

1: Genetics & Development | California State University, Northridge

Introduction to Genetics and Evolution is a college-level class being offered simultaneously to new students at Duke University. The course gives interested people a very basic overview of some principles behind these very fundamental areas of biology. We often hear about new "genome sequences.

For example, the brain of a human embryo looked first like that of a fish, then in turn like that of a reptile, bird, and mammal before becoming clearly human. The embryologist Karl Ernst von Baer opposed this, arguing in that there was no linear sequence as in the great chain of being, based on a single body plan, but a process of epigenesis in which structures differentiate. Von Baer instead recognised four distinct animal body plans: Zoologists then largely abandoned recapitulation, though Ernst Haeckel revived it in Lancelet a chordate, B. Larval tunicate, C. Kowalevsky saw that the notochord 1 and gill slit 5 are shared by tunicates and vertebrates. Morphology biology and Body plan From the early 19th century through most of the 20th century, embryology faced a mystery. Animals were seen to develop into adults of widely differing body plan, often through similar stages, from the egg, but zoologists knew almost nothing about how embryonic development was controlled at the molecular level, and therefore equally little about how developmental processes had evolved. As an example of this, Darwin cited in his book *On the Origin of Species* the shrimp-like larva of the barnacle, whose sessile adults looked nothing like other arthropods; Linnaeus and Cuvier had classified them as molluscs. It took a century before these ideas were shown to be correct. Biologists assumed that an organism was a straightforward reflection of its component genes: Biochemical pathways and, they supposed, new species evolved through mutations in these genes. It was a simple, clear and nearly comprehensive picture: RNA Polymerase, 2: It was a cluster of genes, arranged in a feedback control loop so that its products would only be made when "switched on" by an environmental stimulus. One of these products was an enzyme that splits a sugar, lactose; and lactose itself was the stimulus that switched the genes on. This was a revelation, as it showed for the first time that genes, even in an organism as small as a bacterium, were subject to fine-grained control. The implication was that many other genes were also elaborately regulated. Lewis discovered homeotic genes that regulate embryonic development in *Drosophila* fruit flies, which like all insects are arthropods, one of the major phyla of invertebrate animals. It was evident that the gene must be ancient, dating back to the last common ancestor of bilateral animals before the Ediacaran Period, which began some million years ago. Evo-devo had started to uncover the ways that all animal bodies were built during development. Deep homology Roughly spherical eggs of different animals give rise to extremely different bodies, from jellyfish to lobsters, butterflies to elephants. Many of these organisms share the same structural genes for body-building proteins like collagen and enzymes, but biologists had expected that each group of animals would have its own rules of development. The surprise of evo-devo is that the shaping of bodies is controlled by a rather small percentage of genes, and that these regulatory genes are ancient, shared by all animals. The giraffe does not have a gene for a long neck, any more than the elephant has a gene for a big body. Their bodies are patterned by a system of switching which causes development of different features to begin earlier or later, to occur in this or that part of the embryo, and to continue for more or less time. The step-by-step control of its embryogenesis was visualized by attaching fluorescent dyes of different colours to specific types of protein made by genes expressed in the embryo. Using such a technique, in Walter Gehring found that the *pax-6* gene, vital for forming the eyes of fruit flies, exactly matches an eye-forming gene in mice and humans. The same gene was quickly found in many other groups of animals, such as squid, a cephalopod mollusc. Biologists including Ernst Mayr had believed that eyes had arisen in the animal kingdom at least 40 times, as the anatomy of different types of eye varies widely.

2: Resources | Yuan Laboratory: Genetics, Development, and Evolution

Development Genes and Evolution publishes high-quality reports on all aspects of development biology and evolutionary biology. The journal reports on experimental and bioinformatics work at the systemic, cellular and molecular levels in the field of animal and plant systems, covering key aspects of the following topics.

Society of Friends petitions Congress for abolition of slavery. New York City traffic regulation creates first one-way street. Guillotine first used to execute highwayman Nicolas J. France declares war on Austria, starting French Revolutionary Wars. The dollar is approved as the currency of the United States. The first dollar coin is minted in The French Republic is proclaimed. Congress enacts the Fugitive Slave Law. It allows slaveowners to cross state lines to recapture their slaves. They must then prove ownership in a court of law. In reaction, some Northern states pass personal liberty laws, granting the alleged fugitive slaves the rights to habeas corpus, jury trials, and testimony on their own behalf. These Northern state legislatures also pass anti-kidnapping laws to punish slave-catchers who kidnap free blacks, instead of fugitive slaves. France becomes first country to use the metric system. Eli Whitney invents the cotton gin cotton enGINE , a machine that quickly and easily separates cotton fibers from their seeds, allowing for much greater productivity than manual cotton separation. By reducing the labor of removing seeds, the cotton gin made cotton growing more profitable, thereby raising demand for slave labor. The first federal census of counted , slaves; by , there were 1. Slavery spread from the seaboard to some of the new western territories and states as new cotton fields were planted, and by it thrived in more than half the continent. Hutton proposes geological theory of gradualism. This is the only US flag to have other than thirteen stripes. The first mammoth fossil fully documented by modern science is discovered near the delta of the Lena River in by Ossip Schumachov, a Siberian hunter. Schumachov allows it to thaw a process taking several years until he can retrieve the tusks for sale to the ivory trade in Yakutsk. He then abandons the specimen, allowing it to decay before its recovery. The specimen, which became known as the Adams Mammoth, is stuffed and mounted, and continues to be on display at the Zoological Institute. Charles White publishes An Account of the Regular Gradation in Man, and in Different Animals and Vegetables, a treatise on the great chain of being, showing people of color at the bottom of the human chain. The stone is a fragment of an Egyptian stele with the same inscription in three texts: This side-by-side translation allows historians to translate ancient Egyptian hieroglyphs for the first time. Napoleon Bonaparte becomes First Consul and seizes power in France. To share papers with colleagues around the world, he set up a small paper-sharing section on his personal web page. ORG web site, with the formal goal of providing free, world-wide access to the literature of classical genetics. ESP Rationale Although the methods of molecular biology can seem almost magical to the uninitiated, the original techniques of classical genetics are readily appreciated by one and all: ESP Goal In reading the early works of classical genetics, one is drawn, almost inexorably, into ever more complex models, until molecular explanations begin to seem both necessary and natural. At that point, the tools for understanding genome research are at hand. Assisting readers reach this point was the original goal of The Electronic Scholarly Publishing Project. ESP Usage Usage of the site grew rapidly and has remained high. Faculty began to use the site for their assigned readings. ESP Content When the site began, no journals were making their early content available in digital format. As a result, ESP was obliged to digitize classic literature before it could be made available. Since that funding ended nearly 20 years ago , the project has been operated as a purely volunteer effort. Anyone wishing to assist in these efforts should send an email to Robbins. We also plan to add new reference and pedagogical material. We have already started providing regularly updated, comprehensive bibliographies to the ESP.

3: Evolutionary developmental biology - Wikipedia

*We have developed many genetic and genomic resources and functional tools in a classical ecological and evolutionary model system, monkeyflowers (*Mimulus*), so that we can integrate hard-core genetics, developmental biology, and evolutionary ecology to actually address this problem.*

Introduction In this entry, I will review the history of evolutionary and ecological genetic of research, with the emphasis on the latter. Most investigations have focused on two of the most prominent patterns in nature: The earliest studies attempted to document the action of natural selection in wild populations in support of Darwin. While natural selection is the only evolutionary force that can account for adaptation, several evolutionary forces, acting alone or in combination, can sustain a polymorphism, at least transiently. Thus, assigning causal agency is a much more difficult problem for explanations of polymorphism than it is for adaptation. Conspicuous phenotypic polymorphisms, such as the spotting patterns on butterfly wings or banding patterns of snail shells, were the material of the earliest investigations of natural populations. I will show that the continuing emphasis on detecting natural selection is, at least in part, historical with its roots in the works of its founder, E. Ford, and his collaborators, notably R. In the beginning period, much of the problem of assigning causal agency to the maintenance of genetic polymorphism was resolved by definition rather than by empirical observation see below: Classical Ecological Genetics and Polymorphism. In the later period present, molecular ecological genetics attempts to investigate a less biased sample of genetic polymorphisms, such as allozymes and single nucleotide polymorphisms, but still retains the early emphasis on natural selection as the single most important evolutionary force shaping the hereditary material. Ecological genetics began at a time when the major theoretical aspects of the Modern Synthesis were in place, when the marvels of adaptation were clear, but when few empirical examples of natural selection in action were available. Fisher, in correspondence with S. Wright, quoted in Provine [], p. Very weak natural selection, however, is an impediment to the goal of ecological genetics to illuminate natural selection in action. Thus, the shift in focus to understanding the role of strong natural selection in maintaining genetic polymorphism is understandable. As put by its founder, E. First, whereas the early studies tended to focus on evolution in single populations, there is now a significant emphasis in ecological genetics on the population genetic structure of metapopulations and the roles of migration, extinction, and colonization on evolutionary and adaptive processes. Secondly, whereas the earliest studies emphasized chromosomes and their influence, the advent of biochemical genetics in the late s significantly broadened the phenotype, beginning with the application of electrophoretic methods to population studies. The new emphasis on biochemical phenotype, however, did not change the explanatory or causal framework of the field. Lewontin lie in the controversy over random genetic drift versus natural selection in early ecological genetic research see below. Thirdly, the more recent advent of DNA sequencing initiated the growth of molecular phylogenetics and added not only a new phenotype, but also a more pronounced historical dimension to ecological genetic research. Molecular phylogenetics and comparative sequence analysis have become the primary modern tools for the investigation of the evolutionary patterns and processes that shape DNA sequences. These methods have strengthened inferences regarding biogeography, speciation, and adaptation, especially in regard to the diversification of taxonomic lineages that attends ecological release and adaptive radiations. They have shifted the focus from polymorphism within species to diversification among clades and permitted the investigation of the history of individual genes. Two new patterns in particular have been recognized by these DNA-based methods. It is this conservative aspect of natural selection acting at the molecular level that lends power to the investigation of the genetic architecture of model organisms vis a vis human genetics. The second pattern is the discovery of the existence of ancient polymorphisms, molecular genetic variation whose duration may be greater than that of the species or taxon in which it was discovered. Natural selection, however, still remains the privileged explanatory force in modern sequence studies. Indeed, the search for and documentation of uniquely molecular patterns, such as codon bias and selective sweeps, has, if anything, elevated the focal explanatory power of natural selection in evolutionary studies. In this entry, I will first review classical ecological genetics and then discuss the novel

kinds of processes and explanations that accompanied the expansion of the field from single populations to genetically structured metapopulations and from phenotypic to biochemical and DNA sequence polymorphisms. I will show that the central early controversy over the roles of random genetic drift and natural selection in evolution has continued to this day, notwithstanding the apparent technological refinements afforded by the availability of biochemical and DNA sequence data. That is, finer scale or more reductionistic genetic data has not yet led to a resolution of the original conceptual issues that lie at the foundation of ecological genetics. Classical Ecological Genetics and Polymorphism Historically, the starting point of ecological genetic research has been the discovery of variation within a natural population, i. The subsequent goal is three-fold: Although recurrent mutation in conjunction with mutation can maintain a polymorphism indefinitely at mutation-selection balance, here Ford is clearly interested in a more active role for natural selection in the maintenance of polymorphism. The reasoning stems from the theoretical findings that, in large populations, it is unlikely that the positive and negative effects of an allele or chromosomal inversion on fitness will be exactly balanced and that the number of individuals with a rare neutral mutation is proportional to the number of generations since its origin. In addition, recurrent mutation as a cause of persistent polymorphism was considered most unlikely and, in fact, this evolutionary cause is explicitly excluded from the definition of genetic polymorphism by Ford see above. Hence, neutral genetic polymorphism was considered an exceptionally rare event by the founders of ecological genetics and, consequently, such polymorphisms were the hallmark of strong, active natural selection. Ford further distinguished two types of selective polymorphism, transient polymorphism and balanced polymorphism. This and statements like it reflect the viewpoint that organisms in nature are exquisitely adapted to their environments by the long-acting process of Fisherian gradualism. It is a prelude to the more explicitly adaptationist views found in the current behavioral literature see review in Shuster and Wade This view of the evolutionary process as primarily one of refinement of existing organismal adaptation is an essential part of the Fisherian theory of evolutionary genetics Wade and Goodnight The presumptions of a genetic basis for discontinuous phenotypic polymorphism and its maintenance by natural selection are clear from the writings of Ford cited above but these principles also can be found together in a single statement: Thus, the primary goal of the ecological geneticist is to discern exactly how natural selection is acting to maintain a balanced polymorphism by the relative strength of opposing fitness effects acting on the different sexes or at different stages in the life history of the organism. Fisher first argued that, because every individual has a mother and a father, the mean fitness of males must be equal to the mean fitness of females multiplied by the sex ratio, expressed as the number of females to males i . As a result fitness increases with rarity, and, in this circumstance, whenever the population sex ratio deviates from unity, a gene that increases the numbers of the minority sex at birth will have a selective advantage. In general, the fitnesses of the different types constituting a phenotypic polymorphism must be equal to be maintained within a population by natural selection at a non-zero equilibrium frequency a point recognized by Darwin , p. However, the balance of selective forces for non-sex related or even sex-linked polymorphisms is very different from that required to maintain an equal sex ratio, namely, the necessity that each offspring inherit equally from each sex parent. Using the existence of the separate sexes as an example of a balanced polymorphism is misleading or, at least unrepresentative, of the selective forces necessary to sustain balanced polymorphisms in general. Classical Ecological Genetics, Population Size, and Natural Selection The founding ecological geneticists dismissed any significant role for random genetic drift in evolution. The theoretical interaction of random genetic drift and natural selection for single genes with constant effects can be seen in Figure 1. Fisher in his evolutionary theory assumed that natural populations achieved or sustained the very large sizes as seen in his in correspondence with S. Similarly, according to his intellectual biographer W. With very large N_e , the domain of random genetic drift is greatly restricted even as that of natural selection is expanded see Fig. Thus, the evolutionary domains of natural selection upper and random genetic drift lower are separated by the wavy boundary determined by the effective population size. However, ecological geneticists did not dismiss random genetic drift as a significant evolutionary force for the same reasons that Fisher did. Field observations conducted with the mark-recapture methods developed by ecological geneticists documented generation-to-generation fluctuations in population

size up to or exceeding an order of magnitude in most natural populations studied long term. Thus, small local population sizes were not seen as unusual by ecological geneticists. Despite the not infrequent occurrence of small population sizes where drift would be expected to be most efficacious, random genetic drift was considered an irrelevant evolutionary force in ecological genetics because natural selection was viewed as being particularly strong during periods of population decline. The smallest populations showed little phenotypic variation, which was seen as evidence that they were the most fit or most finely adapted populations. The stressful environmental conditions responsible for the decline in numbers also were seen as causing particularly strong natural selection. Thus, the lack of phenotypic variation in small populations was owing to it having been eliminated by natural selection during the immediately prior period of decline. Conversely, under periods of population increase, natural selection was seen as weaker and more permissive of variation. This concept of relaxed selection provided Ford with a cause for the increase in observations of rare phenotypic variants in large and growing natural populations. If selection pressure increases inversely to population size, then the role of random genetic drift in evolution must be greatly restricted. In addition, Ford, p. Interestingly, Ford and his colleagues believed that genetic subdivision of the sort postulated by Wright would promote rapid evolution but for very different genetic reasons and by different genetic mechanisms natural selection instead of random genetic drift, local selection, and interdemic selection. Here, he proposes a trade-off between specialized adaptation to local conditions in the absence of migration and generalized adaptation to global conditions in the presence of migration. In modern terms, this is called genotype-by-environment interaction, where the selective effect, s , of a gene changes with change in the environment. A gene might be adaptive in one environmental context i . Migration between local environments mixes the adaptive and maladaptive responses to selection and reduces the average magnitude of gene frequency change. In this sense, genotype-by-environment interaction is viewed as an evolutionary constraint because it limits the rate of gene frequency change. The restraint can be removed simply by stopping gene flow or the mixing of genes across different local environments. Thus, the fixed selective effect illustrated in Figure 1, must be considered an average selective effect across environments. That is, he claims interactions among genes, or epistasis, contribute to local adaptation. Thus, Ford invokes genotype-by-environment interactions for fitness as well as gene-gene interactions for fitness in his cases of rapid evolution. Both of these kinds of interactions change the depiction of the threshold separating natural selection from random genetic drift Figure 1 in important ways see below. Before turning to interaction effects, I will examine a representative discussion of ecological genetics of random genetic drift using data from a natural population. The Sewall Wright Effect Several wing coloration variants segregating in a small natural population of the moth, *Panaxia dominula* Fisher and Ford, were investigated using mark-recapture in one of the longest continuous studies of a single population in evolutionary research. The goal of Fisher and Ford was to determine whether year-to-year fluctuations in the frequency of the variants *medionigra*, a heterozygote, and *bimaculata*, a homozygote were better explained by natural selection or by random genetic drift. We do not think, however, that it has been sufficiently emphasized that this fact is fatal to the theory which ascribes particular evolutionary importance to such fluctuations in gene ratios as may occur by chance in very small isolated populations. Thus our analysis, the first in which the relative parts played by random survival and selection in a wild population can be tested, does not support the view that chance fluctuations can be of any significance in evolution. In his response Wright, Wright pointed out, first, that his theory of evolution explicitly involved the simultaneous action of several forces selection, drift, mutation, and migration and he emphatically rejected the paradigm of Fisher and Ford that either selection or drift alone had to be responsible for all of the observed fluctuation in gene frequencies. Wright noted that, in order to reach their statistical conclusion, Ford and Fisher had to include gene frequency data from a decade before the more careful study, notably a period without any estimates of population size. Without this earlier data point, the average fluctuations were much smaller and not significant. He pointed out that, like the mark-recapture estimates of population numbers, the gene frequencies themselves were estimates whose variation, based on the reported sample sizes, accounted for more than half. He then showed that, if one assumed only the unitary explanation of natural selection, then the observed gene frequency fluctuations were so large even without the sampling

variance that the temporal variations in the allelic selection coefficients must range from near lethality or sterility to tremendous advantage *i*. However, Fisher and Ford provided no indication of comparable levels of temporal variation in any environmental factor acting as a selective agent. In an unyielding reply, Fisher and Ford labeled chance or random fluctuations in gene frequency, the Sewall Wright Effect, a term which has endured to the present day as a synonym for random genetic drift. With a larger data set covering several more years, Ford, *p*. Ford also showed that the selective advantage for the rarer of the genes varied widely, from He did not find, however, the expected negative correlation between strength of selection and population size in these data. In the intervening decades, data from a variety of other organisms and natural population had become available and its review led Ford, *p*. Later laboratory research has shown that the expression of the color patterns is sensitive to the thermal environment during development and thus the gene frequency estimates may be subject to significant measurement error, owing to the misclassification of genotypes. This is yet another source of variation, not accounted for in the Ford analyses. In addition, empirical evidence has found, as Wright expected, that temporal fluctuations in population size, large variance among females in fecundity, and sexual selection reduce the effective number to less than half the Fisher-Ford estimate. Cook and Jones]. Ecological geneticists like Ford postulated interactions of the sort that could change the sign of genic selection coefficients with changes in the environment including density or in the genetic background. As the two environments fluctuate in frequency, spatially or temporally, the selective effect of an A allele changes in both magnitude and sign see Figure 2.

4: Evolutionary Genetics (Stanford Encyclopedia of Philosophy)

This unique story offers an introductory conversation to genetics, embryology and evolution, taking us on a historical journey of biology through the ages. Using a series of dialogues between the Greek philosopher Democritus and his disciple Alkimos, we travel through time visiting eminent.

Johann Wolfgang von Goethe first used the word morphology. The origin of the term " morphology " is generally attributed to Johann Wolfgang von Goethe. He was of the opinion that there is an underlying fundamental organisation Bauplan in the diversity of flowering plants. In his book *The Metamorphosis of Plants* , he proposed that the Bauplan enabled us to predict the forms of plants that had not yet been discovered. In the middle centuries, several basic foundations of our current understanding of plant morphology were laid down. Nehemiah Grew , Marcello Malpighi , Robert Hooke , Antonie van Leeuwenhoek , Wilhelm von Nageli were just some of the people who helped build knowledge on plant morphology at various levels of organisation. It was the taxonomical classification of Carl Linnaeus in the eighteenth century though, that generated a firm base for the knowledge to stand on and expand. Wilhelm Hofmeister , one of the most brilliant botanists of his times, was the one to diverge away from the idealist way of pursuing botany. Over the course of his life, he brought an interdisciplinary outlook into botanical thinking. He came up with biophysical explanations on phenomena like phototaxis and geotaxis , and also discovered the alternation of generations in the plant life cycle. The focus shifted from the population level to more reductionist levels. While the first half of the century saw expansion in developmental knowledge at the tissue and the organ level, in the latter half, especially since the s, there has also been a strong impetus on gaining molecular information. Edward Charles Jeffrey was one of the early evo-devo researchers of the 20th century. He performed a comparative analyses of the vasculatures of living and fossil gymnosperms and came to the conclusion that the storage parenchyma has been derived from tracheids. This tradition of evolutionary analyses of plant architectures was further advanced by Katherine Esau , best known for her book *The Plant Anatomy*. Her work focussed on the origin and development of various tissues in different plants. Working with Vernon Cheadle , [8] she also explained the evolutionary specialization of the phloem tissue with respect to its function. It presents plant evolution as the evolution of plant development hology. In this sense it is plant evolutionary developmental biology plant evo-devo. According to Zimmermann, diversity in plant evolution occurs through various developmental processes. Three very basic processes are heterochrony changes in the timing of developmental processes , heterotopy changes in the relative positioning of processes , and heteromorphy changes in form processes. In the meantime, by the beginning of the latter half of the s, *Arabidopsis thaliana* had begun to be used in some developmental studies. The first collection of *Arabidopsis thaliana* mutants were made around Powerful techniques like mutagenesis and complementation were made possible in *Arabidopsis thaliana* via generation of T-DNA containing mutant lines, recombinant plasmids , techniques like transposon tagging etc. Availability of complete physical and genetic maps, [12] RNAi vectors, and rapid transformation protocols are some of the technologies that have significantly altered the scope of the field. Cusset provided a detailed in-depth analysis of the history of plant morphology, including plant development and evolution, from its beginnings to the end of the 20th century. Maize has traditionally been the favorite of plant geneticists, while extensive resources in almost every area of plant physiology and development are available for *Arabidopsis thaliana*. Apart from these, rice , *Antirrhinum majus* , Brassica , and tomato are also being used in a variety of studies. The genomes of *Arabidopsis thaliana* and rice have been completely sequenced, while the others are in process. While Brassica has been used primarily because of its convenient location in the phylogenetic tree in the mustard family, *Antirrhinum majus* is a convenient system for studying leaf architecture. Rice has been traditionally used for studying responses to hormones like abscisic acid and gibberelin as well as responses to stress. However, recently, not just the domesticated rice strain, but also the wild strains have been studied for their underlying genetic architectures. Also, these supposedly crucial genes might not be responsible for the evolutionary origin of that character. For these reasons, a comparative study of plant traits has been proposed as the way to go now. One example of this is

the Floral Genome Project , which envisages to study the evolution of the current patterns in the genetic architecture of the flower through comparative genetic analyses, with a focus on EST sequences. Expressed sequence tag EST sequences of quite a few non-model plants like sugarcane , apple , lotus , barley , cycas , coffee , to name a few, are available freely online. In the process, it intends to make available information for the study of evolution of seeds , cones and evolution of life cycle patterns. Presently the most important sequenced genomes from an evo-devo point of view include those of A. The impact of such a vast amount of information on understanding common underlying developmental mechanisms can easily be realised. Recently, cross-species hybridization has begun to be employed on microarray chips, to study the conservation and divergence in mRNA expression patterns between closely related species. We now have better models for molecular evolution , more refined analysis algorithms and better computing power as a result of advances in computer sciences. Evolution of plant morphology[edit] Overview of plant evolution[edit] Main article: This chert preserved early plants in cellular detail, petrified in volcanic springs. By the middle of the Devonian period most of the features recognised in plants today are present, including roots, leaves and seeds. By the late Devonian, plants had reached a degree of sophistication that allowed them to form forests of tall trees. Evolutionary innovation continued after the Devonian period. Most plant groups were relatively unscathed by the Permo-Triassic extinction event , although the structures of communities changed. Meristems[edit] The meristem architectures differ between angiosperms , gymnosperms and pteridophytes. The gymnosperm vegetative meristem lacks organization into distinct tunica and corpus layers. They possess large cells called central mother cells. In angiosperms , the outermost layer of cells divides anticlinally to generate the new cells, while in gymnosperms, the plane of division in the meristem differs for different cells. However, the apical cells do contain organelles like large vacuoles and starch grains, like the angiosperm meristematic cells. Pteridophytes , like fern , on the other hand, do not possess a multicellular apical meristem. They possess a tetrahedral apical cell, which goes on to form the plant body. Any somatic mutation in this cell can lead to hereditary transmission of that mutation. One can thus see a clear pattern in evolution of the meristematic tissue, from pteridophytes to angiosperms: Pteridophytes, with a single meristematic cell; gymnosperms with a multicellular, but less defined organization ; and finally, angiosperms , with the highest degree of organization. Evolution of plant transcriptional regulation[edit] Transcription factors and transcriptional regulatory networks play key roles in plant development and stress responses, as well as their evolution. During plant landing, many novel transcription factor families emerged and are preferentially wired into the networks of multicellular development, reproduction, and organ development, contributing to more complex morphogenesis of land plants. Origins of the leaf[edit] Further information: The leaf architecture probably arose multiple times in the plant lineage Leaves are the primary photosynthetic organs of a plant. Based on their structure, they are classified into two types - microphylls , that lack complex venation patterns and megaphylls , that are large and with a complex venation. It has been proposed that these structures arose independently. It has been proposed that the before the evolution of leaves , plants had the photosynthetic apparatus on the stems. This spread has been linked to the fall in the atmospheric carbon dioxide concentrations in the late Paleozoic era associated with a rise in density of stomata on leaf surface. This must have allowed for better transpiration rates and gas exchange. It is observed that high trees rarely have large leaves, owing to the obstruction they generate for winds. This obstruction can eventually lead to the tearing of leaves, if they are large. Similarly, trees that grow in temperate or taiga regions have pointed leaves, presumably to prevent nucleation of ice onto the leaf surface and reduce water loss due to transpiration. Herbivory , not only by large mammals, but also small insects has been implicated as a driving force in leaf evolution, an example being plants of the genus *Aciphylla*, that are commonly found in New Zealand. The now-extinct moas birds fed upon these plants, and the spines on the leaves probably discouraged the moas from feeding on them. Other members of *Aciphylla* that did not co-exist with the moas were spineless. This is brought about by ARP genes, which encode transcription factors. Genes of this type have been found in many plants studied till now, and the mechanism i. Expression of KNOX genes in leaves produces complex leaves. It is speculated that the ARP function arose quite early in vascular plant evolution, because members of the primitive group lycophytes also have a functionally similar gene [34] Other players that have a conserved role

in defining leaf primordia are the phytohormone auxin, gibberelin and cytokinin. The diversity of leaves One feature of a plant is its phyllotaxy. The arrangement of leaves on the plant body is such that the plant can maximally harvest light under the given constraints, and hence, one might expect the trait to be genetically robust. However, it may not be so. In maize, a mutation in only one gene called *abp1* abnormal phyllotaxy was enough to change the phyllotaxy of the leaves. It implies that sometimes, mutational tweaking of a single locus on the genome is enough to generate diversity. The *abp1* gene was later on shown to encode a cytokinin response regulator protein. The genes involved in defining this, and the other axes seem to be more or less conserved among higher plants. These proteins deviate some cells in the leaf primordium from the default abaxial state, and make them adaxial. It is believed that in early plants with leaves, the leaves just had one type of surface - the abaxial one. The definition of the adaxial identity occurred some million years after the abaxial identity was established. How the infinite variety of plant leaves is generated is a subject of intense research. Some common themes have emerged. One of the most significant is the involvement of KNOX genes in generating compound leaves, as in tomato see above. But this again is not universal. For example, pea uses a different mechanism for doing the same thing. Changes in these morphogen gradients may also affect the leaf form. Another very important class of regulators of leaf development are the microRNAs, whose role in this process has just begun to be documented. The coming years should see a rapid development in comparative studies on leaf development, with many EST sequences involved in the process coming online. Molecular genetics has also shed light on the relation between radial symmetry characteristic of stems and dorsiventral symmetry typical for leaves. James stated that "it is now widely accepted that In fact, it is simply the timing of the KNOX gene expression! However, recent molecular evidence is at odds to this hypothesis, [43] [44] and further suggests that Gnetales are more closely related to some gymnosperm groups than angiosperms, [45] and that gymnosperms form a distinct clade to the angiosperms,."

5: Plant evolutionary developmental biology - Wikipedia

Originally published in Hungarian, The Story of Genetics, Development and Evolution provides a historical background to the life sciences, with complex scientific concepts stripped down and explained carefully for academics and anyone interested in going back to the roots and philosophies of scientific progress.

6: PubMed Journals will be shut down | NCBI Insights

STADLER GENETICS SYMPOSIA SERIES GENE MANIPULATION IN PLANT IMPROVEMENT Edited by J. Perry Gustafson GENETICS, DEVELOPMENT, AND EVOLUTION Edited by J. Perry Gustafson, G. Ledyard Stebbins, and Francisco J. Ayala.

7: Current Opinion in Genetics & Development - Journal - Elsevier

One outstanding question in biology is the problem of development: how the genetic instructions encoded in the DNA become expressed in the morphological, physiological, and behavioral features of an organism.

8: Home | Yuan Laboratory: Genetics, Development, and Evolution

In Castle, Carpenter, Clarke, Mast, and Barrows published a paper entitled "The effects of inbreeding, cross-breeding, and selection upon the fertility and variability of Drosophila."

9: ESP Timeline: Genetics, Development, and Evolution vs History ()

Development. Development is the process through which an embryo becomes an adult organism and eventually dies. Through development, an organism's genotype is expressed as a phenotype, exposing genes to the action of natural

selection.

Hurricane at Biak A Prophet of Our Time How to Develop Use a Mission Statement Gaggia platinum swing manual St. James guide to Black artists Causality in medicine Giulio Giorello Revelation : nonviolent victory! faithfully persevere in prayer, praise, and worship D20 Critical Locations (d20 Campaigns: d20 Modern) Application of special variance estimators to geodesy Nicotine And Tobacco (Drugs) Mediterranean diet origins and myths Assessing your companys potential Pigs Ahoy! (Picture Puffins) Jews in Siddi Janjira A very short introduction to shakespeare Compile-time analysis of data list-format list correspondences. Vol.II. Statement Guide to New Brunswick for the use of settlers, tourists, and sportsmen V. 16 Nicholas Nickleby. 1938. Kenneth hagin ebooks Clariant annual report 2015 Origins and development of high ability. V. 1. From Parmenides to Wittgenstein Long-term use of sleeping pills in chronic insomnia Milton Kramer Rh Bk Computr Lit V125 The shaping of Maltese throughout the centuries: Linguistic evidence from a diachronic-typological analys Three day road book Saint Marys Press Glossary of Theological Terms (Essentials of Catholic Theology Series) Street Luge in the X Games Do You Know What You Look Like? From fantasy to structure : dada and neo-classicism A walk in the fields. Nightingale Cathy Maxwell. The battling doctors: excerpt from Cai Shun shares the mulberries (Cai Shun fen-shen): yuanben play attri A Christmas wreath Sorting (Mortimers Math) The rendering of nature in early Greek art Grade 7 conversions word problem worksheet Immune Functions of the Vessel Wall (Perfoming Arts Studies,) lcd 10 cm reference manual