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255 The Reference Points in Evolution

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Workshop on
The Reference Points in Evolution

Organized by

P. Alberch and G. A. Dover

P. Alberch
P. Bateson
R. J. Britten
B. C. Clarke
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I N D E X

PROGRAMME

1. Session on role of genomic turnover in evolution

R. FLAVELL	- Molecular processes in the genome and gene evolution; a hypothesis that the most effective members of a multigene family may be preferential substrates for mutational processes which affect gene frequencies.
R.J. BRITTEN	- Long term lineage fitness and the eukaryote genome.
G.A. DOVER	- Molecular drive and the evolution of functional novelties.

2. Session on role of mutation in somatic and germ-line evolution

C. MILSTEIN	- Evolution of antibody diversity.
B.C. CLARKE	- "Mutational order" and evolution.
G.P. WAGNER	- Population genetics theory and the evolution of development.

3. Session on rules of development: universal or particular?

A. GARCIA-BELLIDO	- Syntagmata and compartments.
G.L.G. MIKLOS	- The evolution of genomes and nervous systems. Natural selection may account for the survival of the fittest, but tells us nothing about the arrival of the fittest.
G. OSTER	- Developmental models and morphological evolution.
G.M. EDELMAN	- Topobiology.

4. Session on origins of major bauplans

P. ALBERCH	- The evolution of developmental systems.
S.CONWAY MORRIS	- Adaptive landscapes over geological time.

M. DE RENZI - Role of extinction in evolutionary processes.

A. SEILACHER - Precambrian evolutionary experiments: vendozoa and psammocorallia.

5. Session on developmental constraints and tempo and direction of evolution.

G.B. MÜLLER - Generative roles of development at the origin of morphological novelties.

S. STEARNS - A few comments on constraint.

D.B. WAKE - Heirarchical perspectives on constraints and novelty in evolution.

6. Session on plasticity and assimilation

P. BATESON - Baldwin effect and "genetic assimilation".

G.M. EDELMAN - Neural darwinism: population thinking and higher brain functions.

G.P. WAGNER - The role of developmental plasticity for the mutual adjustment of phenotypic parts.

7. Session on behaviour and evolution

P. BATESON - Behaviour and the tempo of evolution.

A. WILSON - The brain's role in driving body and brain evolution.

A. SEILACHER - Morphologic transformation in the wake of behavioral change.

8. Session on speciation and macroevolution

E.S. VRBA - Some reference points in macroevolution.

D.B. WAKE - Population structure and speciation.

A. FONTDEVILA - Genetic instability in speciation.

A. MOYA - Effect of successive bottlenecks of different sizes on the evolution of positive assortative mating in drosophila.

S. CONWAY MORRIS - Macroevolution and early metazoan evolution.

INTRODUCTORY REMARKS

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Gabriel A. Dover
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One popular and largely misguided image of science is that it's speed of progress is determined by a few men and women of genius, working in isolation, who single-handedly and single-mindedly bring about scientific revolutions in outlook. I suppose the public can be forgiven such an attitude with names like Newton, Darwin and Einstein serving as landmarks where major changes in thinking took place.

I personally do not believe in scientific revolutions, paradigm shifts or heroic charges of valiant Don Quixotes tilting against establishment windmills. Nevertheless, there are critical times in the broad progress of a science, as it accumulates more and more information, when a group of diverse and experienced biologists collectively need to stop and wonder what's it all about?' As one English poet - W.H. Davies - put it:

"What is this life if full of care
We have no time to stand and stare?"

And standing and staring and thinking and wondering is just what we intend to do over the next three days.

The reasons why many of us feel that the luxury of such supine activity is not excessive are because there is indeed an explosion of new and radically different information in the biological sciences, following hard on the heels of techniques that were simply science-fiction only ten years ago.

Right across the board of disciplines of molecular biology, cell biology, developmental biology, behavioural biology, ecology and paleobiology the accumulation of new information is explosive. This increase is bought at great cost and time but - and this is my main point - at the expense of the essential complementary time required to put it all into a wider perspective, one that serves as a framework for properly assessing whether the new data really do challenge old and established assumptions of the ontogeny and phylogeny of organisms.

For many of us that wider perspective is essentially an evolutionary perspective, the great Umbrella-in-the-Sky that brings it all together. Everything that we'll discuss over the next three days is with reference to the fundamental processes that have underwritten the origins, establishment and successes of biological novelties. What are these and where do they reside? Or, to be more colloquial, who is driving the evolutionary bus? Whose foot is on the accelerator and whose foot is on the brake? Do we have manual control of the gear shifts, or are we drifting on automatic? Where is the line between necessity and contingency? Is selection the great unifying principle - the Cosmic Arbitrator of all that functionally succeeds in

evolution - right for all times and for all places? Or are there additional forces stemming from the genome, ontogeny amd behaviour, serving as important reference points of permission and restraint? How can we integrate across levels of organisation and through tiers of time? Can there be a theory of living systems - should we be expecting one - given the chance, historical nature of biological evolution?

It has often been said that experimental biologists should not bother with the overall shape of things but attend to the details - "God is in the details". Well, God might very well be in the details but he/she has to be prised out with the complex tools and dexterity that only a wide ranging group of interests can supply.

Maybe, at the end of our three days, one holy toe will be on show!

1. SESSION ON ROLE OF GENOMIC TURNOVER IN EVOLUTION

REFERENCE POINTS IN EVOLUTION: Molecular Processes in the Genome and Gene Evolution; a Hypothesis that the Most Effective Members of a Multigene Family May be Preferential Substrates for Mutational Processes which affect Gene Frequencies

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There are three sorts of forces that result in changes in the frequency of a gene in a population of individuals: natural selection, genetic drift and molecular processes which directly change the number of copies of a DNA sequence in individuals. The spread of DNA sequences through a population as a result of these latter molecular processes has been called "molecular drive" (Dover, 1982). Examples of these molecular processes are (1) replicative transposition where sequences are duplicated and move to another location because of the special features of transposons (2) unequal crossing over whereby related sequences can be increased or decreased in frequency in somatic or germline cells (3) gene conversion in which one DNA sequence is converted to that of another closely related sequence. If this is biased in favour of one of the sequences then this sequence can accumulate in a population at the expense of the other.

A question frequently asked in discussions of the role of such molecular processes in evolution is "do the processes lead to increases in the frequency of favourable genes which enhance the fitness of individuals"?

In my contribution I speculated using one example that in certain cases they might.

The genes encoding the major 18S and 25S ribosomal RNAs are arranged in tandem arrays at nucleolus organisers. They coevolve within and between loci by unequal crossing and gene conversion processes. These processes facilitate the conservation of genes within a species but also occasionally the amplification of a new variant. As a result of the latter, closely related species often have diverged significantly for the regulatory DNA sequences associated with such genes. Within a species the regulatory DNA sequences presumably coevolve with the genes encoding the regulatory proteins which bind to the regulatory DNA sequences. Does this occur by random amplification of new variants of genes followed by selection on individuals, which in effect tests the efficiency with which the new variants are recognised by the regulatory proteins and hence the efficiency of the locus for synthesising ribosomal RNA. I raised the possibility that the subset of the genes which are preferentially amplified or deleted by unequal crossing over or gene conversion processes is the subset with the optimum affinity for the regulatory proteins. In this model the subset of genes propagated in the species by molecular drive processes are those variants with the highest ability to satisfy the rRNA requirements of the organism. Optimisation of the genotype then would not be by natural selection alone but also by selection of optimal genes at the genome level for spreading through the population. Support for the hypothesis comes from studies on plant ribosomal RNA gene families which are very large, many genes of

which are not transcribed, have a high frequency of methylated cytosine residues and are condensed into heterochromatin (Flavell, R. B., *et al*, 1988; Flavell R. B., 1989). They are thus not available to interact with the transcription machinery, in contrast with the active subset of genes. There is increasing evidence that the active subset are selected from the total in the cell in part by virtue of their ability to interact more efficiently with the regulatory proteins required for their transcription. The possibility can be raised therefore that the genes more accessible to the recombination enzymes might also be this same subset. If so, then the active subset are more likely to be involved in the unequal crossing over processes.

The products of such processes will have either more or fewer copies of the preferred regulatory sequence. Presumably natural selection would eliminate individuals with too few suitable genes and those with more efficient genes would be selected in the populations. Thus, this scenario does not eliminate a role for natural selection but emphasises that the molecular processes provide natural selection processes with individuals with increased numbers of genes adapted to have the optimum combination of regulatory DNA sequences and proteins. Genes with inferior regulatory DNA protein combinations are not preferentially increased by unequal crossing over. This model indicates how rDNA genes coevolve with the regulatory protein genes - the rDNA genes which compete best for the regulatory proteins are preferential substrates for the recombination enzymes. This contrasts with a previous model in which rDNA genes are amplified at random and their association with the regulatory proteins evaluated subsequently by natural selection (Dover & Flavell, 1984).

Finally it should be noted that the hypothesis is based on the premise that not all rRNA genes with the same function are in the same physical state in the chromosomes. This may also be the case for other gene families, the active genes being more accessible to recombination and related enzyme systems. If so, then many mutational processes may affect active genes more readily than inactive genes.

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LONG TERM LINEAGE FITNESS AND THE EUKARYOTE GENOME

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LINEAGES. Each modern species derives from a lineage extending far back in time and each lineage has undergone an immense variety of crises. Modest, usually survivable, crises such as unusual climatic events have been very frequent. More severe crises such as extreme climatic changes or diseases causing massive death occur less often but threaten extinction. Each long lasting lineage may be visualized as a main stem having very many branches each representing the production of closely related species. The great majority of the branches are short as a result of extinction. In addition along the main stems of the long term surviving lineages there have been thousands of events of change that can be termed speciation, some caused by internal genomic changes and some due to environmental changes. Interspersed among the severe events have been extended quiescent periods in which populations have grown and limited amounts of genetic variation have been involved in the evolutionary processes.

FITNESS IN STABLE OR CRISIS CONDITIONS. Fitness of course is determined by an almost indescribably large number of features whereby a given lineage is suited to survive and multiply. The kind of fitness suitable during stable periods is very different from that required during overwhelming crises. While we may not yet specify the required changes in fitness it appears that large genomic variation under crisis conditions could give a decisive advantage and permit a lineage to adapt quickly to changing conditions. Thus the features responsible for fitness under crisis conditions probably differ from those under stable conditions at least by a large rate of production of variation.

CRISES AND GENOMIC CHANGE. Among the many aspects of the genome that might be responsible for excessive variation required in crises are the many copies of mobile elements. Such elements may code for genes or systems that control their rate of copying and insertion into the host genome and perhaps control their excision as well. They may be considered as responsive systems that can be mobilized in times of stress, though we know little enough about the mechanisms and the probabilities involved. Nevertheless the creation of the novelty required for a lineage to pass through a crisis may be dependent on the excessive variation caused by the mobile elements. Changes in the genome due to mobile DNA replication and insertion are of course under natural selection as they influence viability and fertility. However the influence of mobile elements is not easily lost due to active replication and insertion of multiple copies. Thus integrated effects of past

events can be stored as a result of multiple copies- a complex form of molecular "memory". There are other theoretical possibilities for memory including changes in the system of gene regulation whereby, in particular evolutionary lineages, batteries of genes may be turned off and on again in certain stages and tissues. Another source of novelty may derive from re-use of regulatory systems that were significant in the past or from the use of fragments of them. Striking novelty might result if such batteries or organized subsystems were turned on in later lineages in changed circumstances. Our original proposals of 20 years ago included the mobilization of DNA sequences that could modulate the association of batteries of genes into novel regulatory patterns.

PROPOSED LONG TERM LINEAGE FITNESS (LTLF). I am proposing that there is a kind of lineage fitness that is suitable for alternating crises and stable periods and that this fitness is realized over long time intervals. The measure of this kind of fitness is the passage through many crises without going extinct. A reasonable model would be that most members of the lineage would fail to survive but a minority would change and survive. An important aspect of LTLF is rapid response to crisis conditions so that adaptation may occur before extinction. As with any other feature of living systems LTLF is best considered as a product of variation and natural selection. A critical point is the long period of time required for the features of LTLF to be selected. A quiescent or stable period contributes little to LTLF and in principle allows LTLF to deteriorate. A single crisis may lead to improvement in LTLF but it appears that an ultimate requirement is selection over an extended series of crises each of which is severe enough to require increased genetic variation for survival. A central feature of LTLF is the ability to pass through long stable periods without total loss of the important genomic features. Thus there is a requirement for a kind of memory so that a successful lineage is prepared for future crises and as mentioned memory could be based on multiple copies of significant sequences. The genome carries integrated effects of past events that survive for various times depending on the specific nature of the residual sequences and the rate of base substitutions and rearrangement events.

COMPUTER MODEL. A "state" number was stored for each individual and at each generation compared to a varying number representing the environment. The probability of duplication to form progeny was maximum if the numbers matched and reduced if they differed. For each individual three other numbers were stored which determined the probability of mutating the state number as well as the probability of mutating the mutation rate and mutating the mutation of the mutation rate. Each mutation was determined by a pseudorandom number generator. Progeny inherited all numbers though they changed when mutations occurred. The result (averaged over the population and many runs) was that each level of

mutation rate followed a cycle set by the variation of the environment number. Selection was only due to reduced fertility based on comparison of the state of an individual and the environment. Presumably individuals whose state numbers changed to better match the environment did so because the mutation rates at each level were higher and in this way there was indirect selection for each of the upper levels. The upper level mutators are primitive models for LTLF. The system was not tested for the long term with multiple branching lineages, extinction and the gain or loss of the mutators but the results are predictable.

MOBILE DNA AND GYPSY CLASS RETROIDS. The genome of eukaryotes has many features which we are only beginning to appreciate, including the presence of many mobile elements which can be a major source of variation. Mobile elements cause most known mutations in Drosophila and many such mutations in Drosophila or yeast affect the system of gene regulation and may have important effects on the processes of development and the determination of form. The term retroid describes all mobile or infective elements that include the reverse transcriptase (RT) gene whether retrotransposons or retroviruses. Our focus is on the gypsy class- not because they have been shown to be the most important type of mobile DNA that could supply the required elements of a responsive system with the capability of recording past experience- but because we have been working with them and they have potentiality. It is my guess that gypsy class plays a minor role among many other kinds of mobile DNA elements. The gypsy class is defined as retroids which share with each other about 20% or more amino acid sequence identity in the RT gene region and members are known in yeast (TY3) Drosophila (gypsy, 297, 412 etc.) sea urchin (RTE1, RTE5 etc.) pine trees (IFG7) and other plants (viruses CAMV, CERV). Members have been found in all species that have been examined and it is clear at least in yeast, Drosophila and sea urchins that copies have integrated into the DNA in recent times and thus that active (replicating) members exist. The gypsy class is an example of very large numbers of mobile DNA elements of several classes that include sequences that may act as mutagens by insertion or can affect the regulation of genetic activity and may transform by transferring host DNA sequences. The widespread occurrence, preservation by multiple copies, known capabilities as sources of variation and a wide range of as yet unknown potentialities make them candidates for a role in LTLF. Mitochondrial DNA sets a precedent for sequences derived from an external source that are fundamentally important and maintained with a pattern of replication and inheritance that differs from the nuclear DNA. There is no reason to deny that sequences such as mobile or repeated DNA (often thought to be parasitic or selfish) could play a central role in evolutionary processes.

GENOME ORGANIZATION. It seems that the organization of the genome and the network of gene regulation is determined by the requirements of embryonic development and specification of form and by the requirement that the system can evolve and change to meet changing circumstances. This proposal adds to these requirements the ability to maintain LTLF. It seems improbable that an understanding of the organization of the genome will be achieved from the examination of the evolution of models suitable for stable conditions. Because the LTLF may involve multiple copies of sequences it is possible that the organization of the genome is strongly affected by the residual sequences introduced in crises and maintained as a part of LTLF. In addition to mobile DNA, duplicate genes and gene families are also protected from loss by the existence of multiple copies. Multiple copies would be particularly significant for the sequences of binding sites involved in gene control or the genes for transactive factors. They would add evolutionary flexibility for the network of gene control. In each of these cases the duplication mechanisms may be selected because of their value and then form many unused or surplus copies and may even go wild and add the massive quantities of repeated sequences which are often observed. The proposal is that the copies required for LTLF and surplus multiple copies would have a significant effect on genome organization which may ultimately be understood as products or byproducts of Long Term Lineage Fitness.

(Some parts of this abstract were not presented and have been influenced by the discussions at the workshop.)

Molecular drive and the evolution of functional novelties

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Through a quirk of history and some arrogance, both the process of natural selection and its functional product are called 'adaptation'. This is not very satisfactory. In order to consider alternative routes to the establishment of functionally successful novelties we cannot use the term 'adaptation' without causing a good deal of unnecessary confusion. This point was recognised by Gould and Vrba when they introduced the term 'exaptation' to cover all cases where a novel function arose not as a consequence of differences in reproductive success of individuals with and without the function, but as the result of genotypic/phenotypic traits that spread through a population by other means. For example, a trait may have spread through the process of neutral drift which means, by definition, that the mutation in question (and its phenotypic outcome) was neutral with respect to function. However, fixation by diffusion does not preclude the later cooption or exploitation of such traits for some useful function. All organisms endowed with the trait would enjoy the new function. A variant gene hitch-hiking a ride alongside another gene, whose functional trait is under selection, is another potential way of achieving an exaptation.

There is a third route to establishing successful, novel functions which is operationally distinct from selected adaptations and coopted exaptations. This is the adoptational outcome of a cohesively evolving population under molecular drive. In this scenario, the average genotypic/phenotypic composition of a population is changed, not as the result of differential survival or accidents of sampling in the external world, but as a consequence of internal homogenisation/fixation processes of genomic turnover. In an ideal sexual population there can be a slow shift in the mean composition which could allow the population to actively adopt some previously inaccessible component of its existing environment. The cohesive population dynamics of molecular drive are a consequence of the known large disparities in rates between mutation, DNA turnover and sex.[1,2,3] Hence, the gradual replacement of a multigene family (or internally repetitious gene) with a randomly produced variant member gene, more or less in unison across a sexual population, permits two key adjustments vis-a-vis the critical functions of the genes in question. One is the potential for active adoptation, and the other is 'molecular coevolution'. This latter process is achieved when the product of another gene that functionally interacts with the gene family is pressurised to change as a consequence of the changes in the gene family. Several known examples of molecular coevolution point to an involvement of selection on the second component, stimulated as it were by the internal mechanisms that underpin molecular drive.[4]

Taken together, adoptation and molecular coevolution indicate that there are greater degrees of flexibility and tolerance in evolving biological systems, than is to be expected on strict selectional optimisation principles. First, molecules are not necessarily 'locked' into each other as they perform ontogenetic functions, and secondly organisms are not necessarily 'locked' passively into their predetermined environmental

niches.

Many aspects of phenotype (physiology, immunity, morphology and behaviour) are influenced by the products of multigene families and internally repetitious genes. In many of these the activities and consequences of mechanisms of genomic turnover (gene conversion, slippage, unequal crossingover, transposition and RNA-mediated genetic exchanges) have been uncovered; and aspects of molecular coevolutionary changes, maintaining essential cellular functions, are known. The evidence for adoptation is harder to achieve; but for the vast majority of biological functions there is an equal dearth of evidence for selection. The simple observation of an organism at peace with itself and with its environment is no longer sufficient proof of selected adaptations. The superficial description of harmoniously developing and reproductively successful organisms adequately covers all three outcomes of adaptation, exaptation and adoptation. Only through the careful dissection of genomic and developmental operations and the dynamics of the ecology will the relative contributions of selection, drift and molecular drive to any given trait be quantified. This is a problem for experimental evolutionary biology, not semantics.

There are some problems set by the environment the solutions to which are provided by the selection of relatively better suited individuals. There are some problems set by the inherent flux in genetic systems, both as a source of mutation and the populational spreading of such mutations (molecular drive), the solutions to which are provided by internal molecular coevolution and collective adoptation. By the very nature of evolving biological systems it is to be expected that there will be a variety of interactions at several levels between external selection and drift and internal molecular drive[5]. For the moment, how much of a given trait is adapt, exapt or adopt is a question of perspective and preference. Time will tell, and I'm looking forward to the future!

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2. SESSION ON ROLE OF MUTATION IN SOMATIC AND GERM-LINE EVOLUTION

EVOLUTION OF ANTIBODY DIVERSITY

C. Milstein

There are a number of reasons why the immune system offers unique opportunities in understanding evolutionary processes. While recognition molecules which display the basic immunoglobulin fold structure (grouped into the immunoglobulin superfamily) are found in primative organisms, there are unique features which occur only in vertebrates. These are primarily concerned with the generation of somatic diversity, and with the functional link between recognition and effector functions of antibody molecules and T cell receptors.

Antibody molecules and T cell receptors are made of pairs of chains (e.g. heavy and light in antibodies), and each chain is assembled by somatic recombination of gene fragments (e.g. V_H, D_H, J_H and C_H for heavy chains, V_L, J_L and C_L for light chains). All these evolve as gene families, with clear evidence of expansion and contraction processes. This is best recognised in the tandem C-region genes coding for IgG molecules which defines effector functions. For instance, the human γ locus contains four genes very closely related, indicating recent duplication events. The rabbit γ locus consists of a single gene. The mouse γ locus contains four genes of quite distinct sequence, none of them directly related to the four human ones.

Somatic diversification

There are two stages in the somatic generation of diversity. The first involves DNA rearrangement, the second hypermutation. The mechanism of DNA rearrangement is quite old, as it utilises similar recombination signals for antibody and T cell receptor molecules. On the other hand, the generation of primary antibody diversity differs in different vertebrate classes studied - mammals, birds and sharks. In mammals, primary diversity is by combinatorial gene rearrangements, while in birds

this is very limited, and occurs only in embryonic life. Diversity occurs later in the bursa through segmental gene conversion, involving a variety of "pseudogenes". In sharks, the integration occurs within clusters, and may not be combinatorial.

DNA rearrangements establish a huge repertoire of cells, each one expressing a different receptor. This is true for B cells (for production of antibody) and T cells (providing helper and cytotoxic cells). Among these niaive cells, those which are capable of recognising a foreign antigen proliferate to become memory cells.

These processes seem sufficient for T cells, but not for B cells. The affinity of the derived antibody produced following the first stage of antigenic stimulation rarely exceeds 10^7 M^{-1}, and is more commonly around 10^6 M^{-1}, or even less. Mammals have evolved a sophisticated mechanism to further increase the affinity of antibodies towards defined antigens. It is based on the somatic hypermutation of the cells which have been selected for proliferation during the first stage. The way in which antigen drives selection for cells with increasing affinity is poorly understood. The process has the characteristics of a Darwinian process, because it involves:

1. Variation, but only introduced by point mutations. The mutation rate is around 3 x 10^{-4}/bp/generation, and is directed exclusively to the domain concerned with antigen recognition.
2. Selection which, while poorly understood, seems to be driven by competition for antigen as the requirement for cell survival.
3. It is inheritable, but only at the somatic level, among the B-lymphocytes of the individual.

Recently (in collaboration with M. Sharpe, M. Neuberger, A. Surani and others), we have derived transgenic mice which, depending on the details of the transfected DNA, can (or cannot) hypermutate following antigenic stimulus. In the

future, it may be possible to use transgenic animals to compare, within a single cell, the effect of different levels of selective pressures on identical or nearly identical genes.

"Mutational Order" and evolution

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Until the development of fast computers, it has not been possible to study the simultaneous evolutionary behaviour of many genes that contribute to a quantitative character under selection. Recent models of such systems have drawn attention to an important factor in evolutionary divergence, one that has been almost completely neglected since it was discussed by Muller (1939). This factor is the random order in which mutations occur.

Two identical but isolated populations that are subject to identical selection on a quantitative character will diverge at the genetic level because each will accumulate a different array of advantageous mutations. If they were subject to different selection, the populations would also diverge. Thus divergence at the genetic level is to some degree independent of divergence at the level of the character (for example, in morphology). Genetic divergence is necessarily more 'clock-like' than morphological divergence.

If selection moves the character to an optimum, the number of different ways of reaching that optimum can be very large indeed. In our models of a character influenced by five loci, each with 32 possible alleles, the number of genotypes that will give the optimal phenotype is of the order of 10^{13}. With ten loci it is of the order of 10^{28}. Which genotype, or array of genotypes, comes to determine the optimum will depend upon the mutational history of the population.

We have examined the relative importance of mutational order and random genetic drift in bringing about divergence between populations. When selection is strong and populations are large, the effects of mutational order can be a great deal more important than those of random genetic drift.

The observations make sense of many evolutionary phenomena that have been attributed to the Founder Principle, to founder-flush (or flash) cycles, to genetic revolutions, and so on. They explain these phenomena more simply. They also explain some differences between morphological and molecular evolution, and suggest a mechanism for a selectively-driven (but nonetheless stochastic) 'molecular clock'.

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POPULATION GENETICS THEORY AND THE EVOLUTION OF DEVELOPMENT

by

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In this contribution the question is discussed whether the evolution of development can be approached within the limits of the adaptationist program. Based on Fishers fundamental theorem of natural selection (or any modification of it) adaptation can be considered as an equilibration process. Therefore adaptation can be studied with some success by the use of optimality models. There are also aspects of the evolution of development that are within the reach of the adaptationist program: a) adaptations to the environment of the embryo or larva (cenogenetic characters); b) repatterning of developmental pathways due to selection for shorter developmental time. However, more fundamental aspects of development, namely the rules by which genetic variation is transformed into heritable phenotypic variation, are not subject of adaptive optimization in the sense of Fisher. This conclusion is based on the mathematical analysis of two models of modifiers of gene expression. One is the simplest model of evolution of genotype-phenotype mapping, i.e. the classical model of dominance modification. The other is a multilocus model, where one "developmental gene" modifies the expression of quantitative trait loci (QTL), the B-matrix model (Genetics 122, 223-234). Both models have the following features in common: 1) if the population is close to the adaptive optimum of the phenotypic characters, selection on the genotype-phenotype mapping is weak or absent, 2) considerable selection coefficients can only be expected if the genetic system is kicked off the mutation selection equilibrium, and they become small as soon as the phenotypic characters come close to equilibrium. Hence, selection on genotype-phenotype mapping requires either strong and sustained directional selection on at least one character, or other population biological processes that lead to non-equilibrium situations over some period of time (e.g. longlasting hybridization, environmental heterogeneity). Selection on genotype-phenotype mapping is thus a non-equilibrium process, that can not be modeled as a case of local optimization. It is suggested that the evolution of development requires a non-adaptationist approach, although natural selection may play a part.

3. SESSION ON RULES OF DEVELOPMENT: UNIVERSAL OR PARTICULAR?

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Syntagmata and Compartments

The analysis of the evolutionary process has followed two major comparative approaches, that of morphological (homologies, analogies) variants corresponding to a "semantic level" and that of populational (allelic polymorphism) or genomic-structural variants (caryotypes, DNA sequences), corresponding to a "phonetic" level. It is worthwhile exploring a "syntactic" level, based on the existence of operationally coordinated groups of genes (syntagmata) performing invariant developmental operations and of supracellular modules generating morphologies (lineages and compartments).

Syntagmata (s. syntagma, team, see García-Bellido, in Genetics, Development and Evolution, Plenum, 1986) consist of groups of genes, hierarchically organized, that interact by molecular recognition to perform specific and independent operations (such as DNA replication and repair, DNA transcription, protein synthesis in ribosomes, phage morphogenesis, aminoacid and nucleotide metabolism, sporulation and flagellum formation in bacteria, signal transduction in cell division and differentiation, stress, immune and hormone responses, sex determination, segmentation, segment and histotype specification in embryos, etc). Molecular recognition and high connectivity among members of a syntagma lead to their inertia in evolution. Combinations of syntagmata operate within a given cell and different combinations in different cell lineages. The low connectivity between syntagmas allows for combinatorial changes in space and time during Development and Evolution.

Lineages and Compartments. Morphogenesis is the paradigm of Evolution. Most morphogenetic mutations are cell-autonomous or reflect cell-neighbour interactions (at least in *Drosophila*). Morphogenesis, therefore, largely results from the deployment of local controls, as opposite to global specifications. The generation of the morphological space follows 1) strict cell lineages that seggregate by subsequent branchings different cell types ("kinship groups") or 2) association of cells into "equivalent groups" to define pattern elements or 3) into large units of polyclonal origin called "compartments" (see García-Bellido in Phil Trans Roy.Soc. London B 312, 101.1985). The latter subdivide during cell proliferation into new compartments, usually dichotomically. Compartments are specified by selector genes acting in all its cells. Homologous compartments appear in different parts of the embryo generating spatial diversity in a combinatorial fashion. Strictly speaking compartments have been demonstrated by clonal analysis only in segmentation and appendage

formation of *Drosophila*, but their topographic or genetic properties have been found in other developmental processes in insects, in different stages of vertebrate development, in slime molds and in plants.

Modular morphogenesis could be the spatial counterpart to genetic operations as defined by syntagmata, both corresponding to developmental units above cells and genes. Units that may help to rationalize the superficial complexity of the evolutionary changes.

THE EVOLUTION OF GENOMES AND NERVOUS SYSTEMS

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Natural Selection may account for the survival of the fittest, but tells us nothing about the arrival of the fittest.

Many evolutionary investigations are still primarily concerned with the spread of new alleles throughout a population under the aegis of natural selection or drift. This neo-Darwinian approach to "understanding" evolution, even when supplemented with recombinant DNA technologies to assess genetic variation at a finer and finer level, misses the paramount problem, namely the ***origins*** of evolutionary novelties at the genomic level. In order to understand these origins it is firstly necessary to understand the molecular mechanisms that produce them (Dover 1987, John and Miklos 1988). For example, is a new variant the fortuitous combination of two previously separate protein modules? is it the genesis of a new multigene family? is it the addition of a new regulatory component to a circuit in which protein/protein, protein/DNA or protein/RNA interactions are now so altered that major embryological changes now take place?

The major problem with the theory of neo-Darwinism is that it ***does not predict*** what novelties will arise in the future; it is entirely retrospective. It is simply not good enough to argue that favourable traits will be selected for. What one badly needs to know is the set of molecular alternatives from which a choice can be made. Complex structures, be they morphologies or nervous systems are ***not explained*** by natural selection, although it is implicitly understood by many that once selection has been found to act, no more needs to be said. This unsalubrious state of affairs leads to no advances. Inroads cannot be made into the evolution of early genomes and their abilities to produce complex brain structures, if all that is considered is the shuffling of alleles by selection or drift.

The magnitude of the evolutionary problems comes home with quite some force when we consider protein evolution and brain evolution. The roundworm *Caenorhabditis elegans* for example, has about 10,000 transcription units and exactly 302 neurons. The fly, *Drosophila melanogaster,* by contrast, has about 13,000 transcription units and a nervous system of about 200,000 neurons. A human being has about 50,000 transcription units and at least 100,000 ***million*** neurons. A further most important and unappreciated fact is that in the squid *Loligo pealii,* the number of genes active in the optic lobe of the brain is nearly 80 percent the mammalian value! Thus squids and octopuses, which have always been regarded as intelligent creatures (albeit in anecdotal terms), nevertheless come close to rivalling mammals in terms of the molecular investment that has occurred in their nervous systems. Furthermore in the fly, the squid and the human, more than half of the transcription units are active in the adult brain and there has thus been an enormous genetic investment in the setting up and maintenance of neuronal hardware, a point which has rarely been emphasised in evolutionary studies.

The evolution of complex nervous systems has been predicated on sophisticated interacting brain modules during embryogenesis. This evolution of connectivity requires cell proliferation, cell differentiation, cell migration, cell death, the growth and guidance of filopodia, the appropriate recognition of cell surface molecules and ultimately the formation of synapses. The brain can then get on with sampling the unlabelled world and modifying the strengths of its synapes as a result of its interactions (Edelman 1987).

I shall discuss these evolutionary problems in the context of reverse engineering, namely the examination of the functional properties of simple brains by dismantling them using neurogenetic approaches. In organisms such as *C. elegans* and *D. melanogaster,* this can be done by molecular genetics, enhancer trap methodology, recombinant DNA technology, neuroanatomy and behavioural testing. These attempts at examining Cartesian reflex machines are throwing some light on what it ***costs*** (in a genetic sense) to wire up some circuits, and by extrapolation, what it costs to do a full scale wiring job on a human brain for example. Since nervous systems utilize most of the genetic activity of the higher metazoan genomes, surely we should concentrate more on the evolution of neuronal novelty, rather than being bogged down with the hoary old chestnuts of mutations and selection pressures which still do not address, and will never address, the quintessential features of evolution, namely the ***origins*** of novelties and their effects on development.

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DEVELOPMENTAL MODELS AND MORPHOLOGICAL EVOLUTION

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There are many ways to study the phenomenon of morphological evolution, ranging from comparative anatomy to fossil records and molecular genetics. I would like to propose that mathematical models of developmental processes can, in some instances, provide insight into the ways in which morphological changes and novelties may have been incorporated into a species' anatomy. An example of this type of analysis is given in Oster, et al. (1982, 1988). Here we put forth the following argument concerning the morphological evolution of the tetrapod limb. There are several common feature shared by most models of limb development. First, the number and arrangement of cartilage condensations is most strongly influenced by the size and shape of the tissue domain from which the condensing cells are recruited, as well as the parameters controlling the rate and range of chemical and/or mechanical communication amongst cells. Second, the models exhibited discontinuous behavior when certain dimensionless collections of parameters exceeded a critical value. These "bifurcation points" delineated the location, geometry and size of the condensations. These "universal" properties were largely a consequence of the laws of physical chemistry, and so apply whatever the actual mechanism of cartilage formation. On the basis of these properties we were able to place some "developmental constraints" on the limb "developmental program". For example, cartilage condensations must bifurcate, not trifurcate; that is, successive elements can split into two segments or branch into two subordinate branches. This proper ty enables one to classify the sequence of cartilage elements in a rational way, and provides some insight into the probable sequence of events connecting ancestral species.

Recently, we have constructed a developmental model to investigate the process of "convergent extension" wherein embryonic epithelia elongate themselves by directed cell intercalation (Weliky and Oster, 1990; Oster and Weliky 1990). The model is built around the equations for the mechanical forces generated by the cellular cytoskeleton It allows one to hypothesize rules of intercellular interaction and intracellular behavior, and computes the morphogenetic consequences for a population of epithelial cells that are mechanically coupled by apical junctions. For example, we have investigated the extension of the amphibian notochord by cell intercalation. The behavior observed in time lapse cinematography can be mimicked by imposing two rules for inter and intra cellular behavior: (i) contact inhibition of cell protrusion, which generates refractory boundaries between the notochord and the lateral somitic mesoderm; (ii) lateral inhibition of cell protrusion within each cell, which generates polarized cells. Both of these rules are well documented for cells moving **in vitro**. We plan to use this model to study the assembly of various tissues in related species. In this way we can see what alterations in cellular bahavior can convert one morphology into another.

In general, once one has constructed a model for a developmental event, it is then possible to explore the parameter variations required to match ancestral and descendent species in a phylogeny.

Frequently, these parameters refer to some cellular or physical property whose variation controls the tissue geometry. This, in turn, provides a possible scenario for evolutionary change whose validity can be tested against other modes of phylogenetic comparison. While the developmental model technique can not by itself resolve evolutionary issues (there are usually several developmental paths leading to the same final morphologies), nevertheless, the procedure can be a useful adjunct to more conventional analyses.

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T O P O B I O L O G Y

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The development of the modern methodologies of cell biology in the fifties and sixties and of molecular biology in the seventies and eighties has led to a reductionist view of embryonic development that centers on the cell and the gene as functional units of development. The functional units in most inductive and morphogenetic processes in the embryo are not single cells, however, but rather are collectives of interacting cells that give rise to tissues and organs. Can we reconcile a molecular analysis with the fact that form arises epigenetically from the collective interaction of an increasing number of embryonic cells during development? How does the one-dimensional genetic code specify a three-dimensional animal of a given species? To answer these questions, one must link genetic regulation to mechanochemical processes that coordinate cell division, cell movement, and cell death. Recent studies of cell adhesion suggest that one such link is provided by cell adhesion molecules (CAMs) that mediate cell-cell binding, and by substrate adhesion molecules (SAMs) that affect cell movement and transformations of cell states. CAMs are involved in defining cell collectives and their borders as they interact during inductive events in morphogenesis. Networks of SAMs are involved in patterned cell migration. Although CAMs cannot be considered the "cause" of induction, they play key roles among the complex causal chains of inductive interactions involving hormones and growth factors, extracellular matrix components, and cellular receptors.

Cell adhesion molecules (CAMs) function in neurite fasciculation, cell migration, stabilization of maps, and regeration. Each CAM studied so far is specified by a single gene, although the genomic structures of different CAMs vary widely. N-CAM, the first CAM to be characterized, serves as a paradigmatic example of a calcium-independent CAM. Detailed investigation of its structure by cDNA and genomic analysis supports the hypothesis that an N-CAM-like gene was the evolutionary precursor of a family of neurally important adhesion molecules, as well as that of the entire immunoglobulin superfamily. We have recently analyzed cDNAs specifying Ng-CAM and a new CAM, Nr, and have found that both share Ig-like structures. Electron microscopy suggests that several CAMs have a hinged multi-domain structure. CAM binding is generally homophilic, shows highly nonlinear kinetics, and is affected by modulation events that occur in a place-dependent fashion during neural development. These include (for N-CAM): alteration of α2-8-polysialic acid attachment, changes in cell surface expression, and variation of particular domains by alternative RNA splicing.

CAM function in cell sorting depends upon surface density, homophilic binding specificity, and specific cytoskeletal attachment of cytoplasmic CAM domains. Transfected S180 cells expressing a chimeric molecule with an L-CAM extracellular domain and an intracellular N-CAM (sd) domain bound to each other and to cells transfected with an L-CAM. Only L-CAM-transfected cells sorted out, however; cells transfected with N-CAM and the chimeric molecule did not. These data and those on alternative RNA splicing indicate a major role for transmembrane attachment in CAM function.

Antibody perturbation of CAM binding can lead to changes in morphology. Moreover, perturbation of morphology (e.g., in nerve-muscle regeneration) leads to changes in CAM expression, suggesting a series of readjustments in signaling events that control CAM levels. During morphogenesis and regeneration , CAMs are co-regulated with SAMs (substrate adhesion molecules) such as cytotactin to affect cell migration and positioning . Cytotactin may be one of a series of molecules controlled by neural signals that function to discourage cell and neurite migration into particular sites. Recent evidence on cytotactin location in whisker barrels supports this view. CAMs and SAMs thus are both affected by place-dependent dynamic signaling that is essential to normal neural morphogenesis.

In this lecture, I hope to provide a brief summary of these results in a field I have designated "Topobiology", which is concerned with such place-dependent interactions of cell surfaces with other cell surfaces or with substrates that result in changes in cell regulation. My remarks shall be centered about the function of CAMs and SAMs in morphogenesis, using recent experimental results on pattern formation in a variety of tissues as paradigms providing insight into various aspects of the molecular regulation of animal form.

4. SESSION ON ORIGINS OF MAJOR BAUPLANS

THE EVOLUTION OF DEVELOPMENTAL SYSTEMS

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The shape and size of living forms result from a dynamical process of development. A developmental system is composed of a set interactions among gene products and their environment. Oster et al. (1988) and Alberch (1989) have argued that it is spurious to attempt to conceptually separate gene action from, so-called, epigenetic interactions when characterizing the structure of a developmental system, since gene action is both the cause and effect of a developmental process. For example, genes express molecules, such as cell adhesion melecules, which, in turn, control morphogenetic processes. The result of a morphogenetic process may be the spatial rearrengement of cell populations with the consequence that induction events are triggered. Since induction involves the expression of a new battery of genes, it is clear the gene expression is subordinated to a precedent morphogenetic (i.e. "epigenetic") event.

Networks of developmental interactions have emergent properties such as stability, threshold effects ("bifurcations") and non-random transitions among steady states. So far, we have tended to emphasize the question: Given a particular developmental system, what are the evolutionary consequences? But it is equally reasonable to assume that the structure of a deveolpmental system is also amenable to evolve. Recently, Buss (1987) and Wolpert (1990) have addressed this issue from very different perspectives.

Here, I would like to introduce the issue of selection at the level of dynamical systems, i.e., selection on the global properties of systems, such as stability, discontinuity and ordered transformation. It is obvious that biological systems, in general, and genetic-developmental systems, in particular, are a subset of all possible dynamical systems. For example, a dynamical system that is highly unstable against small perturbation, or one that exhibits chaotic behavior is not a very adaptive biological system. Conversely, a system that is so stable to be immune to perturbations, such as genetic mutation, will have limited evolutionary potential.

In other words, there must have been a selection among pattern generating systems favoring the ones that exhibit the adequate balance between stability and potentiality to generate sufficient phenotypic variability. It must be emphasized that we are dealing here with a new level of selection, one that it does not act on the phenotype nor on the genotype, but rather on the emergent properties of the dynamical system of development.

Thus, I will propose the following scenario dealing with the evolution of developmental programs. Early multicellular evolution in the Pre-Cambrian was accompanied by a period of experimentation in rules of cell-cell interaction. These rules exhibited different form-generating potentialities as well as distinct stability properties. Perhaps, the fact that we find a larger number of structural plans of metazoan organization in the fossil record of the Pre-Cambrian and Early Cambrian (e.g. see discussion on this issue by Gould, 1989) is a reflection of this period of experimentation. An additional piece of evidence is that no new Bauplans, or cell types, seem to have appeared since the Cambrian, about 500 million years ago. Since that time morphological diversification has been reduced to variations within a theme. We are confronted with a systematic exploration of the potentialities of a few conserved, and stabilized, developmental systems. In fact, one of the most striking features emerging from recent advances in molecular biology is that the same sets of genes, or morphogenetic molecules, are involved in widely distinct developmental processes and in remotely related taxa (for example, recent literature on homeobox-genes or on cell adhesion molecules).

If we are dealing with variation within a conserved set of rules of gene, and cell interaction, it should not be surprising that a regulatory process such as heterochrony is the predominant mode of evolution.

This hypothesis would also solve one of the most frustrating arguments in evolutionary theory: Why are we unable to create qualitatively new forms in the laboratory? Most experimental manipulations in embryology result in atavistic re-expressions, or deletions, or duplications of already existing features. If we are dealing with an evolutionarily fixed developmental system we are, with our experimentally induced perturbations, only able to explore its potentialities. The obtain the same possible outcomes that for the most part have been realized during the 500 million years of evolution.

Adaptive landscapes over geological time

S. Conway Morris

The graphic power of the concept of the adaptive landscape needs little emphasis, and models of varying complexity have been devised to show how such a landscape might be populated, the peaks accentuated or shifted. In principle the fossil record can provide insights to the changing configuration of adaptive landscapes, at least using morphometrics. In a general sense the documentation of stasis and gradualistic trends is implicit to the landscapes that remain static, although perhaps becoming more rugged, as against those that shift. Explicit portrayal, however, is relatively uncommon. Interesting examples can be called from the study of cephalopods, whose shell coiling lends itself to morphometric analysis. In a study by Ward, for example, shifts in the landscape can be traced, as can occupation of space, vacated by the demise of another group. Other studies, such as those by Foote on early Palaeozoic trilobites, reveal significant shifts in morphological expression leading to a more dispersed landscape.

Such specific examples are complemented by more theoretical approaches adumbrated by Strathmann and Kaufmann. Adaptive landscapes can be seen to evolve. Peaks become more pronounced and some may be vacated by local disasters that have far-reaching consequences. Why the landscape has a given configuration and what determines occupation or loss of adaptively favourable peaks remains conjectural, but it may be premature to assume that other worlds would be radically different from the one revealed by our fossil record.

ROLE OF EXTINCTION IN EVOLUTIONARY PROCESSES

by Miquel De Renzi

After a mass extinction, many ecological niches become free (Valentine). The emergence of major Baupläne took place in a similar ecological situation. According to Gould, mass extinctions are at the third tier in the scales of time and they can undo evolutionary issues at lower tiers. Thus, mass extinctions promote subsequent evolutionary processes, because empty and new niches may be occupied by new species. These processes are adaptive radiations.

For our purposes, predictions about these evolutionary processes may throw some light on how major Baupläne emerged and evolved. As Stanley said, major Baupläne appeared when two internal conditions were fulfilled in the ecological scenario: emergence of an evolutionary novelty (sexuality) and structure of ecosystems (presence of predators). They were the motive for the initial animal radiations, but it is possible that such requirements are also needed for radiations in general.

A family of free niches after a mass extinction may become occupied by species originated during the radiation. At the beginning of the process, a certain sloppiness characterizes the early designs, according to Frazzetta, because selection pressures would be weak in absence of competition. The early radiation of major Baupläne would have also this feature in common.

Evolutionary trends in radiating groups after a mass extinction are not probably ruled in order to get adaptive improvement. Species selection (in the Vrba new definition) and

Vrba's effect hypothesis result in non-adaptive trends. Thus, trends in the initial moments of a radiation could be caused by these mechanisms. When niches became occupied progressively and a gradual saturation took place, competition would have a more relevant role and natural selection would guide later evolutionary trends, with adaptive improvement of organisms in the lineages. It would be also possible that major Baupläne followed these general trends. Echinoderms could be an example of this. Constraints put limits to available variability for adaptation. Perhaps, success is related to developmental systems loosely canalized.

Evolutionary trends are now seen as the issue of internal constraints imposed by development to the morphological change, according to Alberch. In order to test this general hypothesis, we must obtain proofs about the unbiased character of the fossil record in each case (taphonomic biases can produce taphonomic trends) and the absence of randomness with the techniques proposed by Raup.

Adolf Seilacher (Tuebingen and Yale Universities):

PRECAMBRIAN EVOLUTIONARY EXPERIMENTS: VENDOZOA AND PSAMMOCORALLIA.

Precambrian paleontology allows us (1) to search for roots of extant phyla, (2) to enrich the spectrum of known life forms by basic constructions that happened to become extinct, (3) to test the postulated plasticity of early developmental systems, (4) to learn about environmental conditions in the early biosphere.

Among the two groups of fossils here discussed the first one comprises the impressions of "Ediacaran" organisms. The traditional view that they represent the soft-bodied ancestors of various animal phyla is based on general symmetry relationships and biassed by the character of the best studied, mainly Australian, occurrences. Three lines of evidence speak against this interpretation:

1. The actual forms are neither archetypal nor functionally plausible in terms of the claimed affiliations.

2. Ediacaran fossils are found as low-relief molds in clastic sediments -- on sole faces of storm sands in Australia and Russia, on top of graded ash layers in England and Newfoundland and within sandstones in Namibia. Equivalent preservations are unknown in the Phanerozoic.

3. They share a unique quilted-pneu construction that provided rigidity in the absence of hard skeletons, at the same time maximizing the external surface for direct metabolic exchange. This construction also dendrified the contained fluid (possibly syncytial) similar to giant foraminifera or echinoderm ossicles.

During growth, the width of the quilting units was allometrically maintained -- either by the animal-like introduction of new "segments" at the growing edges (Australian and Russian forms) or by fractal subdivision of established units reminiscent of what we see in plant leaves (Newfoundland). In either fabricational mode, basic geometries change readily from radial to unilateral, or to bilateral shapes in which growth proceeded either at both poles or only at one end (Fig.1).

For these reasons, Ediacaran fossils should be considered not as protists, animals or plants (in neontological definition), but as an independent group of organisms. Their developmental plasticity allowed them to evolutionarily switch between symmetry classes that would characterize phyla in more established bauplans. Still they developed very specific and seemingly complex patterns by adopting various self-organizing morphogenetic mechanisms. While their physiology remains uncertain (photo -or chemosymbiosis?), their viability is documented by their worldwide common occurrence -- in spite of a presumably very low fossilization potential -- and by their remarkable evolutionary radiation. Their disappearance at or before the end of the Proterozoic has probably more to do with the emergence of predators than with physical perturbation.

If we discredit typical Ediacaran fossils as direct ancestors, early metazoan phylogeny becomes again a problem. Even if the radiation of bilaterian phyla was a relatively sudden affair connected with the acquisition of mineralized skeletons in the earliest Cambrian --what about the bilaterian stem groups, coelenterates and sponges that must have split long before that event? With regard to Precambrian sponges, the fossil

record is a yet lacking. Acoelomate and coelomate worms are documented by infaunal trace fossils. They sometimes co-occur with Ediacaran impressions and still need to be biomechanically and behaviorally analyzed. Some hemispherical impressions on the sole faces of Precambrian sandstones may also be trace fossils, made by actinian burrows (Bergaueria). This would agree with molecular data (DIANE BRIDGE & LEO BUSS, pers.comm.) suggesting that anthozoa, rather than medusoids or hydrozoans, were the most primitive coelenterates. But did skeletal corals really appear only in the Ordovician, as the oldest Rugosa would suggest? The discovery of the "Psammocorallia" (Figs.2-3) tells us otherwise, though in an unexpected way. Not only did they use sand as building material, but instead of agglutinating the grains externally, they must have swallowed and phagocytized them to make a massive internal skeleton in the place of the mesogloea. The primary function of this skeleton was not protection, but stabilization in sandy and silty bottoms. A "rock in the sock" model (metaphor suggested by MARC McMENAMIN) illustrates how such an animal would be passively scour-implanted in a wave-swept sand. So the most primitive psammocorallian skeletons (including Precambrian forms) are not conical, but hemispherical on the lower, ectodermal side and show concentric growth ridges on the flat upper surface lined by endoderm. Since the sand skeleton was rigily cemented, it could also be used to increase the digestive inner surface of the gastrocoel by ridges that were either mesh-like (Protolyella) or radial(Spatangopsis) or both. Since they were not constrained by the necessity to mineralize in small blisters, psammocorallian septa may have very blunt edges. They are also variable in number.

The fossil record so far indicates that Psammocorallia lasted from the Vendian to the Upper Ordovician and had their greatest diversity in the Lower Cambrian. This evidence, however, may be misleading. Not only have they been described under various affiliations (mostly as medusae). They also require exceptional conditions to be preserved. In the normal case, the seemingly organic cement of the sand skeleton decayed soon after death, so that infaunal worms and trilobites could readily burrow through it. Only in storm layers this skeleton had a chance to be wholly or partly embedded in mud and thus retain its shape and individuality. On the rippled interface between the sandy and the muddy part of a tempestite tentacle impressions may also be preserved (Fig.2).

Preliminary evidence from the Lower Cambrian of Sweden suggests that Psammocorallia were not confined to solitary polyps, but also evolved into colonies with ear- or fan-shaped sand skeletons. Nevertheless they were excluded from reef formation because the internal skeleton and the availability of sand limited their potential for hard-substrate cementation and elevator growth.

Conclusions:

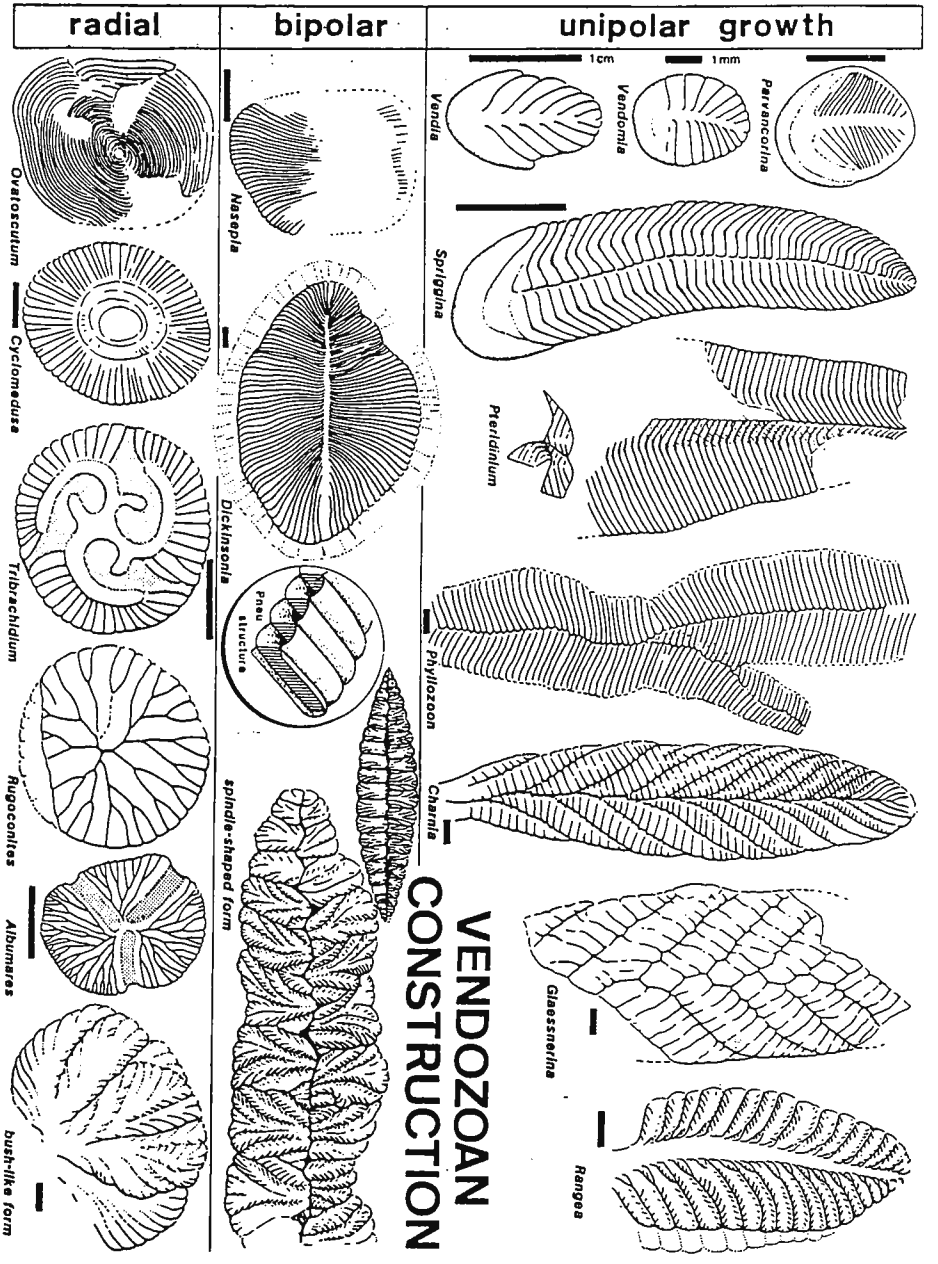
1. "Ediacaran"fossils (Vendozoa) represent a failed experiment of Precambrian evolution rather than the ancestors of modern animals and plants. Their morphological diversity is based on the adoption of simple morphogenetic principles and shows a remarkable plasticity with regard to basic symmetries.

2.The Psammocorallia extend the anthozoan record back into the Precambrian. At the same time, they too, represent a failed experiment, because the choice of an internal sand skeleton --rather than a biomineralized exoskeleton of calcite (Rugosa) or aragonite (Scleractinia) -- implied morphogenetic and ecologic constraints and licences that set them well apart from later radiations of the coral bauplan.

Fig.1: In spite of their great diversity with regard to symmetry and segmental or fractal subdivision, "Ediacaran" fossils share an unusual preservation and a peculiar construction (quilted pneu mattresses). Therefore they are here interpreteted not as ancestors of modern animals or plants, but as members of an extinct group of organisms (Vendozoa), whose basic symmetries were still plastic compared to more advanced developmental systems (From Seilacher 1989).

Fig.2: The massive internal sand skeletons of Psammocorallia (new term) served primarily for stabilization on wave-swept sandy bottoms. In storm sands of the Lower Cambrian Mickwitzia Sandstone (Sweden), Protolyella is always found with the hemispherical,ectodermal side down and the flat endodermal side up. This and the alignment along ripple troughs, as well as rocking marks in the direction of wave action, suggest passive implantation. Note also the reticulate ridge pattern by which the endodermal surface was increased as an alternative to septa. -- Blockdiagrams after slabs in the Riiksmuseum, Stockholm; loose specimens in collection of Jan Johansson.

Fig.3: In the sandcoral Spatangopsis, the endodermal surface is increased by septa in varying numbers (3-5) and the outline becomes star-shaped by extension of either the interseptal or, more commonly, the septal margins. In the propeller-shaped form (upper right) the ectodermal surface has become reduced to a small pad at the base, while the tuberculate septa form the bulk of the skeleton. (Specimens from Jan Johansson). In the rippled slab (Riiksmuseum, Stockholm) faint tentacle impressions are preserved around self-implanted specimens. Scales 1 cm.



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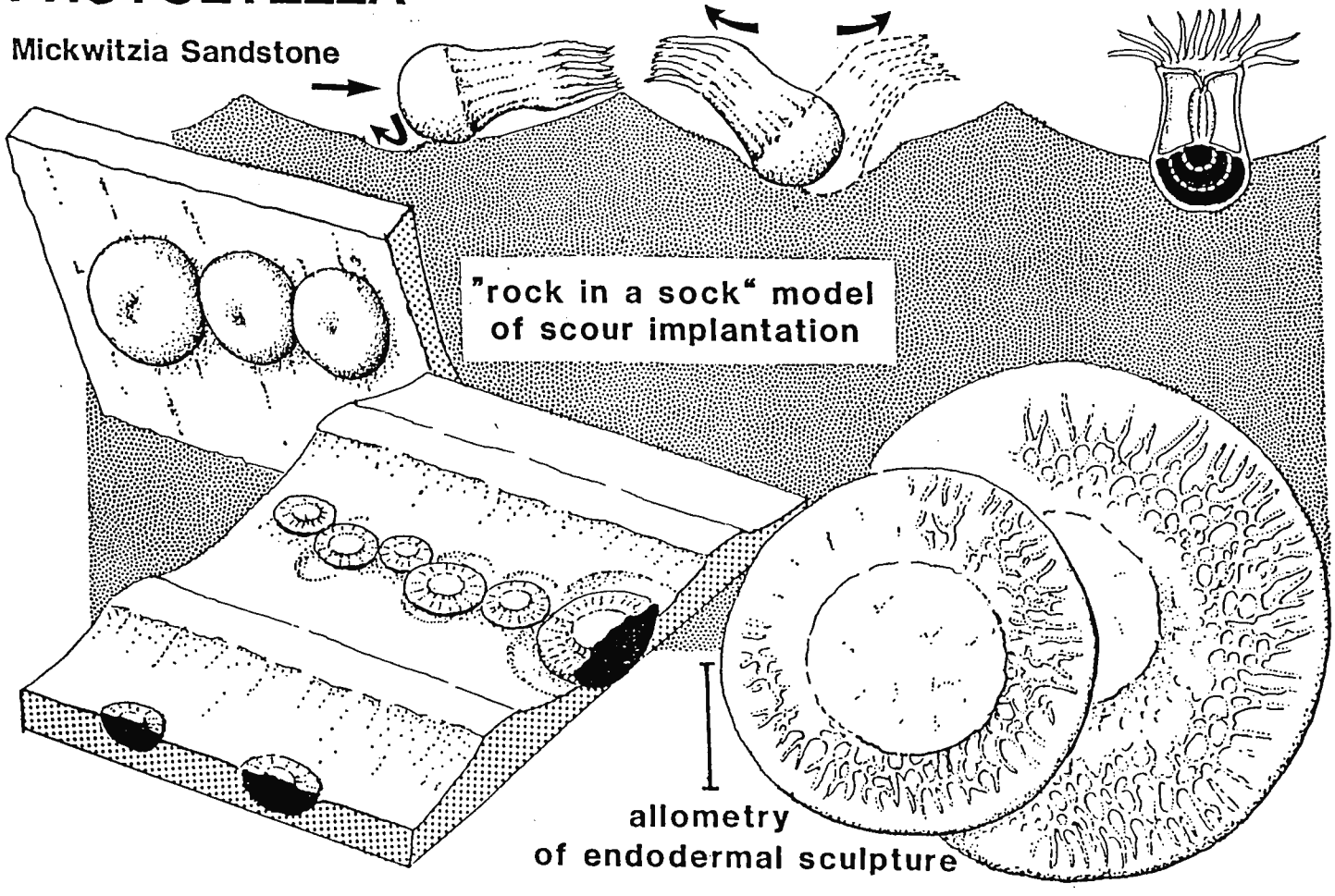

5. SESSION ON DEVELOPMENTAL CONSTRAINTS AND TEMPO AND DIRECTION OF EVOLUTION

GENERATIVE ROLES OF DEVELOPMENT AT THE ORIGIN OF MORPHOLOGICAL NOVELTIES.

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Morphological novelties are qualitatively new structures that arise discontinuously in phenotypic evolution. The origin of such structural innovations is still a controversial issue in evolutionary biology. For decades explanations of novelty have oscillated between micro- and macroevolutionary concepts, without arriving at the formulation of a testable model. Most of the evoked scenarios are genetic, reflecting the search for a direct causation of novelties. In contrast, the hypothesis presented here is primarily epigenetic, assuming an indirect causation based on the systems properties of development.

Morphological evolution is essentially a modification of size and proportion of characters. Neo-Darwinian mechanisms acting on these parameters gradually alter the developmental systems that produce the characters. Developmental systems, however, have steady state properties with non-continuous boundaries. Evolutionary alterations of a particular system can eventually reach thresholds specific to the system, which may lie in critical blastema size, cell number, morphogen concentration, temporal or spatial aspects of induction, etc. Transgression of such thresholds can interrupt developmental interactions or initiate new ones, resulting in a modified tissue response. A new phenotypic feature arising from such a modified tissue reaction is then a by-product of the primary evolutionary alteration of a developmental system.

For example, selection acting on beak proportions in certain birds leads to an elongation of the posterior part of the mandible which, upon contact with the occipital bone, forms a new articulation with the cranium. This basi-occipital joint, a novelty in bird morphology, must have formed automatically when the mandible reached a threshold size in development and initiated on both bones the tissue interactions involved in joint formation. The new joint forms because skeletal tissues have the capacity to react upon mechanical stimulation with a host of cellular processes that result in the

formation of articulations. In this case, no gene level innovation or particular selection for joint formation is required for the generation of a new structure. However, not necessarily the results of new tissue interactions are immediately expressed in the adult phenotype. They may first exist as transitory structures in ontogeny and can at a later time become the basis for a novelty emerging rapidly in the evolution of an organismic lineage (Müller and Streicher 1989).

This scenario identifies a causal mechanism for the origin of novelties, but the causality lies in the systems properties of development (epigenetics) and is only indirectly related to the neo-Darwinian processes involved in the modification of a specific morphological component of the evolving organism. The majority of morphological novelties possibly arise as epigenetic side-effects of evolutionary modifications to quantitative parameters of development (Müller 1990). Only secondarily the rudiments of a new character are themselves exposed to selection and population genetic mechanisms.

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A few comments on constraint for Session 5.
Steve Stearns

Adaptation and Constraint

These words represent the poles of a continuum of possible biological explanations. Both are often used naively. Most traits are affected by a mixture of adaptation and constraint, and methods are available for identifying and weighting those contributions. Definitions of adaptation and constraint can be arranged in sequences of increasing sophistication. The naive definition is the same for each: all patterns are adaptive, and all patterns are constrained. Biologists exist who believe in one or the other definition, which are, however, mutually exclusive.

More sophisticated definitions of adaptation:

(1) The functional definition.- According to Williams (1966) and Curio (1973), an adaptation is a *change* in a phenotype that occurs in response to a specific environmental signal and has a clear functional relationship to that signal that results in an improvement in growth, survival, or reproduction. Otherwise, it does not appear. For example, waterfleas produce spines and elongate helmets in response to dissolved molecules that indicate the presence of invertebrate predators that prey less effectively on spiny, helmeted *Daphnia*. Helmets and spines are costly, individuals that do not produce them have higher reproductive rates, and when predators are not present, the spines and helmets are not produced. This definition is most appropriately applied to variation within populations.

(2) The phylogenetic definition.- Given a phylogenetic tree indicating species relationships and the evolutionary sequence in which traits appeared, Coddington (1988) suggests that we only apply the word adaptation to homologous traits that are derived, unique to a single species, and functionally associated with a change in habitat and selection pressure that is also unique to that species. This stringent definition, appropriate in the phylogenetic context, ignores variation within populations (see above) and lineage-specific selection (see next) that produces adaptations that can be older than an individual species. It also encounters one problem and creates another (Harvey and Pagel, 1991). By requiring that we have knowledge of both current and ancestral character state and habitat, it asks for details that can almost never be produced, and by restricting the use of the word adaptation to homologs, it rules out the extremely useful procedure of using convergence as evidence for adaptation.

(3) Adaptation through lineage-specific selection pressures.- If entire lineages encounter selection pressures that differ consistently from those of

other lineages, one should be able to speak of adaptations older than individual species and detectable by comparisons among lineages. An example would be selection for locomotion in cetaceans (whales) as compared with their relatives the artiodactyls (sheep, antelope, and their relatives). The entire cetacean order lives in aquatic environments that select for a fusiform body that slips efficiently through the water propelled by fins. The entire artiodactyl order moves about on legs in a terrestrial environment that selects for efficient running, jumping, and turning. Just as compelling are examples of active selection of the same habitat by all species within a lineage, as is the case with the planktonic larvae of all the wormlike species in the Phylum Phoronidae, which have been selecting shallow beds of clean marine sand to settle in for hundreds of millions of years. The adult forms then predictably encounter only the selection pressures associated with that particular habitat.

The strongest selection pressures on a trait originate not in the environment but in the other traits making up the individual. The traits of a single individual encounter each other reliably in every generation and *must* fit together to produce a functioning organism. This kind of selection is strong. Because traits move through lineages together, this kind of lineage-specific selection produces complex, precise adjustments of several traits to each other when the traits have been interacting with each other for a long time - longer than the lifetime of the species, perhaps longer than that of the genus or family.

(4) Two microevolutionary definitions of adaptation.- These definitions are aimed at testing hypotheses with risky experiments. (1) An adaptation is the state of a trait predicted to be in that state and no other by an optimality model if the prediction has been tested by using mutations or phenocopies to perturb the phenotype away from the optimal state and it has been demonstrated that the fitness of the perturbed phenotypes is lower than the fitness of the optimal one. This has been achieved through clutch size manipulations, with consequences most clearly worked out for kestrels by Daan et al. (1990). (2) An adaptation is the state of a trait such that every time a given factor changes in the environment, the trait evolves to the same new state, and every time the factor changes back to its original state, the trait does also. I know of no good examples where the second definition has been applied in practice.

More sophisticated definitions of constraint:

(1) The casual phylogenetic definition: This holds that any pattern or state that can be attributed to phylogeny, as opposed to recent microevolution within the currently existing population, is a constraint. For example, all birds in the Order Procellariformes have a clutch of only one egg. The casual phylogenetic definition of constraint would take this as evidence that no member of this order *could* evolve a clutch size of two. While the conclusion does not follow from the evidence, it is helpful as an alternative used to sharpen the naive adaptationist hypothesis that a clutch size of one is actively maintained by natural selection in every species of the entire order. A more sophisticated

definition of constraint helps to sharpen a less sophisticated defini-tion of adaptation. This also works the other way round.

(2) The biomechanical definition.- This is relatively uncontroversial. It asserts that organisms are constrained to obey the laws of physics and chemistry. Examples include the need for terrestrial tetrapods to increase the cross-sectional area of their limbs as their body mass increases and the necessity for the surface area of lungs and guts to increase in proportion to body mass rather than some linear measure of size.

(3) The systems definition of constraint.- This is the most biological, and most interesting, definition of constraint, for it suggests a new research program. It claims that fixation of key traits leads to progressive integration, irreversible change, and constraint. The key idea is that once one trait becomes fixed, other functionally related traits are less free to vary, and that the longer one trait has been fixed, the more other traits have also been subsequently fixed. The functional interconnections of these fixed traits constitute organismal integration and make it first difficult, then impossible, for evolution to proceed in reverse to the original state. This definition of constraint suggests two testable hypotheses.

First, if we can establish the order in which two traits have evolved (cf. Maddison), the older of the two traits should be more deeply integrated into the organism, more buffered against genetic change. If we induce mutations with radiation or chemical mutagens, the older traits should vary less than the more recent ones in response to the same level of mutagenic treatment.

Second, suppose that we can compare the same variable trait in two closely related species. In one species, several functionally related traits are fixed. In the other, none of those traits are fixed, all still vary. If we select the target trait, it should display a larger and more rapid response to selection in the species where all traits still vary than in the species in which some functionally

Comments:

(1) Not all biologists have agreed on clear definitions of adaptation and constraint. Those given above cover much of the range of opinion but do not exhaust it.

(2) It is a mistake to frame an evolutionary question as a matter of *either* adaptation *or* constraint. The two interact in the causation of every pattern and determination of every state of every trait that I can think of. Adaptation plays its clearest role in cases of convergence, whereas the systems sort of constraint plays its strongest role in the preservation of lineage-specific patterns of organismal integration over long time spans.

(3) We can distinguish between patterns that can be interpreted as *adaptive*, including those detected in broad comparisons across taxa, and processes leading to *adaptation* that can be investigated as mechanisms operating within populations. The scope of proper application of the term adaptive is

much broader than that of the word adaptation, which should be reserved for cases satisfying either the phylogenetic or the microevolutionary definition.

(4) After a trait has been thoroughly scrutinized with theory and experiment, the question, Is this thing an adaptation or is it a constraint?, may no longer be interesting. Well-investigated traits are often determined by an intimate interaction of natural selection and internal structure, and their states are such complex mixtures of "adaptation" and "constraint" that the manner in which they are determined becomes more interesting and more important than the summary labels that rather inaccurately describe the categories of forces involved in the determination.

(5) We are always forced by the complexity of nature to concentrate on some aspects and ignore others. The things ignored are often described as "constraints" on the things investigated in detail. One can, however, include some of the things previously ignored and ignore some of the things previously included. When that is done, the traits previously described as constraints may look like adaptations themselves.

Lineage-specific constraints on growth modulate the expression of genetic variation

(1) *Drosophila* age and maturity (Gebhardt and Stearns, 1988) (slides)

(2) *Daphnia* age and maturity (Ebert, in prep.) (slides)

Energy allocation can constrain genetic correlations **not** *to change sign*

(1) Y-models (Stearns, de Jong, and Newman, in prep.) (slide)

Consequences

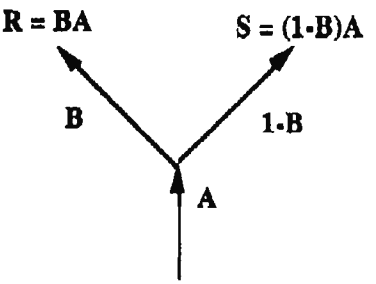
Intrinsic, epigenetic factors play a dominant role in modulating the
These factors - e.g. mode of growth - differ among lineages.

This has consequences for:

- the maintenance of genetic variation

- for the lineage-specificity of the response to selection.

Environmentally-induced changes in magnitude and sign of genetic covariances do occur. However, the genetic correlations of two plastic traits do not always change sign. What sorts of pairs of traits should show sign change, and what sorts of pairs should not? Pairs of traits that are functionally coupled, such as two traits both drawing on the same resource pool within one individual, should have genetic correlations that do not change sign. Those that are not functionally coupled are not so constrained - their pleiotropy is not structured - and would be more likely to show a sign change. If so, then the causes of the deeply rooted, stable genetic covariances that do not change sign are to be sought not in the genes but in epigenesis - physiology and development. Modifying the example developed by van Noordwijk and de Jong[39]:



There is a tradeoff in energy used between reproduction (R) and survival (S). The total amount of energy acquired is set by A, where $A = R + S$. The fraction of energy allocated to reproduction is determined by B, so $R_i = B_iA$ and the fraction allocated to survival is what is left, i.e. $S_i = (1-B_i)A$, with B_i assumed to be genetic. For any fixed level of resource A, the covariance between R and S is negative, as the traits R and S are related by structured pleiotropy.

The message is not that genetics is unimportant, but that genetic correlations are only a superficial representation of the genetic variation that underlies epigenesis. An understanding of epigenesis is required to reveal both the causes of constraints and the causes of genetic correlations.

Heirarchical Perspectives on Constraints and Novelty in Evolution

David B. Wake

Homoplasy refers to evolved similarity and can arise when two taxa evolve by parallelism, convergence, or reversal. Homoplasy is common, and while some of it can be attributed to response to selection, much of it is the result of limited options arising from developmental and other constraints on evolution. Miniaturization is salamanders is an example of a homoplasy that arises from a complex interaction of adaptive processes and constraints, and can be used to illustrate ways in which these phenomena combine to produce new structural and functional features in evolution.

There are three levels in the heirarchy I consider: populational, organismal, and genomic. I assume that miniaturization arises as an adaptive response to selection manifest at the level of the population - such as r-selection for reproduction at earlier ages and hence smaller sizes, or use of physical refuges from predation, such as beetle channels under the bark of logs. So, there is downward causation on the organismal from the populational level. Genome size is an unsually important parameter in salamander evolutionary biology, for salamanders have by far the largest genomes among terrestrial vertebrates (approaching 90 pg DNA per haploid nucleus). The correlation of genome size with cell-level phenomena such as cell size, cell division rate, and cell metabolic rate is well established. So, there is upward causation the the organismal from the genomic level. The organismal level is caught in a "squeeze".

These very small salamanders (as small as 15 mm body size) have very large cells, and there are a number of consequences. One is that the skull is very underdeveloped, and there is a very large cranial fontanelle. This is novelty by reduction, and is not especially interesting. Of greater interest is that so few cells are present that certain pre-cartilage condensations fail to form, and new arrangements of carpal and tarsal elements result. A structural arrangement that is a biomechanical constraint in the tongue-firing mechanism fails to form, and the result is a new simplified arrangement that is the most efficient firing system yet found. This is a functional innovation.

There are organismal-wide consequences, and even in the brain profound changes occur. One of these is the persistence of and elaboration of ipsilateral retinofugal projections, which are lost through a kind of cell level competition in most other vertebrates. This leads to a novel structural feature that has strong functional implications for binocular vision associated with the new feeding system.

There are some common themes associated with miniaturization, but others are more lineage-specific and circumstance dependent. For example, four-toed salamanders have evolved three times in one family alone, all in miniatures. But vastly increased cell size can make salamanders effectively smaller than they seem when measured with a simple meter stick. Integration of such information in a hierarchical context will improve our understanding of morphological evolution.

6. SESSION ON PLASTICITY AND ASSIMILATION

Baldwin effect and "genetic assimilation"

Patrick Bateson

Sub-Department of Animal Behaviour, University of Cambridge

The idea that an individual's capacity to adapt to new circumstances may play an important part in evolution ("organic selection") was proposed independently by Baldwin, Lloyd-Morgan and Osborn. It is hardly ever mentioned in modern text-books and is often dismissed incorrectly as Lamarckian. Waddington's evidence that (a) environmental change may expose a greater amount of genetic variation than was previously apparent and then used for purposes of artificial selection and (b) his ideas about "genetic assimilation" have also been widely misunderstood. Although he wasn't always consistent, Waddington himself believed (correctly) that his proposal for evolutionary change was not the same as the Baldwin effect. The differences in the two evolutionary hypotheses may be summarized as follows:

Baldwin (Organic selection)

Stage 1. Individuals adapt physiologically or behaviourally to a challenge from the environment and, by so doing, most if not all members of a population survive potential extinction.

Stage 2. Some individuals produce the adaptive character at lower cost (e.g. without learning) and, by degrees, Darwinian evolution takes place.

Stage 3. The adaptive character can now be expressed even in the absence of a "training" effect from the environment.

Waddington (Genetic assimilation)

Stage 1. Some individuals develop differently from others when challenged by the environment.

Stage 2. Those individuals that express a given character are better able to survive for reasons that are not necessarily connected with the challenge. If the environmental challenge recurs, the adaptive character increased in frequency by the normal process of Darwinian evolution.

Stage 3. Under what are probably rare circumstances involving special features of each individual's developmental system, the evolved character is expressed even when individuals are not challenged by the environment.

Whereas the "organic selection" hypothesis proposes an appropriate and rapid response to environmental change and initial survival by virtually all members of the population that have been so challenged, Waddington's hypothesis proposes a haphazard and frequently slow response to a challenge in which only a sub-set of the population survive. The two processes are at opposite ends of three continua. My own view is that the second stage of genetic assimilation depends on a relatively unlikely developmental scenario and, therefore, the full process postulated by Waddington has not been very important. However, I believe that the Baldwin effect has been much more important in evolution than conventional wisdom would suggest. The behavioural aspects of adaptability involved in that evolutionary process and the first stages of the process in which Waddington was interested are discussed further in the abstract on behaviour and the tempo of evolution.

NEURAL DARWINISM: POPULATION THINKING AND HIGHER BRAIN FUNCTIONS

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The Neurosciences Institute
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Recent progress in neurobiology has renewed our conviction that psychological functions cannot be understood in isolation from the biology of the brain. Current views of higher brain functions are largely based on the notions of computation and information processing. These views suggest that the brain is a Turing machine. Various lines of evidence appear to be incompatible with this view and suggest that perception follows a set of selectional principles along the lines first suggested by Charles Darwin. A theory of selection to account for perceptual categorization has been formulated. To test the consistency of this theory of neuronal group selection, a set of automata based on its principles has been constructed. These automata have performances that resemble perceptual categorization in animals with complex brains. A movie showing the performance of one of these machines (Darwin III) will be shown in this lecture and the possibility that selective recognition automata may become useful will be discussed.

THE ROLE OF DEVELOPMENTAL PLASTICITY FOR THE MUTUAL ADJUSTMENT OF PHENOTYPIC PARTS

GÜNTER P. WAGNER, University of Vienna

The possible evolutionary significance of developmental plasticity will be discussed in the light of results from population genetic theory. Developmental plasticity is defined as context dependency of the growth and development of an organ. This definition considers the dependency of a character from its intra-organismal environment and is not the same as phenotypic plasticity, which considers the influence of the extraorganismal environment on the expression of genetic variation. At least in some cases (for instance the functional adaptation of the liver or the plasticity of mammalian skeleton) developmental plasticity can be seen as a way to achieve a mutual adjustment of the growth and differentiation of functionally coupled characters.

Developmental plasticity may thus be able to supress the production of non-functional and therefore non-adaptive variants. This regulatory potential of developmental plasticity is of obvious advantage for the individual, as it provides the opportunity to compensate acquired deficiencies. Whether the suppression of non-functional variation is also of evolutionary significance is an open question. Regulation is at least not necessary for the coordinated change of functionally integrated traits by mutation and selection. This is obvious form theoretical as well as from empirical evidence. However, theory also suggests that regulation (= suppression of non-adaptive variation) facilitates adaptation by natural selection. Therefore the possibility exists that developmental plasticity may convey long term evolutionary advantages, as long as there are no direct disadvantages to the individuum.

7. SESSION ON BEHAVIOUR AND EVOLUTION

Behaviour and the tempo of evolution

Patrick Bateson

Sub-Department of Animal Behaviour, University of Cambridge

Four consequences of behaviour are likely to affect the rate of evolution. Many of the ideas are summarised in Bateson (1988), although I have taken them further here.

1. Animals are able to modify their behaviour in response to changed conditions, most obviously by learning. This allows evolutionary change that, otherwise, would probably have been prevented by the death of the animals exposed to those conditions. Ontogenetic adaptation to some environments may be costly for animals equipped with particular kinds of genotype. They can do it, but there is a more efficient way. Evolving efficient specific mechanisms, such as a particular unlearned feature detector, does not mean, however, that the general adaptability would have been lost.

2. By their behaviour animals often expose themselves to new conditions which may reveal heritable variability. This opens up possibilities for evolutionary changes which would not otherwise have taken place.

3. Animals make active choices and the results of their choices have consequences for subsequent evolution, the most famous example being the results of selective mating. When a learning process is involved, such as imprinting in mate choice, then the evolutionary ratcheting process may proceed more rapidly because heritable change is only required in the characteristics that are chosen and not in the the characteristics involved in making a choice. Relatively unexplored evolutionary processes such as "molecular drive" may also interact with behaviour through choice or "adoption" as Gabby Dover calls it. Even though the cohesively evolving population of organisms may develop a feature that would have been maladaptive in the environment in which their ancestors lived, they can move to another environment where the feature works or, at least, is not a handicap.

4. By their behaviour, animals change the physical or the social conditions with which they and their descendants have to cope and thereby affect the subsequent course of evolution. An evolutionary ratcheting mechanism could operate in predator-prey relations as well as in both competitive and

cooperative social relationships within a species. I emphatically agree with Alan Wilson that imitation and cultural transmission is a part of this cluster of mechanisms and was especially important in hominid evolution. However, I also think that other cognitive capacities, learning abilities and elaboration of communication systems are likely to have been involved in the general phenomenon.

The forms of behaviour that can affect the rate of evolution often require relatively complex neural processing, although the first two processes could well have been important in simple organisms. In general, though, it would not be surprising if the rate of behaviourally induced evolutionary change was related to neural capacity and had been especially frequent in complex animals such as birds and mammals. The third process is likely to produce directional change in evolution but would not be expected to feed back on to the cognitive capacity of the brain. However, the fourth process unquestionably would be expected to have such a feed-back effect. Being clever accelerates the evolutionary of becoming cleverer. In other words, it is possible to recognise several independent ways in which behaviour could influence the tempo of evolution in different ways.

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Allan Wilson

The Brain's Role in Driving Body and Brain Evolution

Perhaps the most important gifts made by molecular biology to evolutionary biology are (1) A new and universal way of measuring approximate *time of common ancestry*, i.e., *branching time*, for any pair of genomes. (2) The concept of *biological distance*, which invites us to violate the structure-function paradigm that has ruled biology (including biochemistry and natural history).

EXAMINING THE BASIS FOR MORPHOLOGICAL EVOLUTION

Quantification of Body Evolution

In order to examine the molecular basis of evolution at the organismal level, it is essential to measure both molecular and organismal evolution. With a standard set of linear measurements of bones from all parts of the body, it has been possible to estimate the extent of difference in body plan for any pair of tetrapod vertebrates (Table 1). This estimate, termed morphological distance correlates with distance in the classical taxonomic hierarchy (Fig. 1). The correlation validates morphological distance as a measure of body evolution.

Morphological Rates Correlate with Relative Size of the Brain

Morphological distance divided by time since common ancestry provides an estimate of rate of morphological evolution. The highest rates of morphological evolution are found within the genus *Homo* on the lineage leading to *Homo sapiens sapiens*. Next, come other hominoids, then songbirds, other mammals, other birds, and finally reptiles and amphibians. Relative size of the brain conforms to the same series (Table 2, Fig. 2). One way of explaining this correlation is to suppose that the brain drives organismal evolution, while having apparently no impact on point-mutational evolution in the nuclear genome (Fig. 2).

Brain Size has Risen Hyper-exponentially

We know from fossil studies that the relative size of the brain in early amphibians was about the same as in modern amphibians. It follows that there has been a 100 - fold rise in the relative size of the brain on the lineage leading from early amphibians to humans. Phylogenetic analysis (Fig. 3) suggests that this increase has been hyper-exponential (Fig. 4) as has the increase on the lineage leading to songbirds (Fig. 5). Probably, the tempo of anatomical evolution has also risen (Fig. 6) according to the same hyperexponential law, given the correlation shown in Fig. 2.

How the Brain Drives Body Evolution

The mechanism by which the brain drives body evolution may consist of 3 steps:
1. The rise of a new behaviour in one individual.
2. Social propagation of the new behaviour among individuals of that species.
3. Selection for mutant genes with effects on the body that complement the new behaviour.
Steps 1 and 2 constitute a "cultural shift" (or a "round of cultural evolution"). Such shifts are

known to occur not only in humans but also in other mammals and songbirds. The capacity for such shifts is proportional to relative brain size (Table 3).

How the Brain Drives its Own Evolution

Each round of cultural evolution is expected to select not only for "body" mutations but also for "brain" mutations that improve the ability of organisms to detect, evaluate and copy the advantageous innovative acts of other individuals. New knowledge and its diffusion is thus the catalyst for both body and brain evolution.

Population Biology

The speed and effectiveness of social transmission are expected to depend on the structure and dynamics of populations (Fig. 7). Those vertebrates with the biggest brains (e.g. songbirds and primates) are highly mobile and able to communicate over long distances. Furthermore, if it is true that the basic equation of adaptive evolution is $E = 4N\mu s$, where μ is the mutation rate to advantageous alleles and s is the selective advantage, the fastest evolution in response to a cultural shift will occur in big populations. Small populations will not be efficient at fixing such alleles.

Uncoupling or Peaking Out

When the interval between one cultural shift and the next one becomes very short, as in humans, the opportunity to make a genetic response (step 3) diminishes. From that point onwards, the link between cultural and genetic evolution weakens progressively (Fig. 8). Perhaps this is why the brain stopped getting bigger 100,000 years ago. Cultural evolution can then begin to drive itself directly. At this stage, cultural shifts select among cultural units not for body or brain mutations but for increased capacity to innovate and catch on.

The Implication of Predictability

The observations summarised here were made possible by the "molecular biological" approach, and the model they lead to implies that the *overall rate* and *direction* of evolution above the molecular level are *predictable*. Once a nervous system has evolved any capacity for innovation and social propagation, a positive feedback loop is thereby completed. This loop leads inevitably to a system that innovates and propagates faster and faster. Perhaps evolutionary biology can help us to predict the future!

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Fig. 1

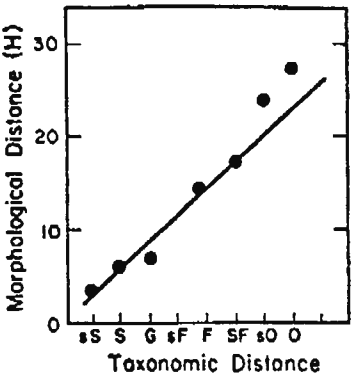
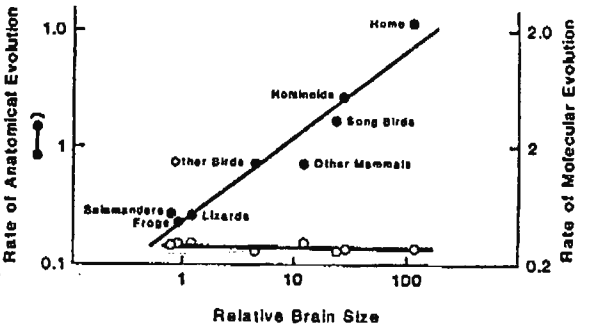


Fig. 2



The points represent morphological distances among independent pairs of birds as a function of distance in the taxonomic hierarchy. The line, by contrast, is for the H values coming from comparisons of frogs, lizards and mammals.

$$H = 0.1 \sum_{i=1}^{8} |x_i - y_i|$$

Fig. 3

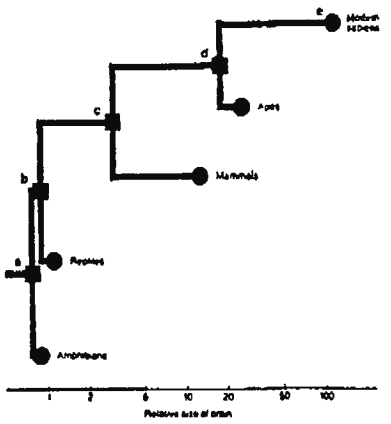


Fig. 4

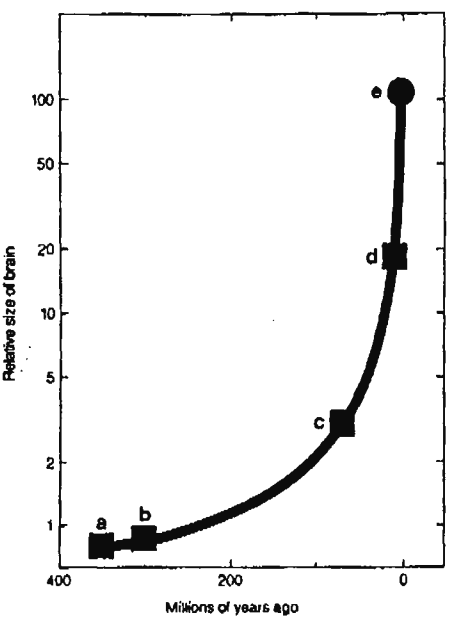


Fig. 5

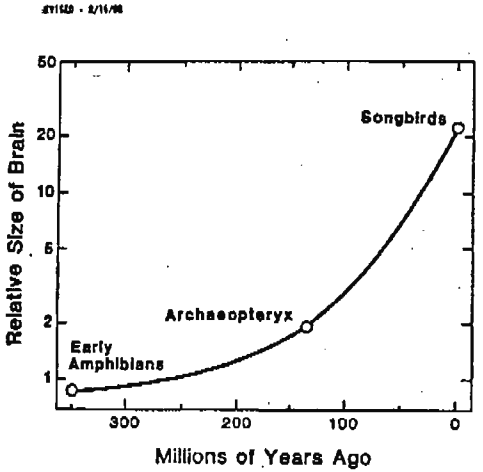


Fig. 6

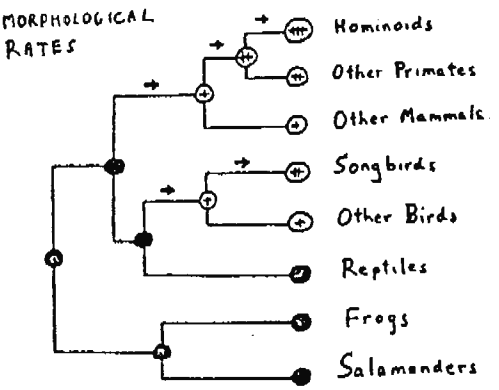


Fig. 7

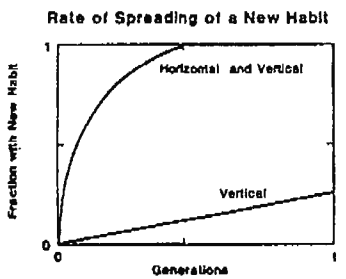


Fig. 8

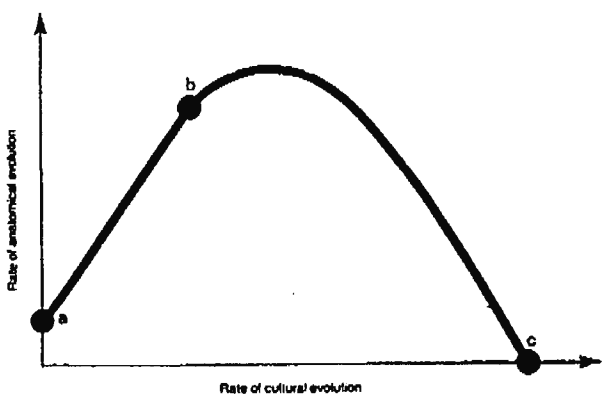


Table 1. Relative Lengths of Morphological Traits in Humans and Chimpanzees.

Trait	Relative Length of Trait: Humans x_i	Chimpanzees y_i	Difference $[x_i - y_i]$
Backbone	393	361	32
Shank	236	174	62
Forearm	167	201	34
Head (length)	70	108	38
Head (width)	59	63	4
Toe	48	51	3
Eye-nostril	15	17	2
Nostril-lip	12	25	13
All traits	1000	1000	190

Table 2. Brain size in relation to rate of anatomical evolution

Taxonomic group	Relative brain size*	Anatomical rate†
Homo	114	>10
Hominoids‡	26	2.5
Songbirds	23	1.6
Other mammals	12	0.7
Other birds	4.3	0.7
Lizards	1.2	0.25
Frogs	0.9	0.23
Salamanders	0.8	0.26

Table 3. DISTRIBUTION OF LEARNING ABILITY

Type of learning	Invertebrates: Most	Invertebrates: Social	Vertebrates: Cold	Vertebrates: Warm	Vertebrates: Humans
Social					
1. Teaching	-	-	-	-	+
2. Imitation	-	-	-	±	+
3. Primitive*	-	±	±	+	+
Individual	+	+	+	+	+

* Social facilitation and local enhancement.

Adolf Seilacher (Tuebingen and Yale Universities)

MORPHOLOGIC TRANSFORMATION IN THE WAKE OF BEHAVIORAL CHANGE.

Constructional morphology, in its initial version, was meant as a working procedure to explain a given structure as a compromise between phylogenetic, fabricational (= morphogenetic) and functional constraints and licenses. Environment was left outside. This becomes inadequate if we compare different taxa, because each species selects from an amorphous environment a different set of factors with varying priorities. This "effective environment" defines the reference points of its fitness and should properly be included in the diagnosis. Because this would be an impossible task for most modern (let alone fossil) species, taxonomists have settled on listing only the collectible, i.e. morphological characters. Nevertheless we should not forget this shortcoming when we try to understand evolutionary processes.

No matter whether the effective environment changes relative to extrinsic (climatic and paleogeographic shifts; prey extinction; new predators etc.) or by intrinsic factors (mating; locomotion; foraging; settlement paterns) the initial step is likely to be behavioral, because behavior establishes the structure of the effective environment.

Morphological change will commonly follow in a second step. It is likely to be punctuated, because it commomly involves the adoption of modular morphogenetic processes from the menu of epigenetic variability. If we deal with self-organizing features related to deterministic chaos (zebra patterns; fractal structures etc.) or to mechanical rules (pneu structures), we may also expect that the generating processes become secondarily "tamed" to conform to a specific functional paradigm.

Two examples may illustrate the role of behavior in morphological transformation. Firstly, S.PETERS (in press) has cited the case of crossbills -- birds whose extravagant beak construction enables them to pick the seeds from pine cones. In fabricational terms, horny beaks grow as a bivalved system of marginally accreting cones.In crossbills, the two beaks miss each other at the tips so that they can grow into unconstrained spirals.The same may happen in starlings, but without the habit of pine-cone feeding it remains a teratological character.

The second example are colonial incrusters on gastropod shells inhabited by hermit crabs. In this situation, species of bryozoans, hydrozoans, zoantharians and scleractinians have modified their growth programs in specific ways. Firstly, the incrusters enlarge the original gastropd shell, but in a planispiral rather than the original helicospiral mode. Secondly, the incrusters develop a horn, or wing, on either side. In the hydrozoan Kerunia (Eocene of Egypt) an additional horn, or tail, developed on the rear side as soon as the crustacean host had stopped to grow.

In the adaptationist stance, Kerunia-like symbioses would be considered as convergent evolution towards a state that suits both partners: the host can remain in the same shell without risking its life when moving into a new home. Cnidarian incrusters also provide him with nematocyst protection. The incruster gains from beeing held upright and allowed to maximize its feeding area. But who controls such a growth program in an anarchic colony?

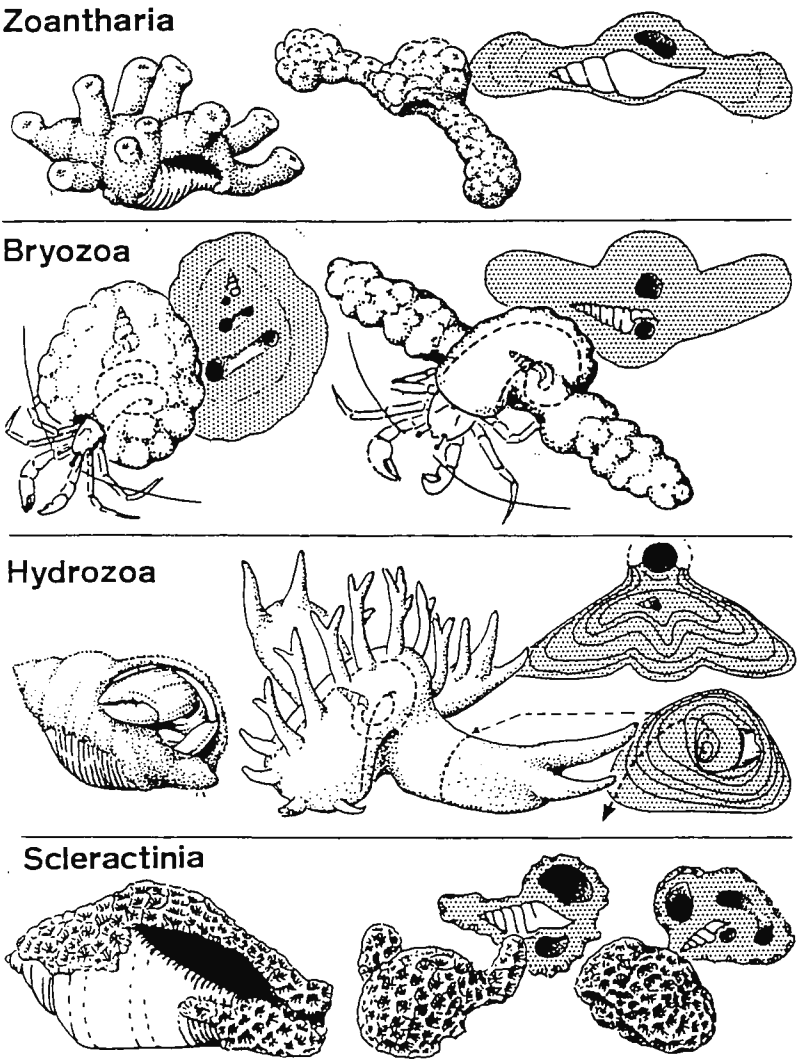
Alternatively, the phenomenon may be interpreted as a cybernetic system, in which the activity and growth of the crustacean inhabitant automatically controls the growth of the incruster. The shell edge part of the colony grows faster because it gets the bread crumbs of the host's meals.Horn growth follows the rotation axis (sometimes with a helicospiral component) because in this direction immersion into the mud is minimal over time.Even the equivalence between the two lateral horns (either both slender or both fat) is automatically controlled, since any imbalance would starve the heavier side by mud-immersion, while the other side proliferates, If we accept this epigenetic model, a change in larval settling behavior (on hermitized shells instead of any kind of hard substrate) suffices to enter the whole Kerunia syndrome.

Conclusions:

1. In an epigenetic view, morphological transformation is likely to be punctuated because it implies the adoption of modular morphogenetic processes. Adopted processes tend to first be neutral and only then become "tamed" towards specific functions by Darwinian selection.
2. Morphological transformation is commonly induced by behavioral changes that alter the effective environment and thereby the reference points of evolution.

Fig.1: The planispiral extension of the original gastropod shell and the addition of lateral horns in colonial incrusters of various affiliation can be explained by a cybernetic system dominated by the growth and actions of the hermit crab host.

COLONIAL PAGURID PICKABACKS



8. SESSION ON SPECIATION AND MACROEVOLUTION

Conference: "REFERENCE POINTS IN EVOLUTION", held by Fundacion Juan March, September, 1990, Madrid, Spain.

Some Reference Points in Macroevolution

Extended Abstract

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Knowledge of paleoenvironmental changes has increased rapidly in recent years. For instance, three astronomically-caused climatic cycles - the Milankovitch cycles - have been documented, with periodicities of ~100,000, 41,000, and 23,000 years. During the Plio-Pleistocene they involved not only large-scale expansion and retreat of polar ice, but also major climatic and vegetational changes in the terrestrial tropics (review in Vrba, 1988]. These cycles, in some form, must have accompanied the entire history of life - a constant 'background ' climatic cycling. Over longer time periods the cyclic mean and mode underwent major changes, for instance during the Plio-Pleistocene near 2.5myr and 0.8myr ago. The cyclic amplitudes were large [at least for some past periods and many areas on earth] relative to the habitat-tolerances of most extant species. Evidence is mounting that most known species survived the 'background' cycles by the passive response of geographic shifting and vicariance of their distributions, without significant evolution and speciation. I will mention some hypotheses we are testing [with R. DeSalle, J. Gatesy, R. Vaisnys], that posit an important role, for the major and less frequent shifts in the Milankovitch cycles, in the evolution of phenotypic novelty and trends, and in the origin of new species.

The "Turnover-Pulse Hypothesis" [Vrba, 1985] states that : Speciations and extinctions do not occur unless initiated by changes in the physical environment. Thus, most lineage turnover in the history of life has occurred in pulses, nearly (geologically) synchronous <u>across diverse phylogenies</u>, and in synchrony with changes in the physical environment. Most turnover-pulses are small peaks involving few lineages and/or restricted geographic areas. Some are massive and of global extent. Under this view, biotic interactions, like predation or competition, occurring on

their own in the absence of physical changes, are not sufficient to cause speciation or extinction. Physical changes are needed to 'kick the system off balance' as it were. Of course, they do this by causing a host of biotic changes. We are currently gathering a combination of cladistic data using morphology, the fossil record, and mtDNA sequences of African antelopes to test the predictions of a restricted version of the turnover-pulse hypothesis : that the major global climatic changes, that in the climatic record occurred from one to several millions of years apart, accounted for the vast majority of lineage branching events.

The 'comparative method' can be used effectively to test evolutionary hypotheses. Once one has a well-supported cladogram from one data set [say, mtDNA sequences], one can compare with it several variables that distinguish species and clades, such as organismal breadth of food-item intake, and tolerance of vegetation types, rainfall, temperature and substrates; and genetic variability, population structure and mobility. I tested whether lineages of biome specialists, because they are more vulnerable to climatic changes, speciated and became extinct more frequently than generalists. The results on twenty African mammals clades supported this, and rejected some other hypotheses, such as that differences in birth rates, and gene flow between populations, might influence macroevolution [Vrba, 1987].

If such climatic influences on macroevolution were generally supported, it would imply several things : Climatically-induced vicariance, resulting in small isolated populations, is important to speciation; and so is phenotypic selection in new environments. We would next want to find out <u>how</u> these agencies act. But this would only be half the story. The question of how novelty arises in the first place, before it can ever be selectively sorted, has been neglected in evolutionary theory. Among other things I would like to find out what heterochronic biases are likely to be introduced, by ontogenetic responses to particular climatic conditions, into the phenotypic spectrum on offer to selection.

The new macroevolutionary studies are expected to result in new theory,

relative to the NeoDarwinian tradition. Theory can be new because it negates elements of, or because it adds elements to the old. I suggest that, at the very least, the new compound data, on how the paleoclimatic record is associated through long time with molecular and phenotypic distributions in genealogies, will lead to additional theory.

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ABSTRACT

Population Structure and Speciation

David B. Wake

There is renewed interest in species and speciational processes. Two extremes of viewpoint are a strict nominalism, to which Van Valen's question - "Why, other than for names, do we need species?" - applies, and a new essentialism, exemplified by the great current interest in the "Recognition concept" of Patterson, with its focus on the fertilization system and mate recognition systems as being the essential elements in origin and recognition of species. There are a spectrum of views between these extremes.

In order to make progresss, we must ask - "to what use is the species concept to be put?". On the one hand, species are seen as outcomes, incidental by-products of a vast diversity of processes. On the other, species are seen as active players in evolutionary and phylogenetic processes. This is not the same dichotomy as that above, and in fact we have a complex of axes that only makes the entire species question increasingly difficult.

For me species are units of phylogeny. They are what fix traits phylogenetically. But this is strictly a result of a sorting process and the speciation is neither the source of the sorting nor of the evolutionary traits that are sorted. I argue, using examples from detailed population-level studies of salamanders in my lab and those of my colleagues, that species are incidental by-products, and that, for the most part, there is no process of speciation (although I do not deny that some processes have as their outcome the production of new species). There are, however, processes that lead to species formation, and one of the most important of these is manifest in population dynamics in time and space.

When one examines the distribution of alleles in space one can infer the level of genetic cohesion (although time and distance are necessarily confounded at present). One finds a relationship between the increase of genetic distance with geographic distance that is characteristic for different taxa. For example, in salamanders there are enormously large Fst values, and it can be argued that the world is relatively enormous for them. In contrast, for most birds the Fst values are relatively low, and so the world is relatively small for them. So, using appropriately scaling and inferring something about gene flow through space and time, one can make inferences concerning genetic cohesion, or lack thereof, and hence be guided in drawing lines between species.

This approach, which I illustrate with some detailed examples in the presentation, will result in more rather than fewer species. While it does not necessarily produce the monophyletic species that workers such as Cracraft desires (it is less than a "maximalist" approach), it is much more useful for understanding the degree of biological diversity in groups and in biogeographic regions than prevailing approaches.

GENETIC INSTABILITY IN SPECIATION

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Two models are prevalent among population evolutionists to explain speciation: the gradualistic model and the disorganization model. In both models the roles of reproductive isolation and population variability are crucial. The gradualistic explanation predicts a correlation between overall genetic divergence, as a measure of evolutionary time, and reproductive isolation. However, several studies suggest that the transition from one taxon without significant reproductive isolation (subspecies or geographical races) to another taxon where the reproductive isolation is already important (semispecies or incipient species) may be achieved without further genetic (allozyme) divergence. These experimental evidences would favor the view that crucial steps in reproductive isolation may be independent of allozyme evolution.

The understanding of speciation is, thus, dependent on the genetic architecture of reproductive isolation. Experiments with Drosophila interspecific hybrids prove that the number of sterility factors is enourmous and can be classified into two types. First, there are many X-linked specific factors distributed all over the X chromosome, any one of which (or a few of them) produces sterility by itself. Second, there are many non-specific factors spread all over the autosomes, which produce dominant sterility only when accumulated in critical amounts. This unambigous dispersive nature of sterility factors requires as a counterpart a dispersive molecular architecture of genetic functions acting in concert during the spermatogenesis. Here, I propose that the dispersed structure of middle repetitive DNA is compatible with these results. Moreover, one outstanding property of these DNA sequences is, under certain circumstances, their ability to transpose throughout the genome in a short time. This would favor the observation of a fast evolution of the reproductive isolation without any further genetic differentiation.

The disorganization of the genome mediated by founder effects requires a whole series of population bottlenecks to produce the necessary gene frequency shifts and fixations. This model predicts the depletion of aditive genetic variability in founder lines. Population geneticists, in general, discard mutation as a main agent to restore variability in founder events and adhere to the classic idea that recombination is sufficient to this purpose. Mutation, as a source of variation, has been considered more as a

passive mechanism that constantly insuflate random variability into populations than as an active performer of evolutionary change. However, the putative constant and steady rate of genetic mutations has been challenged by some historical observations of high mutation rates in natural populations. In general the causes of enhanced mutation rates are unknown, but in some cases natural hybridization and environmental stress have been advanced as triggers of mutational instability.

Recently, there is ample evidence that intraspecific hybridization between certain populations or strains in D.melanogaster produces high genetic instability that generates a series of abnormal traits in hybrid progenies, including sterility and a high frequency of new chromosomal rearrangements and mutations. The biological similarities between intraspecific hybrid dysgenesis and interspecific hybrid abnormalities have been pointed out several times. Recent studies of natural and experimental hybrids show elevated chromosomal mutation rates. In our laboratory high frequencies of new chromosome rearrangements have been induced by introgressive hybridization. These results on interspecific hybrid genetic instability are so similar to intraspecific hybrid dysgenesis that both may be considered as the result of the same genetic phenomenon, namely the activation of mobile elements through hybridization. In our laboratory, preliminary results show that the rate of transposition in Drosophila interspecific hybrids is higher than in inbred lines, but both rates seem to be higher than expected under normal conditions, suggesting that genetic instability is induced not only by hybridization but also by inbreeding.

At present there is increasing evidence that mobile element transposition is also induced by environmental stress. Most stressful population circumstances described as critical to speciation may be linked to episodes of genetic instability. As an example, Wright's shifting balance theory implies an ecological context in which both environmental and genomic stresses are present in marginal unstable demes. This may help to understand how genetic variability can be restored by insertional transposition in critical moments of species formation. Similarly, in the disorganization theory transposition mutability would provide also the needed supply of genetic variability advocated to explain many episodes of founder speciation. Another critical moment of speciation under the gradualistic model is when incipient species meet in zones of secondary contact before they have completed their genetic isolation. New genetic novelties may be produced by the genetic instability created in the hybrids. In Drosophila, some new inversions may be selected for several reasons. First, they may prevent recombination in chromosomal segments longer than the critical size for sterility, thus maintaining in their carriers reproductive

isolation at a maximum. Second, some of these segments covered by inversions may also include coadapted gene complexes. Any inversion sharing both properties would be selected because homozygotes will be perfectly adapted and their genetic isolation maintained through the lowest level of hybrid fertility. If these ideas are accepted, critical evolutionary change would be a discontinuous process in which populations would have to wait for stressful events (ecological or genetic) in order to acquire a new evolutionary pattern through genetic transposition. As I envisage the process, natural selection would still be the guiding force of Evolution, but its role would be much conditioned by the evolutionary potential of the unstable genome.

EFFECT OF SUCCESSIVE BOTTLENECKS OF DIFFERENT SIZES ON THE EVOLUTION OF POSITIVE ASSORTATIVE MATING IN DROSOPHILA

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Genetic drift and particularly founder effects have been postulated by a number of authors as necessary for the formation of new species, in addition of natural selection.

The most explicit model on founder-mediated evolution has been the one of Carson (1975). Carson derived this model by considering the extraordinary evolutive radiation of genus Drosophila in the Hawaiian Islands, where island-specific species seem to have arisen from colonizations by small propagules -perhaps a single gravid female- coming from nearby islands (Carson and Kaneshiro, 1976). He proposed also a experimental way to test the model, the founder-flush-crash protocol where "competent single propagules can be obtained, an artificial flush and crash cycle induced and the results examined" (Carson, 1971). In this paper we show the results given by an experiment designed to test this founder effect hypothesis.

Two populations of Drosophila pseudoobscura were chosen as ancestral populations for the protocol. They were established in June 1984 combining a number of flies from captures at two localities (BC=Bryce Canyon, USA, and M=Mexico), and hence each one represents the respective local population (they are not artificial polyhybrid populations, as were criticised in previous experiments).

In December 1984, 27 derived populations were initiated from BC ancestral population (BCA) and 18 from M ancestral population (MA). Ancestral as well as derived populations were cultured in bottles.

Each derived (colonizer) population was founded with N virgin pairs, being N = 1, 3, 5, 7, or 9. Then, we allowed them to grow exponentially (flush phase). At each generation only 100 flies are taken to continue the population, and the rest is discarded. These 100 flies are distributed in 5 bottles. Every 100 flies are randomly chosen from the former generation bottles. Thus we can get an exponential growth with a limited number of bottles. During flush a lot of recombinant genotypes are thought to appear. Due to the little restrictive culture conditions (about 10 adult females per bottle) most new genotypes will survive, and due to the flush itself some of them will become dominant in the population. Derived populations are thought to evolve in this way from ancestral and one from another.

After 4 to 7 generations a crash is induced. All the emergence of two bottles of the last flush generation is entered in a single bottle. Among the emergence of this bottle, N virgin pairs are picked up to begin another flush-crash cycle. These flies are survivers of the more stringent selective conditions (more than 100 adult females per bottle) of the crash generation, and therefore good competitors are selected among the novel genotypes.

Two sets of inbred control populations have been considered. One set consists of six "endogamic" populations, three obtained from each ancestral population, and maintained by eight generations of brother x sister matings and then by serial transfer. The other set consists of six "prima" populations undergoing flush-crash cycles but with a (one-pair) bottleneck lasting three generations instead of only one. The BCA x MA cross stands for a non-flush non-bottleneck control.

We performed multiple choice mating tests with 12 6-day-old virgin males and females of two populations, by putting them together in mating chambers during 45 min. At least four replications were done for each test. In order to discriminate flies from each population we clipped the tip of the wings in two of the four sex-population combinations. Data was analyzed with the Y assortative mating index (Ringo, 1987):

$$Y = \frac{\sqrt{(AD/BC)}-1}{\sqrt{(AD/BC)}+1} ,$$

where A and D are the numbers of homogamic matings and B and C the numbers of heterogamic matings. The statistic X2(Y), chi-square distributed with one-degree of freedom, can be used to test Y:

$$X2(Y) = \frac{(\ln AD/BC)^2}{1/A+1/B+1/C+1/D}$$

Y ranges from -1 to +1, where negative and positive values stand for negative and positive assortative mating, and zero for random mating.

More details on material and methods can be found in Galiana et al. (1989).

RESULTS AND DISCUSSION

Four sets of experiences have been carried out. In the first one (4th cycle, beginning in October 1986) we chose ancestrals plus ten derived populations, one per bottleneck size and origin. In the second one (5th cycle, January 1987) we took ancestrals plus all populations founded with 1 or 3 pairs. In the third one (7th cycle, October 1988) we used ancestrals plus all derived populations with bottleneck sizes of 5, 7 and 9

pairs; furthermore, the 15 mating experiments implying populations MA, BCA, M3, BC2, M7, and BC7, already tested at 4th and 5th cycles, were repeated again. The fourth set corresponded to prima (7th cycle, July 1988) and endogamic populations.

Summarizing, there is a total of 40,257 matings recorded. They represent about 75% of the maximum number of possible matings. There is no evidence of positive assortative mating among control crossses, except one case (out of 36) between prima populations (and only at the 0.05 level). The BCA x MA cross has always yielded a non significant deviation from random mating (Y values of 0.081, 0.068, 0.135 for 4th, 5th and 7th cycles, respectively).

All other mating experiencies can be divided in two types: those involving one ancestral and one derived population and those between derived populations. From a total of 118 ancestral-derived crosses 11 (9.2%) showed significant possitive assortative mating, 9 at the 0.05 level and 2 at the 0.01 level, and 5 (4.2%) showed significant negative assortative mating at 0.05 level. The two only significant crosses at the 0.01 level were between population BC22 (N=7) and either BCA or MA:

BC22 x BCA Y=0.287 BC22 x MA Y=0.280

Among the 370 between-derived crosses 36 (9.7%) showed significant positive assortative mating (23 at the 0.05 level and 13 at the 0.01 level), and only 4 (1.1%) significant negative assortative mating (3 at 0.05 level and 1 at 0.01). Considering bottleneck size, crosses between populations founded with 1 or 3 pairs showed (19 crosses at the 5th cycle, 11.1%) an almost two-fold number of significant positive assortative mating cases than populations founded with 5, 7 or 9 pairs (9 crosses at the 7th cycle, 6.1%). The difference is bigger if we consider the 0.01 level of significance.

In both types of crosses the fraction of positive assortative mating exceeds the one expected by chance.

The highest Y values correspond to the lowest bottleneck sizes, i.e. 1 and 3 pairs:

M7 (3p) x BC10(3p) Y=0.527
M3 (1p) x BC11(3p) Y=0.412
BC33(1p) x BC32(1p) Y=0.390
M12 (3p) x BC12(3p) Y=0.374
M3 (1p) x BC7 (3p) Y=0.363

Sixteen populations are not involved in any significant cross, and almost all of them belong to the wider bottlenecks (2 5-pair, 5 7-pair, and 8 9-pair populations). On the other hand, some derived populations are involved several times in homogamic crosses. Populations M3 (1-pair) and BC7 (3-pair) are found in 5 out of 18 tested crosses; M14 (5-pair) in 4 out of 15; BC32 (1-pair), M5 (1-pair) and BC12 (3-pair) in 3 out Of 18; BC22 (7-pair) in 2 out of 8, etc. Populations M3 and BC7 not only show strong significant assortative mating against the rest of

populations, but also between them in all three times that they were tested in mating experinces. All this indicates the stability of the achieved positive assortative mating.

M3 x BC7 Y=0.293(4th) Y=0.363(5th) Y=0.161(7th)

We have attained partial assortative mating after a founder-flush-crash protocol. There is a clear bias towards positive assortative mating in individual crosses as well as in accumulated data. The appearance of ethological barriers following this protocol supports Carson's model of speciation.

Only one founder-flush-crash experiment succeeded in the past to obtain stable significant assortative mating, the one carried out by Powell also with D. pseudoobscura (Dodd and Powell, 1985). Another experiment by Ringo with D. simulans (Ringo et al., 1985) gave little and erratic assortative mating, being the main result the lowering of mating propensities of derived populations (Ringo, 1987); D. simulans was probably a bad competent species for such an experiment, because of its cosmopolitan nature, its little resistance to inbreeding, and its short recombinational map (see Templeton, 1980).

Only one-pair derived populations had been studied in those previous experiments. Our one-pair populations show 3 cases of significant positive assortative mating, 13.0% (1 at 0.01 level). Powell obtained a higher fraction, but after removing some experimental populations. We have proved that very narrow bottlenecks are optimal for the evolution of assortative mating in flush-crash experiments, and this finding supports the assumption of Carson that species can originate from a propagule of just one male and one female, or a little more than that.

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Macroevolution and early metazoan evolution

S. Conway Morris

Notwithstanding the many imperfections of the fossil record, it is clear that the early Palaeozoic (ca. 550-450 Myr) saw an unprecedented diversification of metazoans. This is evident from (a) skeletal remains, albeit often fragmented and incomplete, (c) trace fossils, of vital importance because they reflect the innovation of behavioural repertoires of most soft-bodied animals, and (c) Burgess Shale-type faunas that include a number of seemingly problematic forms like Anomalocaris and Hallucigenia.

In terms of orthodox taxonomy this diversification is encapsulated in the oft-repeated statement that most phyla and classes evolved during this interval, with much of the rest of the Phanerozoic seeing an exploration of variations on a theme rather than wholesale novelty.

There are several popular, and not necessarily mutually incompatible, hypotheses to explain the rise of so many Bauplan over a geologically short interval. These include a subdued adaptive landscape and ease of transition from one point to another, possibly assisted by low levels of competition. Intrinsic controls have focussed on ease of developmental re-regulation, with a fluid genome permitting repatterning. More arcane proposals include a prevalence of laterally transferred genetic information.

With growing knowledge of developmental regulation and the role of heterochrony, the differences and similarities in metazoan architecture are beginning to become more clear. Fundamental similarities in some developmental genes suggest that aspects such as segmentation may have

evolved at an early stage of metazoan phylogeny. Study of sequences, such as ribosomal RNA, is also presenting new insights into metazoan phylogeny.

In all these discussions, however, the details of the fossil record, especially recent advances in the earliest skeletal faunas and Burgess Shale-type faunas, has not been incorporated fully in the discussions. The palaeontological record has been largely treated from an essentialist stance, whereas it could be argued that the morphological range is not only defined by end-members but also a wide range of intermediates that define a type of morphological continuum. Weeding out of this range of morphologies followed by rediversification of the surviving taxa to give the major clades that we define as phyla and classes is evident. This is not to deny that macroevolutionary processes and alterations in developmental sequences did not play a part in early metazoan diversification, but the historical opportunities of a filling ecological barrel seem to be of considerable significance in understanding this evolutionary episode.

CONCLUDING REMARKS

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As my fellow co-organizer of this conference, Gabriel Dover, points out in the introduction, the advent of radically new information makes it imperative for scientists to get together and wonder what it is all about. Evolutionary biology is no exception, with the added ingredient that since its inception it has been an interdisciplinary field. The breadth of areas of inquiry with direct relevance to evolution makes it even more important to have meetings that allow scientists from different disciplines to share and discuss recent developments in their respective fields and speculate on their implications. This is basically what we did at this workshop.

To set a meeting, however, is not sufficient; there is also a need of succesful communication among scientists from ever more and more jargonized and specialized fields. It would be foolish to attempt to summarize the main conclusions, if any, of a meeting in this sort. For such a reason I have choosen to comment on the subject of interdisciplinary communication. This was an aspect on which the workshop was particularly succesful, not only in my opinion but also corroborated by the comments of many participants.

Towards the end of the seventies the advent of new and powerful molecular techniques, combined with a reassesment of the nature of the fossil record, made it evident that a critical re-evaluation of the neo-Darwinian paradigm was in order. I believe that a critical turning point in the setting up of a revised, or expanded, theory of evolution occurred in a major symposium around the theme of "macroevolution" held in Chicago (Fall of 1980). The meeting, was attended by most leading evolutionists including some historical figures of the neodarwinian theory such as Sewall Wright and Leynard Stebbins. The discussions that occurred there clearly identified the major ingredients of a potential new synthesis. In particular, there was agreement in the need to incorporate the new developments in molecular and developmental biology, reasses the role of natural selection, and quantitatively evaluate the patterns of evolution as evidenced in the fossil record. The Chicago meeting had a large repercusion in the popular press and it served to catalyze a variety of subsequent smaller workshops. Curiously, the organizers felt at the time that nothing new had been said and decided it was not necessary to publish the proceedings. Later, selected articles from the symposium were published by the journal EVOLUTION in 1982, and other presentations appeared in prestigious trade journals such as SCIENCE and PALEOBIOLOGY. In retrospecty, it must have been one of the very few times in which a symposium volume would have been of historical interest.

I had the opportunity to participate, in one of the workshops that originated from the excitement triggered by the Chicago Symposium. It was organized by the Dahlem Foundation and held in Berlin in 1981 (Bonner, J. ed. 1982, Evolution and Development, Springer-Verlag, Berlin). Its objetive was very similar to the current Juan March Workshop, which consisted in bringing molecular and developmental biologists together with morphologists, ecologists and paleobiologists.

As I sat listening to the discussions of the past three days, I could not resist comparing the atmosphere among these three meetings. Chicago was key in identifying the main issues and triggering polarized controversies and polemics. It generated excitement. Berlin was somehow anti-climatic because, with the enlightement from hindsight, it was evident that it was premature. There was no possibility of constructive dialogue between evolutionists and molecular biologists because they were not speaking the same language. Most of the time was spent explaining to the opposite camp why what one worked on was worth exploring. There was no common ground.

Nine years afterwards, the situation has dramatically changed. Today there is no need to justify yourself; evolutionists are convinced that molecular biology cannot be ignored since it is providing important new insights and changing the structure of the theory of evolution. Simultaneously, more and more, molecular biologists are discovering Dobzhansky's "ditto" that claims that "nothing makes sense except under the light of evolution". Similarly, controversies within evolutionary biologists, such as selection vs. constraint or punctuated equilibrium vs. phyletic gradualism, which polarized the discussions in 1980, played a a very minor role in this meeting. The atmosphere was a congenial one, interested and conducive to a constructive debate of results and ideas.

I cannot integrate the concepts that were presented, and which are reported in this booklet, but I believe most of the participants felt this change in the atmosphere of the debate. The new conceptual framework that evolutionists were demanding in Chicago-1980 may already be here. But, perhaps, we are never able to experience the present because when it creeps on us, we interpret it in terms of the past.

LIST OF INVITED SPEAKERS

Workshop on

THE REFERENCE POINTS IN EVOLUTION

List of Invited Speakers

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THE REFERENCE POINTS IN EVOLUTION

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Course on DNA - Protein Interaction.

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J. Burgyan, J. R. Díaz Ruiz, W. G. Dougherty, F. García-Arenal, W. L. Gerlach, A. L. Haenni, E. M. J. Jaspars, D. L. Nuss, P. Palukaitis, Y. Watanabe and M. Zaitlin.

254 **Advanced Course Biochemistry and Genetics of Yeast.**
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