100 to 300 adenosines as a polyA tail to RNA 3' ends. Methylated guanosine can add to RNA 5' ends.

adenosine-to-inosine editing
RNA can alter {adenosine-to-inosine editing} (A-to-I editing), especially in primate Alu repeats.

methylation

To regulate gene expression, cell or virus mechanisms can add methyl groups {DNA methylation} {methylation} to cytosines preceding guanines {CG pair}.

virus

Virus can methylate host genes to inactivate them.

cancer

Cancer genes often have demethylated cytosines in promoters.

drugs

Valproic acid tranquilizer and decitabine chemotherapy agent remove methyl groups from DNA or prevent methylation. Procaine affects DNA methylation.

purposes

Researchers methylate nucleotides to prevent cutting by restriction enzymes. Promoter methylation can suppress gene expression.

post-translation

After translation {post-translation}, proteins can add side groups, go to special locations, and bind to lipids, sugars, and proteins.

recoding

Cells, perhaps only neurons, can substitute RNA bases at three-dimensional loops {recoding}.

reverse transcriptase

Enzymes {reverse transcriptase} can make DNA from RNA, typically making mRNA into cDNA. Hundreds of genes code enzymes that can make DNA from RNA.

RNA catalyst

RNAs can be catalysts {RNA catalyst}.

RNase-P RNA part splits tyrosine-tRNA precursor to make tRNA.

Fungus-mitochondria mRNA and rRNA precursors, and bacteriophage mRNA precursors {Class I self-splicing}, can catalyze themselves to remove introns, using guanosine as cofactor. Introns have further processing to make different RNA catalysts.

Yeast and fungus mitochondria mRNA precursors, and Chlamydomonas chloroplast mRNA precursors {Class II self-splicing}, can catalyze themselves to remove introns, using no cofactors.

Some protozoa edit transcribed RNA to make correct reading frames, possibly using RNA catalysts.

Mammals edit intestine transcribed apolipoprotein B mRNA, possibly using RNA catalyst.

BIOL>Genetics>Post-Transcription>Restriction Enzyme

restriction enzyme

Enzymes {restriction enzyme} can cleave nucleotide sequences at sites. 150 enzymes {endonuclease}, such as FokI and NotI, cut DNA near 4-base to 8-base recognition sequences.

ends

Restriction enzymes can leave ends {blunt end} with paired bases or ends {sticky end} with overlaps. Sticky ends can bind to other sticky ends and then DNA ligase can seal them, allowing splicing with other DNA fragments. Blunt ends can become sticky by terminal transferase, which adds polyA or polyT to one strand. Blunt ends can become sticky by attaching a DNA linker, with recognition sites, to blunt ends and then cleaving with restriction enzyme.

middle

Endonucleases cut nucleic acids at sequence sites not at end. Pancreatic ribonuclease, T1 ribonuclease, and other ribonucleases cut only RNA. Bacterial restriction endonucleases and other deoxyribonucleases cut only double-stranded DNA.

exonuclease

S1 nuclease {exonuclease} pares back RNA and single-stranded DNA ends. Sticky ends can become blunt ends by removing single-stranded DNA using S1 nuclease.

BIOL>Genetics>Post-Transcription>Splicing

RNA splicing

Genes that make mRNA have exon regions for translation and intron regions not for translation.

introns

RNAs typically have several introns. Introns came from bacteria or, if protein folding requires them, have always been in genes. After transcription, mechanisms {RNA splicing}| splice introns out.

exons

Exons typically are functional domains, and proteins have different functional domains. Exons can mix in different ways to make membrane-bound or secretable proteins or to make proteins for different development stages or different tissues.

process

After mRNA leaves cell nucleus, cell processes splice out introns and join exons {mRNA splicing}, to make mRNA for translation. Introns have 5' sequences and 3' sequences.

spliceosome

Large ribonucleotide and protein particles {spliceosome} perform splicing. Spliceosomes have U1 and U2 small nuclear ribonucleoproteins, U1 and U2 small nuclear ribonucleic acids, and SF2, U2AF, and other proteins. Intron 5' ends split first. Intermediate RNAs have lariat shapes, because introns bind to themselves with 2'-5' bonds. Enzymes cut 3' ends, and other enzymes join exon ends. Introns leave as lariats, because introns bind to themselves with 2'-5' bonds to make circles.

splicing regulatory protein

Proteins {splicing regulatory protein} (SR protein) can determine which exons to keep, by binding to exonic splicing enhancer (ESE) or exonic splicing suppressor (ESS). SR protein is for fruitfly sex determination.

alternative splicing

Protein actions can block RNA 5' sites after transcription, allowing only other splicing sites {alternative splicing}. Alternative splicing results in different-size and different-function proteins.

self-splicing RNA

RNAs can splice pieces together, using mechanisms {self-splicing RNA} different than spliceosomes.

BIOL>Genetics>Post-Transcription>Transposition

transposition of DNA

DNA sequences {transposon, DNA} can excise themselves and then insert at other genome locations {transposition, DNA}|. Transposons code for enzymes that recognize DNA splice sites.

methylation

Methylation inactivates transposons.

bacteria

Bacteria have Tn3 and Tn10 transposons with DNA insertion sequences (IS). Tn3 transposons code enzymes that act at transposon-resolvase sites to allow recombination, so they copy themselves, place copies at new sites, and leave originals.

bacteria: Agrobacterium

Agrobacterium infects plants with Ti plasmid.

yeast

Yeast has Ty elements, whose delta-element direct repeats have promoters. Ty elements contain reverse transcriptase.

Yeast MAT genes have mating-type alleles. Yeasts have two mating types, a and alpha. After mating, mating type changes to opposite mating type, as HO endonuclease cuts MAT site. a-gene and alpha-gene copies are far from MAT sites. Copies are templates to reconstruct MAT site as opposite mating type {gene conversion} {replicative transposition}.

Yeast sterile (STE) genes code for a and alpha pheromones, which stop cell growth and change cell shape. Pheromones combine both mating types to form diploids, causing yeast to mate. STE proteins are G-protein subunits (STE4) (STE18), protein kinases, and transcription factors (STE12). STE proteins (STE2) (STE3) can bind factors.

maize

Maize has Ac and Ds transposable elements.

retrovirus
Retroviruses have direct repeats with promoters and contain reverse transcriptase to allow transposition.
trypanosome
Trypanosomes use gene conversion to vary surface glycoproteins (VSG).
fruitfly
Drosophila have P elements. Drosophila have copia elements, which have direct repeats with promoters.

transposon
Fruitfly P elements and other transposition elements can code for enzymes that recognize DNA splice sites. By opening and closing splice sites, genes {transposon, genetics} {jumping gene} can excise and insert between any two splice sites.

retroposon
Reverse transcriptase can make DNA {retrotransposon} {retroposon} from RNA, and DNA can insert back into genome at special sites. Virus-gene fragments can copy themselves and insert in genomes. DNA from retrovirus RNA {human endogenous retrovirus} (Hervs) is 1% of human genome.

transposase
All species have 750-base to 5000-base sequences that code for enzymes {transposase} that recognize DNA sites just beyond both transposase-gene ends.
process
Sites have 10-base to 40-base inverted repeats. Transposase enzymes recognize inverted repeats and cut out transposase-gene sequence between sites. Transposases recognize inverted repeat at other locations in genomes, plasmids, or phages and cut sequence to place transposase-gene sequence in those locations. If two transposons are near each other, transposases can cut at the farthest ends and both transposons, and any DNA between them {complex transposon}, can transpose as one sequence to inverted repeats at other locations.

BIOL>Genetics>Algorithms

gene expression algorithm
Gene arrays can test for gene expression {gene expression, algorithms}.
array algorithms
Gene-expression-array algorithms automatically find background, errors, fiducials, normalization, signal values, spatial cross-talk, spots, replicate aggregates, and clustering.
gene expression analysis
Gene-expression analysis compares different tissues or conditions to find gene-expression patterns. Genes in the same biochemical pathways, genes with similar chemical reactions, and genes for similar cell processes have similar regulation and have similar gene-expression patterns.
gene expression visualization
To visualize expression patterns, expression spaces can have dimension number equal to experiment number. Experiments determine gene-expression ratios, which are expression-space points or vectors. Similar genes have points that cluster near each other in expression space.
Expression matrices have column number equal to experiment number. Gene-expression ratios are expression-matrix rows. Algorithms sort rows and columns to cluster up-regulated and down-regulated genes and/or experiments. Expression-matrix cells can have colors, such as red for up-regulated, green for down-regulated, and black for control levels.
cluster analysis
Using distance measures, genes and/or experiments can cluster. Clustering algorithms include hierarchical, self-organizing maps, K-means, fuzzy C-means, and expectation maximization. Statistical techniques identify gene classes and/or experiment classes and assign shared features. Hierarchical clustering makes hierarchies. Self-organizing maps group equal categories. Error-weighted gene-expression clustering retrofits clustering algorithm information to use error-propagation information.
assay multiplexing
Several assays can be simultaneous, or several samples can be in same wells {multiplexing, assays}.

BIOL>Genetics>Algorithms>Sequence Alignment

BLAST algorithm
Basic Local Alignment Search Tool {BLAST algorithm} searches sequence databases for similar sequences.

ClustalW
Algorithms {ClustalW algorithm} can align multiple sequences.

Comparative Sequencing Analysis
Nucleotide or amino-acid sequences can align {Comparative Sequencing Analysis} (CSA).

FASTA
Algorithms {FASTA algorithm} can search sequence databases for similar sequences.

MSA2.1 algorithm
Algorithms {MSA2.1 algorithm} can align multiple sequences.

Smith-Waterman algorithm
Nucleotide and amino-acid sequences can align using algorithms {Smith-Waterman algorithm} {Gotoh-Smith-Waterman algorithm} or filtering algorithms {Chang-Marr algorithm} {Filtered Smith-Waterman algorithm}.

BIOL>Genetics>Recombinant DNA

recombinant DNA
Restriction-enzyme techniques can recombine nucleic-acid sequences {recombinant DNA}|.

BIOL>Genetics>Recombinant DNA>Sample

sample of DNA
Experiment assays can analyze physical substances {sample, DNA}. Samples come from subjects.

aliquot of sample
Diluting main sample {aliquot}| creates secondary samples.

parent sample
Samples {parent sample} can make aliquots.

logging of samples
Sample information is in databases {logging}.

replicate of sample
Most experiments test samples by the same method more than once {replicate, sample}|.

BIOL>Genetics>Recombinant DNA>Amplification

DNA amplification
Techniques {amplification, DNA} {DNA amplification} can increase number of DNA-fragment copies. In vivo amplification amplifies repeat sequences in fragile X syndrome. In vitro amplification uses cloning or polymerase chain reactions.

purposes
Amplified DNA indicates mutations, translocations, viral and bacterial infections, sex, genealogy, living and extinct species differences, and forensic identification.

DNA synthesis
To make probes or primers, first blocking-group covers 5' or 3' hydroxyl groups of two nucleotides. Then other two hydroxyl-groups react to make phosphodiester bonds. Then acid or base removes blockers. Process repeats to elongate chain.

Amplified Fragment Length Polymorphism

After restriction-enzyme digestion, DNA fragments can amplify, and relative lengths indicate polymorphisms {Amplified Fragment Length Polymorphism} (AFLP).

cuvette

After electrophoresis, DNA fragments flow in transparent tubes {cuvette}|, and lasers excite dyes.

hybridization of DNA

Two complementary DNA or RNA single strands can form a double-stranded molecule {hybridization, DNA}|. Two nucleic-acid strands can pair by hydrogen-bonding A and T, or A and U in RNA, and C and G. DNA or DNA and RNA complementary-strand nitrogenous bases can have hydrogen bonding.

arrays

All array spots have hybridization, as cartridge holds array in position. Hybridization measurement depends on dye sensitivity and dynamic range. If array spots are close together, they can cross-hybridize. Evaporation also causes problems, so arrays have humectants, lids, or dewpoint controls. Spotting pins must be 0.2 mm small and clean. Alternatives to spotting include acoustic focusing, multi-nozzle piezoelectric jets, and continuous solid pin spotting. Probes, cDNA arrays, and oligonucleotide arrays are alternative hybridization methods.

polymerase chain reaction

Methods {polymerase chain reaction}| (PCR) can make many DNA-sequence copies using heat-stable polymerase, 20-base primers complementary to + strand at one sequence end, and 20-base primers complementary to - strand at other end. Synthesized strands are additional templates, so process doubles copies each primer-annealing, strand-elongation, and dissociation cycle.

purpose

PCR can detect defined sequences in DNA samples. PCR can make stutter bands and add bands resulting from extra nucleotide addition by Taq polymerase.

mRNA amplification

DNA has small amounts, but mRNA has much larger amounts. First, reverse transcription converts mRNA to cDNA and then PCR amplifies cDNA (RT-PCR).

DNA amplification

Machines heat DNA double helix to 94 C for several minutes to make single-stranded DNA. Solution contains DNA polymerase from heat-tolerant organisms and the four bases.

When temperature lowers to 30 C to 65 C for 30 seconds, 20-nucleotide primer DNA binds to DNA, outside region to copy. One primer is for 5' strand, and one primer is for 3' strand. Annealing puts complementary 20-base primer at both ends.

Machines raise temperature to 72 C for some minutes, to allow DNA polymerase and bases to extend both primers beyond other primer region. Now both double-helix molecules have primer on one end and extend beyond other primer on other end. Elongating both strands uses heat-stable DNA polymerase, which synthesizes DNA.

Machines heat DNA to 94 C for several minutes again to extend same primers through other primer at strand ends. Now all synthesized-strand lengths are the same, from one primer through other primer. There are now four DNAs.

Cycles make twice as many DNA strands, and process uses new and old strands again, making chain reactions. Repeating process 30 to 60 times makes millions of copies.

primers

Primers can be genome repetitive sequences, such as Alu repeats. Alu repeats are 300 bases, but smaller region varies little in humans. Alu repeats are in both directions.

primers: nested

After one PCR, second primer that binds inside copied sequence {nested primer} can amplify shorter sequences.

primers: concentration

If one primer has high concentration and one has low, system makes mostly single-stranded DNA {asymmetric PCR}, with no chain reaction.

contamination

Contamination with wrong DNA is common. Negative controls make sure correct DNA amplifies.

BIOL>Genetics>Recombinant DNA>Amplification>DNA Sequence

adapter sequence
Sequence tags {adapter sequence} are in probes.

oligonucleotide
Single-stranded DNA sequences {oligonucleotide}| {oligo} can have less than 61 bases.

primer for nucleic acid
To add deoxyribonucleotides to nucleic acid by DNA polymerase requires oligonucleotides {primer, DNA}|.

probe for nucleic acid
Short RNAs or single-stranded DNAs {probe, DNA} {DNA probe} can detect complementary base sequences by hybridization. Probes have 25 to 60 bases and can have 3'-hexyl-amine. Probes attach to last 1500 base pairs closer to transcript 3' ends, where genes have unique short DNA regions. Bacteria and yeast genes have unique primers. Higher organisms have three million different expressed sequence tags (EST).

process
High-concentration purified probes are in 96, 384, or 1536 wells on plastic microtiter plates. Robots take probes from microtiter plate to make same number of spots on glass slides, one slide for each RNA sample to test. Multiple probes test each gene.

zipcode
Nucleotide sequences {zipcode} can attach to molecules to allow probe complementary nucleotide sequence {zipcode complement} to hybridize.

BIOL>Genetics>Recombinant DNA>DNA Sequencing

DNA sequencing
Genomes can have known sequences {DNA sequencing}. H. influenzae has 1.8 million bases and 800 genes. E. coli has 4.5 million bases and 2000 genes. Saccharomyces yeast has 12 million bases and 6000 genes. P. falciparum has 30 million bases and 6500 genes. Caenorhabditis elegans roundworm nematode has 100 million bases and 10000 genes. Arabidopsis thaliana weed has 120 million bases and 20000 genes. Drosophila melanogaster fruitfly has 165 million bases. Fugu rubripes is zebrafish. Mus musculus mouse has 3000 million bases. Humans have 3500 million bases and 30000 genes.

methods
Sequencing {plus-minus method} can elongate DNA sequences using DNA polymerase.

Sequencing {Maxam-Gilbert sequencing method} can chemically degrade labeled, short DNA chains at G, C, A and G, and T and C to make fragments and then electrophorese all four, separately or together, to separate by size.

Sequencing {Sanger sequencing method} can elongate DNA chains and randomly terminate them with nucleotides that cannot bind to next ribose, using A, G, T, and C 2',3'-dideoxynucleoside triphosphates, and then electrophoreses all four, separately or together, to separate by size.

Mixing differently labeled clones {multiplex DNA sequencing} allows easier processing. Labels identify clones.

DNA-fragment ends can have fluorescent dyes, which respond to laser light. Dye terminator attaches to nucleotide 3' ends. Dye primer attaches to 5' ends. Longer fragments have higher signals. Fragments separate by electrophoresis in gels {horizontal ultrathin gel electrophoresis} (HUGE) or capillary tubes {capillary gel electrophoresis}. Because charges are equal, fragments leave gel or tube by size.

Scanning tunneling electron microscopes can sequence DNA strands by wand distance needed to maintain constant voltage. They can sequence 40000-base DNA fragments one base at a time. Exonuclease removes end nucleotide. Shining laser light and recording with photomultiplier reads nucleotide type.

Gas or liquid mixtures can separate using gas chromatography, liquid chromatography, supercritical fluid chromatography, or capillary electrophoresis.

contig
Computers overlap sequence information about DNA fragments {contig, sequencing} to build longer sequences, to map large fragments and then chromosomes.

dendrogram
Cluster hierarchies can look like tree diagrams {dendrogram, sequencing}.

DNA library
If many DNA fragments insert into many bacteria, plate colonies can account for all DNA fragments {DNA library} from foreign organisms.

homology in DNA sequence
DNA analyses include comparing DNA sequences. Sequences of same gene from different organisms can align somewhat {homology, DNA}| {homologous sequences}.

BIOL>Genetics>Recombinant DNA>DNA Sequencing>Sites

sequence-tagged connector
Probes hybridize with clone and fragment regions. Overlapping DNA fragments hybridize to same probe. 20-base oligonucleotides can be probes to find overlapping DNA fragments. For clone ends, random sequences can be probes {sequence-tagged connector} (STC). Probes can have minor-groove binder to enhance exact hybridization, allowing shorter probes.

sequence-tagged site
Processing identifies unique 200-base to 500-base sequences, with unique primers, from known locations {sequence-tagged site} (STS). Perhaps, clones share STS.

BIOL>Genetics>Recombinant DNA>DNA Sequencing>Dye

electropherogram
After DNA fragments exit capillary, plot {electropherogram} shows relative dye concentration versus time expressed as frame number. In electropherograms, small peaks {pull-up peak} can appear under main dye peaks. Incorrect dyes, dye contamination, or capillary or fluid-property changes after spectral calibration can cause pull-up peaks.

DNA labeling
In direct methods, mRNA-AAAAA + reverse transcriptase + Oligo-dT Primer + dNTPs + Cy3 and Cy5 or SymJAZ dye-dNTP -> Dye-cDNA {DNA labeling}.
In random priming methods, mRNA + reverse transcriptase + T7-T20-24 + MuLV -> DNA/RNA + hydrolysis -> cDNA first strand + Bst DNA polymerase + ligase + pN8-9 -> T7-ds cDNA + dye-UTP + T7 RNA polymerase + IVT -> labeled cRNA.
In RNase H methods, mRNA + reverse transcriptase -> DNA/RNA + RNase H -> DNA/RNA + DNA polymerase + ligase -> T7-ds cDNA + dye-UTP + T7 RNA polymerase + IVT -> labeled cRNA.
purposes
DNA labeling can measure labeled-cRNA dye incorporation, reverse-transcriptase conversion, fluorescence-specific activity, minimum RNA, maximum RNA, IVT amplification, total amplification, and length.
controls
Control reagents aid spot finding, image analysis, and signal quantification. Array probes monitor spotting, labeling, hybridization, printing, attachment, and features. Labeling controls monitor enzyme activity, target stability, and dye incorporation during labeling protocols. Hybridization controls monitor mixing, stringency, and washing during array-hybridization protocol. Printing and attachment controls monitor array manufacturing, probe attachment, and lot-to-lot variability. Feature controls normalize signal variability.

BIOL>Genetics>Recombinant DNA>DNA Sequencing>Overlap

chromosome walking
DNA analyses include finding sequences longer than cloned DNAs by looking for their overlaps. First clone can screen whole-genome clone library for overlapping sequences. If overlap, second clone can screen, and so on, to build longer and longer sequences {chromosome walking}.

polony sequencing
DNA sequencing can use modified shotgun methods {polony sequencing}.

BIOL>Genetics>Recombinant DNA>DNA Sequencing>Separation

fragment analysis
DNA-fragment mixtures can separate fragments by lengths {fragment analysis}.

lane on gel
Electrophoresis gels have band sequences {lane}, starting from top sample bands.

fragment separation
Electrophoresis separates eluted DNA fragments, to compare peak separations, spectral separations, and spatial separations {fragment separation}.

retention time
Compounds less soluble in stationary phase elute faster {retention time, elution}.

BIOL>Genetics>Recombinant DNA>DNA Sequencing>Blotting

Northern blotting
DNA analyses can separate cell RNAs or mRNAs on gels and transfer gel-band contents to filters, where RNAs can hybridize to known RNA or cDNA sequences {Northern blotting}. Northern blotting compares mRNAs to cDNAs to study gene expression.

Southern blotting
DNA analyses can separate DNA fragments on gels and transfer gel-band contents to filters, where DNA fragments can hybridize to known DNA sequences {Southern blotting}. Southern blotting can detect gene rearrangements that make antibodies and T-cell receptors. It can detect disease-caused gene rearrangements and deletions. It can detect related genes in organisms and homologous genes from different species. It can detect mRNA-splicing-caused intron removal and exon use. It can detect mRNA splicing to make alternative proteins. It can detect nested genes.

BIOL>Genetics>Recombinant DNA>Gene Expression

gene expression
DNA transcription makes tRNA, rRNA, and mRNA {gene expression}|.
purposes
Gene expression studies gene functions, regulation, and interactions. Hybridization measures gene expression for gene discovery, gene identification, biochemical pathways, and disease mechanisms.
probes
Human-genome arrays have probes for all genes. Human-transcriptome arrays have probes for all transcripts. SNP arrays have all SNPs. Arrays can have immune, toxicity, or cancer-gene probes.

antisense RNA
RNA or single-strand DNA oligonucleotides {antisense RNA}|, complementary to cell mRNAs, can bind to mRNA and prevent gene expression. Antisense RNAs can be in vectors, or techniques can inject them into cells.

expressed sequence tag
300-base to 500-base sequences {expressed sequence tag} (EST) are specific to expressed gene regions, typically at 3' ends. ESTs map gene chromosomal locations from several tissues, recover corresponding gene sequences by electronic-database similarity searching, and retrieve complete cDNA clones for further analysis. Whole-genome shotgun sequencing using EST assembly reduces redundancy and creates longer consensus sequences.

expression ratio
For gene-probe spots and dyes, software calculates ratios {expression ratio} {gene expression ratio}: normalized expression level divided by normalized expression level for control gene. Average expression ratio is 1. If expression ratio is greater than or equal to 2 {up-regulated, expression} or less than or equal to 0.5 {down-regulated, expression},

genes have significant expression {differentially expressed}. Expression-ratio base-two logarithm averages 0, is +1 if expression ratio is 2, and is -1 if expression ratio is 0.5.

gene distance
Gene similarity measures can be distances {gene distance} between expression vectors in expression space.
metric
Distances can have metrics {metric distance}. Distance can always be positive. Distance between point and itself can always be 0. Euclidean distance between two points can always be less than or equal to sum of distance from first point to third point and distance from third point to second point {triangle rule}.
metric: Euclidean distance
Euclidean distances can be differences in point coordinates. Euclidean distances are metric.
semi-metric
Distance measures {semi-metric distance} can be always positive and have distance between point and itself always zero, but not obey triangle rule.

scaling method
To emphasize variation amounts, especially for timed experiments, methods {scaling method} can reduce large expression-ratio values by changing expression-ratio range. Scaling can set average logarithm to zero {mean centering}, by subtracting baseline value. Scaling can adjust logarithm range to -1 to +1. Scaling can normalize expression-vector magnitudes to 1.

serial analysis of gene expression
Gene-expression technologies can use cell extracts from different tissues, same tissues under different conditions, or same tissues under same conditions, over time sequences {serial analysis of gene expression} (SAGE) {expressed RNA}. From RNA, two cell extracts from same tissues under same conditions can make first-strand cDNA labeled with fluorescent dye, one with Cy3 and one with Cy5. Purified labeled cDNA solution soaks slides at optimum temperatures for times. Robots measure slide-spot probe-DNA and labeled-cDNA hybridization.

BIOL>Genetics>Recombinant DNA>Gene Expression>Regulation

down-regulated
Compared to control level, genes can have less expression {down-regulated, gene}. Less expression under same conditions indicates similar biological functions.

up-regulated
Compared to control level, genes can have more expression {up-regulated, gene}. More expression under same conditions indicates similar biological functions.

BIOL>Genetics>Recombinant DNA>Gene Expression>Experiment

experiment
Artificial situations {experiment} can test hypotheses or answer questions. Genomics experiments use one or more assays, samples, and markers.

Random Ratio Dilution
Arrays can have random sets of spots with various concentrations and known green-intensity vs. red-intensity ratios {Random Ratio Dilution series test} (RRD). Automated spot finding works at the 85% level. Variation coefficient {coefficient of variance} (CV) is less than 20%.

reader of arrays
Lasers can fluoresce microarray to read sample results {reader, microarray} {microarray reader} {scanner, microarray} {microarray scanner}. Displays can zoom, track, and normalize arrays or array sets. Dual red/green lasers need constant laser-spot size and large field depth. Scanning simultaneously minimizes spatial crosstalk. Microarrays are in automatic loaders to maintain positions.

standard sample

Control samples {standard sample} calibrate instruments or methods.

BIOL>Genetics>Recombinant DNA>Gene Expression>Experiment>Array

array of molecules
Oligonucleotides attach to plates {array} in rectangular patterns, to test one sample for hybridization.
plates
Plates can be silicon chips {DNA chip}, plastic blocks with small wells {microarray, plate}, optical-fiber tips {bead array}, or glass slides {planar array}.
process
For example, plastic blocks have wells. Wells have reactive-chemical solutions to assay samples. Array probes samples by hybridizing oligonucleotides to sample RNAs or cDNAs. Reader detects hybridization amount using light. Statistical and comparative calculations follow.

master plate
Sample plates {master plate} stored in freezers can make daughter plates.

daughter plate
Master plates supply other plates {daughter plate}.

microarray
Arrays {microarray} can have 9x9-spot matrices at hundreds of positions, to test many genes against one or more test oligonucleotides, plus controls and fiducial-probes.

microtiter plate
Plates {microtiter plate} can have small wells.

well of array
Sample plates contain pits {well, array} that can hold one or more samples.

BIOL>Genetics>Recombinant DNA>Cloning

cloning general
DNA fragments inserted into host nucleic acids can replicate in host organisms {cloning}|.
hosts: bacteria
Plasmids can insert up to 1000 bases. 50,000-base bacteriophage viruses can infect bacteria and can insert up to 15,000 bases. 300,000-base bacterial artificial chromosome DNA can have all bacterial-chromosome functional regions. Cosmids can hold 45,000 bases between cos sites. Gene-product secretion is preferable to harvesting cells.
In bacteria hosts, eukaryote proteins do not fold properly. Foreign proteins can kill bacteria. Bacteria have no post-translation enzymes.
hosts: yeast
Gene-product secretion is preferable to harvesting cells. In yeast hosts, proteases can destroy generated proteins.
For yeast hosts, replicating nucleic acid can be yeast artificial chromosomes.
Two-micron-circle yeast plasmid has replication origin that makes many copies per cell cycle. Other plasmids that use autonomously replicating sequence, sometimes helped by centromere sequence, make one or two copies per cell cycle. Yeast plasmids {shuttle vector} can work in bacteria.
Yeast vectors {integrating vector} with no replication origin integrate gene into yeast genome.
hosts: plants
For plant hosts, replicating nucleic acid can be Ti plasmid.
hosts: insects
For insect hosts, replicating nucleic acid can be baculovirus. Insect cell cultures have high costs. Gene-product secretion is preferable to harvesting cells.
hosts: mammals
For eukaryotic hosts, replicating nucleic acid can be virus or retrovirus. Mammalian cell culture has highest costs. Gene-product secretion is preferable to harvesting cells.
DNA fragment

DNA fragments can come from foreign organisms by cutting chromosomal DNA into DNA fragments using restriction enzymes. DNA fragments can come from mRNA by making cDNA from mRNA using reverse transcriptase and then making double-stranded DNA from cDNA. Synthesis methods can synthesize DNA.

polylinker

DNA fragments have polylinkers added at both ends, to allow nested cuts by different restriction enzymes.

insertion

DNA fragments can link into replicating nucleic acids using restriction enzymes to cut both nucleic acids and then allowing recombination.

selection

After replicating nucleic acids go into hosts, agents kill hosts if they do not have protecting genes in replicating nucleic acids. For example, bacteria with no plasmids die, because plasmids have genes to protect against antibiotics.

DNA

Host cells that live have DNA fragments, for extraction or secretion. Hybridization can test extracted or secreted DNA for DNA fragments. DNA sequencing can test for DNA fragments. Antibody binding or direct protein assays can test extractions or secretions for DNA-fragment gene products.

cell ablation

Toxic changed or foreign genes destroy tissue {cell ablation, cloning}.

clone

Organisms, cells, and molecules can duplicate {clone}|.

colony of bacteria

Bacteria {colony, bacteria}| can grow on media.

restriction map

DNA analyses can cleave chromosomes by restriction enzymes to make DNA fragments, separate fragments by size, and use fragment overlaps to mark relative restriction-enzyme-site positions {restriction map}.

BIOL>Genetics>Recombinant DNA>Cloning>Linker

linker for nucleic acid

Blunt ends can become sticky by attaching DNA {linker} containing recognition sites to blunt ends and then cleaving with restriction enzymes.

polylinker

DNA fragments inserted into replicating nucleic acids can have many possible restriction enzyme sites {polylinker}, to allow nested cuts by different restriction enzymes.

BIOL>Genetics>Recombinant DNA>Cloning>Marker

marker in DNA

Inheritable DNA-sequence positions {marker}| are restriction-enzyme cutting sites, fragment-length polymorphisms, genes, minisatellite DNAs, or microsatellite DNAs. Markers have inheritance patterns.

marker gene

Replicated nucleic acids have added genes {marker gene}, to indicate foreign-DNA insertion and DNA replication.

bacteria

Hosts with added antibiotic resistance genes make proteins that resist antibiotics, whereas hosts with no such genes die. Beta-galactosidase gene makes protein that metabolizes galactose and makes color. Hosts with no beta-galactosidase gene have no color.

yeast

Yeast can grow without leucine if they have LEU gene, without histidine if they have HIS3 gene, without lysine if they have LYS2 gene, without tryptophan if they have TRP1 gene, and without uracil if they have URA3 gene.

plants

Genes {beta-glucuronidase gene} {GUS gene} can make protein that makes glucuronides. Plants have no glucuronides, so E. coli GUS genes can be markers for plants. Firefly luciferase gene makes light. Luciferase genes can be reporter genes for plants.

mammals

Thymidine kinase (tk) gene makes protein that makes thymidine triphosphate {thymidylate}. Mammalian cells (tk-) can have no thymidine kinase gene, so thymidine kinase genes can mark cells (tk+). Aminopterin inhibits all other thymidylate synthesis pathways, so only thymidine kinase gene can make thymidylate.

drugs

G418 inhibits protein synthesis and causes cell death. Aminoglycoside phosphotransferase (APH) gene makes protein that inactivates G418.

Methotrexate inhibits dihydrofolate reductase and causes cell death. Methotrexate-resistant dihydrofolate reductase (DHFR) gene makes protein that resists methotrexate.

Hygromycin-B inhibits protein synthesis and causes cell death. Hygromycin-B-phosphotransferase gene makes protein that alters hygromycin-B.

Mycophenolic acid inhibits GMP synthesis and causes cell death. Xanthine-guanine phosphoribosyltransferase (XGPRT) gene allows GMP synthesis from xanthine.

9-beta-D-xylofuranoyladenine (Xyl-A) damages DNA and causes cell death. Adenosine deaminase (ADA) gene metabolizes Xyl-A.

reporter gene

Replicating nucleic acids can have added genes {reporter gene} that catalyze reactions used to report that promoters are working or not, for gene-expression or transcription-factor studies. For example, chloramphenicol acetyltransferase gene (CAT) reacts with chloramphenicol. Reporter genes are after promoters, to provide direct promoter-activity assays.

BIOL>Genetics>Recombinant DNA>Cloning>Methods

electroporation

If electric fields make holes in bacterial membranes {electroporation}, plasmids can enter bacteria.

heat shock

Plasmids can enter bacteria during short high-heat periods {heat shock}|, in concentrated calcium-chloride solution.

liposome

Lipid vesicles {liposome}| with DNA or protein can fuse with cell membranes and enter cells.

BIOL>Genetics>Recombinant DNA>Cloning>Transformation

transformation by DNA

Replicating nucleic acids can go into host organisms to make different organisms {transformation, DNA}|. Plasmids can enter by heat shock or electroporation. Bacteriophages can infect bacteria naturally. Transforming prokaryotic cells has high success rate.

genetically modified organism

Soy, maize, and other organisms {genetically modified organism} (GMO) can have deliberate genetic changes by genetic engineering.

knockout gene

Replacing genes with bad genes {knockout gene} makes animals that lack proteins. Transgenes can insert into normal gene positions, causing gene-function loss and affecting development.

transfection

Genes can transfer into eukaryotic-cell genomes {transfection}|. Mice, plants, and yeast have only one transfection per thousand cells. DNA can go to cell nucleus but not enter genome, so gene expresses until DNA breaks down {transient expression}. Transfection takes time. Mammalian cell lines must be immortal. Cell culture requires many cells.

types

Inject DNA fragments into cell nucleus {microinjection}. Precipitate DNA fragments with calcium phosphate, so cell-culture cells absorb precipitated DNA by endocytosis. Make liposome lipid vesicles, with DNA inside, that can fuse with cell membranes and enter cells. Fire tungsten microbullets, with DNA fused to them, into plant cells, to penetrate cell wall.

types: virus

Viruses can transfect. Omitting coat proteins prevents virus formation, so cells do not die.

Monkey COS cells include most SV40-virus DNA and make T antigen, which binds to SV40 replication origin. Plasmids with SV40 replication origin can transfect COS cells. Vaccinia virus is large and can hold bacteriophage RNA polymerase. Plasmids with bacteriophage promoter can transfect cells and suppress cell mRNAs. Insect baculovirus DNA is large and can hold genes in coat-protein DNA.

types: retrovirus

Retroviruses can go into all mammalian cells. Retroviruses first place provirus DNA sequence in genomes and then make retroviral RNA. The next stage {packaging, virus} makes complete viruses by adding coat proteins. Then cells die and release viruses. For transfection, experimenters remove packaging genes from retrovirus {helper-free}, to prevent making complete viruses, so cells live.

transgenic mice

Changed or foreign genes can enter mouse embryo cells {transgenic mice} at chromosomal positions. Transgenic-mice descendants have changed or foreign genes and have new proteins.

organism

Mammals have cell and tissue interactions, so testing requires whole organisms.

process: injection

SV40, Moloney murine leukemia virus (MoMLV), or mouse mammary tumor virus (MMTV) microinjection can put changed or foreign DNA into cells. Cloned-gene microinjection into fertilized egg pronuclei can put changed or foreign DNA into cells.

process: cell addition

Mice embryos can change by adding altered cells. Mouse blastocysts have inner-cell {embryonic stem cell, blastocyst} (ES cell) layers, which can culture with fibroblasts or with leukemia inhibiting factor to prevent further differentiation. Embryonic stem cells can uptake and insert genes by homologous recombination. Then ES cells go into mouse embryos.

marker

Neo gene resists G418. ES cells with neo gene resist G418 and live.

embryonic development

In embryos, tissue-specific regulators express changed or foreign genes in one tissue but not different tissues. If changed or foreign genes are toxic, they destroy tissue {cell ablation, toxin}. Ablated cells prevent subsequent tissue development, allowing embryo location and function tracking {cell lineage study}. Retrovirus with E. coli lacZ reporter can trace tissue differentiation and cell migration.

transgenic tissue

Chinese-hamster ovary (CHO) cells {transgenic tissue} can track transgenic effects. Mammary glands can express transgenes.

BIOL>Genetics>Recombinant DNA>Cloning>Vector

cloning vector

DNA or RNA sequences {cloning vector}| can contain DNA or RNA from other sources and can replicate in host organisms. Vectors include plasmids, phages, retroviruses, cosmids, baculoviruses, bacterial artificial chromosomes, and yeast artificial chromosomes.

35S promoter

Cauliflower-Mosaic-Virus promoters {35S promoter} can be in soy, maize, and other genetically modified organisms.

BIOL>Genetics>Recombinant DNA>Cloning>Vector>Bacteria

Bacterial Artificial Chromosome
Vectors {Bacterial Artificial Chromosome} (BAC) derived from F-factor plasmids can clone 100,000-base to 300,000-base DNA fragments in Escherichia coli.

cosmid
Cloning-vector plasmids {cosmid} can contain lambda-phage cos gene, infect E. coli, and clone DNA fragments up to 45,000 bases between phage-end cos sites.

plasmid
Bacteria can have 5000-base circular DNAs {plasmid}| that can insert up to 1000 bases. Cells can have 10 to 200 independently replicating plasmids {relaxed-control plasmid}. Plasmids {stringent-control plasmid} can replicate together with bacterial chromosomes. Artificial plasmids can be cloning vectors.

BIOL>Genetics>Recombinant DNA>Cloning>Vector>Yeast

yeast artificial chromosome
For yeast hosts, replicating nucleic acids can be artificial DNA with all yeast-chromosome functional regions {yeast artificial chromosome} (YAC). YAC replicates like yeast chromosomes.
parts
Yeast artificial chromosomes contain autonomously replicating sequence, centromere (CEN), and telomeres.
gene size
YAC can hold 100,000 bases. Several YACs can undergo homologous recombination to create complete genes from fragments.

autonomously replicating sequence
Yeast artificial chromosomes contain sequences {autonomously replicating sequence} (ARS) for replication.

BIOL>Genetics>DNA Regulation

regulation of DNA
Factors that bind to DNA-control-region binding sites can regulate gene expression {regulation, DNA}| {DNA regulation}. Carbon-atom methylation regulates gene expression by changing binding sites. Environmental factors methylate or demethylate gene-control regions by affecting transmethylase enzymes.

chromatin remodeling gene
Genes {chromatin remodeling gene} can control transcription by allowing transcription factors to reach DNA. They can be tumor suppressor genes {hSNF5/INI1 gene} for malignant rhabdoid tumors (MRT) and central-nervous-system cancers {CNS cancer}, such as choroid plexus tumors, medulloblastomas, and central primitive neuroectodermal tumors (cPNET).

genetic circuit biology
Genes can produce repressors and derepressors to make effect patterns {genetic circuit, biology}. Differing gene repression and derepression causes cell differentiation.

aptamer
In bacteria, long RNA riboswitches have ends {aptamer} that bind to other molecules to act as sensors and have ends {expression platform, RNA riboswitch} that change structurally by making hairpins, or not, to affect protein translation or RNA transcription.

BIOL>Genetics>DNA Regulation>Protein

cysteine protease
Cathepsin S and other proteases {cysteine protease} can cleave proteins to activate pathways. Cysteine proteases have poor regulation in some diseases. Cathepsin S activates antigen receptor MHC-II, which initiates T-cell immune responses. Eph receptor kinases and ephrins affect cardiovascular function, nerve regeneration, and cancer.

derepression
Nuclear acidic proteins can bind to histones to unblock DNA reading {derepression}.

DNA footprinting
Techniques {DNA footprinting} can measure protein binding to DNA without measuring gene expression or protein synthesis. Protein binding to DNA sites prevents DNAase enzyme from cutting DNA. If protein binds to DNA, protein-DNA complex moves more slowly in gels than DNA with no protein {mobility-shift assay}, so slower moving fragments have bound proteins.

epothilone
Myxobacterium S. cellulosum epothilone A, epothilone B, and epothilone D polyketides {epothilone} stabilize microtubules and interfere with cell division. They are like Taxol but more water-soluble.

hepatic nuclear factor
Factors {hepatic nuclear factor-1-alpha} {HNF-1-alpha} can have dimerization domains, which have mini-zipper four-helix-bundle (4HBs) superfamilies. Low transcription factor affects glucose-metabolism regulation, because dimers bind anti-parallel to coactivator protein {DCoH protein} to start insulin secretion in response to glucose.

histone
Basic proteins {histone}| can bind to DNA to make chromosome chromatin structure. Histones can methylate to regulate DNA expression.

ligase
Enzymes {ligase} can join slightly-separated DNA-fragment ends already hydrogen-bonded to other strands, using other strands as templates to add missing bases.

mutS protein
Proteins {mutS protein} can find imperfect DNA helices and uses mutH and mutL proteins to correct them.

nuclear acidic protein
Proteins {nuclear acidic protein}| can bind to histones to unblock DNA reading for derepression.

P300 protein
Regulators {P300 protein} can add acetyl groups to histones.

repression of DNA
Histones surround chromosomal DNA and block polymerase DNA reading {repression, DNA}| {DNA repression}.

RNase
Enzymes {RNase} can cut RNA. RNase A cuts hybridized DNA-RNA at mismatched bases.

transcription factor
Regulatory proteins or ribonucleic acids {transcription factor}| bind before and after genes. Transcription factors and DNA regions differ for different genes. Typically, genes have several regions, for transcription-factor sets. Eukaryote DNA has transcription-factor recognition sites at gene 5' and 3' ends.

Fos
C-fos genes make Fos protein transcription factors.

TATAA
TATAA sites are at 5' ends, just before mRNA transcription-start sites.

GC box
GC boxes are at 5' ends, just before mRNA transcription-start sites.

CCAAT
CCAAT sites are at 5' ends, just before mRNA transcription-start sites.

mRNA enhancer

50-base to 150-base mRNA-enhancer sites can be at 3' ends, 5' ends, or anywhere. They have redundant regions. They react to signal molecules, heat, metal ions, growth factors, or hormones. They contain regions that suppress other-cell-type transcription.

AAUAAA

AAUAAA sites at 3' ends act as signals to cut mRNA 10 to 30 bases away and then add polyA tails.

zinc finger

RNA-polymerase-III 50-base internal-control regions have two regions that bind zinc.

transcription factors: classes

Eukaryotes have transcription-factor classes that bind to DNA-regulatory-region sites: RNA polymerase II promoter, homeodomain, zinc finger, leucine zipper, and helix-loop-helix.

transcription factors: RNA polymerase II promoters

Eukaryotes have transcription factors that bind to RNA polymerase II promoters. Eukaryote promoters have DNA-binding sites and transcriptional-activation sites. Transcription factors help RNA polymerase bind to promoters or change reaction rates. TFIID binds to TATAA sites. TFIIA binds before TATAA sites. TFIIB works with RNA polymerase II. TFIIE binds after RNA polymerase II sites.

transcription factors: homeodomain binding proteins

Homeodomain binding proteins have one helix lying in DNA major groove and another helix lying across DNA to contact other proteins. Fruitfly homeotic genes control body development and contain 180-base homeobox control regions that have helix-turn-helix homeodomain found in most development genes. Vertebrate Hox genes are similar.

400 million years ago, Hox Ubx regulatory-gene mutations caused sea-dwelling arthropods with limbs on all body segments to evolve into terrestrial six-legged insects. Ubx regulates many other genes to prevent fruitfly (Drosophila) thorax-limb development, allow some brine-shrimp (Artemia) thorax-limb development, and allow other-crustacean thorax limbs.

transcription factors: zinc finger

Zinc-finger binding proteins {Kruppel protein} have repeated cysteines and histidines involved with zinc, as in SV40 early-gene GC-box Sp1, steroid-receptor proteins, and gap-gene proteins.

transcription factors: leucine zipper

Leucine-zipper binding proteins, such as FOS oncogene and JUN oncogene proteins, have four or five leucines, seven amino acids apart and just after arginine and lysine regions, that make dimers that bind to DNA.

transcription factors: helix-loop-helix

Helix-loop-helix binding proteins have regions, with arginine and lysine, that bind to DNA and make dimers, as in MyoD-gene and Myc-gene proteins.

BIOL>Genetics>DNA Regulation>Repression

corepressor

Small molecules {corepressor} can bind to repressors to aid repression.

derepressor

Molecules {derepressor} can bind to repressors at allosteric sites to release repressors from operators.

inducer of repressor

Small molecules {inducer} can bind to repressors to block repression.

BIOL>Genetics>Virus

virus genetics

SV40 monkey virus and mouse polyoma virus {virus, genetics}| have circular DNA with 10 genes.

replication phases

In replication early phase, cells make T antigen. In late phase, viral DNA replicates, and cells make coat proteins.

complementary DNA

RNA tumor viruses make complementary DNA by reverse transcriptase. Complementary DNA makes double-stranded DNA that enters host genome and makes RNA virus.

RNA

Tobacco mosaic virus, influenza virus, poliovirus, RNA phages, and other RNA viruses have single-stranded RNA, which replicates using RNA replicase. Single-stranded RNA also acts as mRNA to make viral proteins.

coat protein
Coat proteins surround virus and phage nucleic acid. M13-phage gene III codes coat protein. Genes cloned into Gene III appear on phage surfaces {phage display}. Tobacco mosaic viruses and other mild plant viruses have coat proteins that protect against worse viruses.

T antigen
In replication early phase, cells make viral proteins {T antigen} {tumor protein} for virus DNA replication.

TT virus
Circinoviridae single-stranded circular DNA {TT virus} (TTV) is similar to Circoviridae DNA.

virus-like particle
Virus structural proteins can arrange to make particles {virus-like particle} (VLP) with virus shapes and sizes.

BIOL>Biology>History>Genetics

Gregor Mendel [Mendel, Gregor]
biologist
März, Austria
1863 to 1866
Experiments in Plant Hybridization [1865]
He lived 1822 to 1884 and developed Mendel's inheritance laws by studying dominant and recessive characteristics of pea-plant independent and discrete heredity units.

Francis Galton [Galton, Francis]
biologist
England
1869 to 1883
Hereditary Genius [1869]; English Men of Science [1874]; Inquiries into Human Faculty and Its Development [1883]
He lived 1822 to 1911 and studied human mental-property and physical-property genetics. He collected and classified fingerprints {fingerprinting}. He studied human individual differences, using imagery, psychological questionnaires, twin life histories, and family and talented-people educational backgrounds. He developed the correlation coefficient. He participated in scientific exploration to unexplored Africa.
He discovered air pressure systems and invented weather maps [1875]. He invented a polyhedron {Galton's Polyhedron} of possible structural forms to which organisms can jump. More intellectually gifted people have less vivid imagery [1883].

Walter Flemming [Flemming, Walter]
biologist
USA
1870 to 1879
He lived 1843 to 1905 and studied mitosis [1870], meiosis, and chromatin role [1879].

August Weismann [Weismann, August]
biologist
Germany
1883 to 1902
On Inheritance [1883]; Essays upon Heredity and Kindred Biological Problems [1889]; Lecture on Descendency Theory [1902]
He lived 1833 to 1914. Specialized cells carry genetic information {germ line} {germ plasm theory} [1883]. Selection can operate at levels below and above organisms.

Hugo de Vries [de Vries, Hugo]
botanist
Netherlands

1889 to 1905
Theory of Mutations [1901]; Species and Varieties: Their Origin by Mutation [1905]
He lived 1848 to 1935, studied evening-primrose mutations [1900], and developed inheritance laws based on cell factors {pangenesis, de Vries} [1889]. Plants can jump from form to form, unconstrained by structures. Phylogenesis results from species selection.

William Bateson [Bateson, William]
biologist
England
1894
Materials for the Study of Variation [1894]
He lived 1861 to 1926 and invented the word genetics for heredity study. Genes carry genetic information and are in chromosomes. New species come from repeated-body-segment structure and number changes. Such modifications can lead to similarity with existing part {homeosis, Bateson}. Parts can have jumps. For example, upper thoracic vertebrae can have no ribs or lower cervical vertebrae can have ribs.

Frans Alfons Janssens [Janssens, Frans Alfons]
biologist
Germany
1909
Theory of Crossing-over [1909]
He lived 1863 to 1924 and studied crossing-over.

Thomas Hunt Morgan [Morgan, Thomas Hunt]
biologist
USA
1909 to 1915
Mechanism of Mendelian Heredity [1915]
He lived 1866 to 1945, studied gene linkage, and invented linkage maps, using fruit flies [1909 to 1915]. Genes are in chromosomes.

Archibald E. Garrod [Garrod, Archibald E.]
biologist
England
1909 to 1923
Inborn Errors of Metabolism [1923]
He lived 1857 to 1936 and studied genetics [1909].

Ronald Aylmer Fisher [Fisher, Ronald Aylmer]
statistician/geneticist
Scotland
1920 to 1938
Statistical Methods for Research Workers [1925]; Genetical Theory of Natural Selection [1930]; Design of Experiments [1935]; Statistical Tables for Biological, Agricultural, and Medical Research [1938]
He lived 1890 to 1962. He developed statistical-significance methods {analysis of variance, Fisher} and Fisher experiment-design theory [1920]. Mendelian inheritance in large populations with great variety can result in gradual evolution, but blending inheritance does not work. Variation frequency varies inversely with variation magnitude. Natural selection can increase allele frequency.

Hermann J. Muller [Muller, Hermann J.]
biologist
USA
1926 to 1951
Development of the Gene Theory [1951]
He lived 1890 to 1967. X-rays mutate fruitfly cells [1926]. Many mutations cause cancer [1951].

Richard Goldschmidt [Goldschmidt, Richard]
biologist
Germany/USA
1940
Material Basis of Evolution [1940]
He lived 1878 to 1958 and studied gypsy moths. Genes {rate gene} can control rates and regulate other genes.

George Beadle [Beadle, George]
biologist
USA
1941
Genetic Control of Biochemical Reactions in Neurospora [1941: with Edward L. Tatum]
He lived 1903 to 1989. One gene makes one protein [1941].

Edward Tatum [Tatum, Edward]
biologist
USA
1941
Genetic Control of Biochemical Reactions in Neurospora [1941: with George Beadle]
He lived 1909 to 1975. One gene makes one protein.

Oswald Avery [Avery, Oswald]
biologist
USA
1943 to 1944
He lived 1877 to 1955. DNA transfers from cell to cell in chromosomes. DNA contains gene information to transform cells. He studied pneumococcus deadly S strain, with smooth surface, and mild R strain, with rough surface.

George Gaylord Simpson [Simpson, George Gaylord]
biologist
USA
1944 to 1964
Tempo and Mode in Evolution [1944]; Meaning of Evolution [1949]; Major Features of Evolution [1953]; Principles of Animal Taxonomy [1961]; This View of Life [1964]
He lived 1902 to 1984. DNA transfers from cell to cell in chromosomes. DNA contains information to transform cells.

Barbara McClintock [McClintock, Barbara]
biologist
USA
1951
She lived 1902 to 1992 and studied corn transposable elements {jumping gene, McClintock} [1951].

Rosalind Franklin [Franklin, Rosalind]
biologist
England
1953
She lived 1920 to 1958 and performed x-ray crystallography of DNA indicating it was double helix [1953].

James Watson [Watson, James]
biologist
USA
1953 to 1980
Double Helix [1980]
He lived 1928 to ? and calculated that DNA was double helix [1953].

Francis H. C. Crick [Crick, Francis H. C.]
biologist
England/USA
1953 to 1994
Thinking about the Brain [1979]; Problem of Consciousness [1992: with Christof Koch]; Astonishing Hypothesis: The Scientific Search for the Soul [1994]
He lived 1916 to 2004 and calculated that DNA was double helix [1953]. Perhaps, consciousness depends on thalamus and cortex layers 4 and 6 [1994].

Jacques Monod [Monod, Jacques]
biologist
France
1961 to 1971
Chance and Necessity: An Essay on the Natural Philosophy of Modern Biology [1971]
He lived 1910 to 1976 and studied DNA repression and expression in Lac operon [1961].

Marshall Nirenberg [Nirenberg, Marshall]
biologist
USA
1962
He lived 1927 to ? and found DNA and RNA triplet code [1962].

Ralph Brinster [Brinster, Ralph]
biologist
USA
1969 to 1974
He lived 1932 to ?, cloned foreign genes, and expressed repressed genes in mice [1974].

R. Wall [Wall, R.]/Philip Leder [Leder, Philip]
biologist
USA
1978
Genes rearrange themselves in early infancy [1978]. Antibody genes can join joining gene by deleting DNA between them. Joining genes join to trunk genes, which determine mobility level. Joined genes determine antigen.

Sidney Brenner [Brenner, Sidney]
biochemist
USA
1983
He lived 1927 to ? and helped determine worm and human genetic codes [1982].

Richard H. Scheller [Scheller, Richard H.]/Richard Axel [Axel, Richard]
biologist
USA
1984
How Genes Control an Innate Behavior [1984]

Mario Capecchi [Capecchi, Mario]/Oliver Smythies [Smythies, Oliver]
biologist
USA/Canada
1990
They invented gene knockouts in mice [1990].

Craig Venter [Venter, Craig]
biologist
USA

1995 to 2001

He organized scientists to sequence a free-living organism [1995] and the human genome [2001]. Haemophilus influenzae bacterium has 1000 genes with 1,800,000 bp.

Robert Waterston [Waterston, Robert]/John Sulston [Sulston, John]

biologist

USA/England

1998

C. elegans genome

They organized scientists to sequence C. elegans animal genome [1998].

Richard Gibbs [Gibbs, Richard]/Eric Green [Green, Eric]/Eric Lander [Lander, Eric]/Richard McCombie [McCombie, Richard]/Douglas Smith [Smith, Douglas]/Bruce Roe [Roe, Bruce]/Elbert Branscomb [Branscomb, Elbert]/Ian Jackson [Jackson, Ian]/Steve Brown [Brown, Steve]/Peter Little [Little, Peter]/Jane Rogers [Rogers, Jane]/Duncan Campbell [Campbell, Duncan]

biologist

USA

2002

They organized scientists to sequence mouse genome.