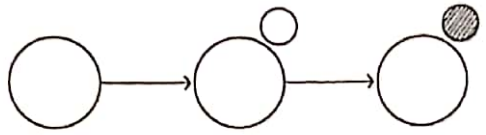
1.1 Synthetic Darwenism

(a) Peripatric or Transilience Speciation

A founder effect model of allopatric speciation in which the new species is formed from a small population isolated (bud off) at the edge or periphery of the ancestral (parental) population of geographic range.

Speciation is speedy due to genetic drift and fixation of random alleles.



Ancestral (Parental) New species

Example: Plumage variation of kingfisher (*Tanyisptera hydrocharis galeata*) of New Guinea.

(b) Vicariant Speciation

In this type of speciation, a large widespread population are separated by the emergence of an extrinsic or topographic or ecological barrier and one or both populations diverge from ancestral population (state).

Example: Emergence of isthmus Panama in the Pliocene divided many marine organism into pacific and caribean population.

Neutral theory and Synthetic theory at the molecular level

All regions of a gene do not mutate equally in all lineages at all times. Some regions in a structure of a gene (DNA) are constraint for change while others are susceptible to incidental change. The constraint region of within the structure of a gene directly affects the gene product.

The rate of mutation at the constraint sites in the gene is slow, but is faster in the other regions that do not affect function of the gene product.

(i) The **Shine-Dalgarno Sequence** (SDS) in the leader region, TATA sequence in the promoter region and the base at the second position of the codons are constraint sequences of a functional gene.

(ii) If random base replacements occur in the SDS, the resulting mRNA would fail to bind to the smaller subunit of ribosome and affects translation.

(iii) If mutation occurs in TATA sequence, the RNA polymerase would fail to bind with promoter and affects transcription.

(iv) If mutation occurs in the second position of the codon, it would often result in an altered amino acid of the polypeptide chain.

(v) If mutation occurs in coding region due to loss or gain of a base, it would often change the frame-shift, resulting in the formation of biologically inactive protein.

(vi) Under such conditions, the mutations in the constraint region of a gene are often harmful while those in non-constraint regions are neither harmful nor useful but neutral in activity.

Neutral theory of molecular evolution describes the fate of purely neutral mutation, i.e., those that neither enhance nor lower fitness. One possible fate is that a mutation will become fixed, i.e., attains a frequency of 1.0 — entirely by chance.

(vii) The probability that this will occur equals 'U', the rate at which neutral mutation arises. In each generation, therefore, probability is 'U' that a mutation that occured as sometime in the past will become fixed.

After the passage of 't' generation, the fraction of mutation that will have become fixed is, therefore, $\lambda = Ut$.

(viii) If two species diverged from a common ancestor 't' generation ago, the expected fraction of fixed mutation in both species is $D = 2\lambda t$, since various mutations have become fixed in both lineages. If the mutation in question are base pair changes, a fraction $D = 2\lambda t$ of the base pairs of gene should differ between the species assuming that all base pairs are equally likely to mutate. Thus, the average mutation per base pair per generation is $U = D/2t$.

Thus, we can estimate U if we can measure the fraction of base pairs in a gene that differ between the two species (D) and if we can estimate the number of generation since they diverged from their common ancestor (t).

If U_0 is the rate of selectively neutral mutation per gene per generation, the substitution rate (the rate of replacement in a population) is independent of population size and is $k = U_0$ per generation (the substitution per unit time is k/g where 'g' is the length of generation). Thus, two population of a species that have been isolated for 't' generation are expected to differ by $2U_0t$ substitution.

(ix) Variation within a population at equilibrium measured the frequency of hetrozygotes per nucleotide site is $4NeU_0$, where Ne = effective populaion size. The quantity of $4NeU_0$ is often denotd by θ.

(x) The neutral mutation θ can be estimated by 'S', the number of segregating (variable) nucleotide sites in a sample of gene copies (sequence) or by 'd' the average number of nucleotide differ as between pairs of sequences in a sample.

(xi) Natural selection can modify these pattern in three ways:

(a) **Purifying selection**: Eleminates or reduces the frequency of deleterious mutation in a population.

(b) **Positive selection** (directional): It fixes a sequence genes that includes advantageus mutation.

(c) **Balancing selection**: Owing to a factor such as heterozygote advantage, frequency dependent selection or variable selection maintains variant sequences in a population.

- **Reconciliation between Neutral theory and Synthetic theory**

(i) During a given interval, the number of nucleotide or amino acid replacement is found to be rare in a locality in a particular season. This may be the result of **natural selection**.

(ii) During the adjustment of an evolutionary lineage to a new environment, simultaneous changes are required in many functions. Then chance itself can cause an abrupt increase in the rate of genetic changes.

(iii) In a particular season of the annual climatic cycle, some species become rare in a locality and abundant in other seasons. The rarity is the bottleneck of the species. When species passes through a population bottleneck the neutral alleles can gain momentous importance and in the right combination, they may become dominant in the genetic makeup of the population for survival and reproduction. If the function of a gene does not change in the period of its evolution, there is no reason to expect fluctuation in rate at which it evolves.

(iv) The magnitude of the variation makes it possible to assert that most differences among alleles in a population are adaptively neutral. They are unselectd variation. In contrasts neo-Darwinians are accustomed to thinking of evolution resulting from accumulation of favourable or beneficial mutation.

Here a conflict arises between Darwinian and neutralists.

The reconciliation of the two points of view lies in that even though majority of the mutations are neutral, a few may have adaptive effect and they would be able to supply enough raw materials for the novelties by natural selection.

- **State briefly the Neutral theory of Molecular evolution**

At the molecular level most evolutionary changes and most variation within and between the species is not caused by natural selection, but by genetic drift of mutant alleles that are neutral.

(i) A neutral mutation is one that does not affect an organisms ability to survive and reproduce. In population genetics, mutations in which natural selection does not affect the spread of the mutation in a species are termed **neutral mutation**.

(ii) Neutral mutations that are inheritable and not linked to any genes under selection will either be lost or will replace all other alleles of the gene. This loss or fixation of

the genes proceeds on the basis of random sampling, i.e., known as a **genetic drift.**

(iii) A neutral mutation that is in linkage disequilibrium with other alleles that are under selection may proceed to loss or fixation via genetic hitchhiking and or back ground selection. The rate of fixation is the rate at which gene mutate to selectively neutral alleles.

The rate of fixation is equal to the neutral mutation rate. Suppose, the population size is N and each generation, a fraction of μ of the 2N copies of gene, mutate to selectively neutral alleles. Let also assume each new mutant is unique. In each generation selectively neutral mutation appear in the population will be $2N\mu$. As each mutant is unique and its frequency will be $\frac{1}{2}N$. This probability of fixation of new mutation will be $\frac{1}{2}N$. Number of each mutant appearing in each generation is $2n\mu$. This rate of fixation of selectively neutral mutant is $2N\mu \times \frac{1}{2}N = \mu$. Therefore, for selectively neutral mutation the rate of molecular evolution is equal to rate at which the mutation occurs in population.

(iv) Many mutations in genome may decrease organisms ability to reproduce (fitness). These mutations are selected against and not passed on to 'future generations'. The most commonly observed mutations defectable as variations in organism and populations appear to have no visible effect in fitness of individuals and are therefore neutral.

(v) The rate of evolution does not depend on population size, or the efficiency of selection peculiarities of mating system. Furthermore, if neutral mutation rate is constant, the nucleotide and amino acid substitution should occur in clockwise fashion in all evolving lineages. The neutral theory has had an enormous impact on the study of evolute at molecular level.

(vi) Neutral mutations are also the basis for using molecular clocks to identify speciation and adaptive radiation.

MOLECULAR PHYLOGENY

The graphic representation of evolutionary relationship among biological entities, i.e., phylogenic tree (individual population, species or higher taxa) based on the divergence observed within a single homologous gene by using a combination of molecular data (such as DNA and protein sequences, presence or absence of transposable element and gene order data) and statistical technique is called **molecular phylogeny** or **phylogenies.**

Most phylogenetic trees generated by molecular data analyses and are prone to uncertainties which may differ in some respect from the true tree is sometimes called **inferred tree.**

- **Features:**
  - (i) All living things (both extant and extinct) on the earth share a single common ancestor that lived 4 billion years (approx) ago.
  - (ii) All phylogenetic trees include some portion of their common ancestor with branches which connect two/more adjancent nodes.
  - (iii) Terminal nodes indicate the latest taxa and internal node represent the common ancestors before branching.
  - (iv) The length of the branches indicate the degree of divergence between the **genes** represented by the **nodes.** Internal nodes represent a common ancestor before branching.
  - (v) As internal node representing a common ancestor to all other nodes is called **rooted tree.**

    In **unrooted** trees, there is no common ancestors, the tree specifies only the relationship between nodes.
  - (vi) Rooted trees provides information on the past evolutionary event, that led to the organisms or DNA sequences being studied. Unrooted trees does not tell us there evolutionary pathway.

- **Methods of Reconstruction of Phylogenic relationship**
  - A. Distance-Matrix approach
  - B. Parsimony based approach
  - C. Maximum likelyhood approach.