

Topic : DSE 3 (UNIT 1 : EVOLUTION OF MICROBIAL GENOME)

SALIENT FEATURES OF SEQUENCED BACTERIAL GENOME

- Bacterial genomes can range in size anywhere from 139 kbp to 13,000 kbp. Recent advances in sequencing technology led to the discovery of a high correlation between the number of genes and the genome size of bacteria, suggesting that bacteria have relatively small amounts of junk DNA.
- Studies have since shown that a large number of bacterial species have undergone genomic degradation resulting in a decrease in genome size from their ancestral state. Over the years, researchers have proposed several theories to explain the general trend of bacterial genome decay and the relatively small size of bacterial genomes. Compelling evidence indicates that the apparent degradation of bacterial genomes is owed to a deletional bias.
- In prokaryotes, most of the genome (85-90%) is non-repetitive DNA, which means coding DNA mainly forms it, while non-coding regions only take a small part. Most biological entities that are more complex than a virus sometimes or always carry additional genetic material besides that which resides in their chromosomes. In some contexts, such as sequencing the genome of a pathogenic microbe, “genome” is meant to include information stored on this auxiliary material, which is carried in plasmids. In such circumstances then, “genome” describes all of the genes and information on non-coding DNA that have the potential to be present.
- Amongst species of bacteria, there is relatively little variation in genome size when compared with the genome sizes of other major groups of life. Genome size is of little relevance when considering the number of functional genes in eukaryotic species. In bacteria however, the strong correlation between the number of genes and the genome size makes the size of bacterial genomes an interesting topic for research and discussion. The general trends of bacterial evolution indicate that bacteria started as free-living organisms. Evolutionary paths led some bacteria to become pathogens and symbionts.

- The lifestyles of bacteria play an integral role in their respective genome sizes. Free-living bacteria have the largest genomes out of the three types of bacteria; however, they have fewer pseudogenes than bacteria that have recently acquired pathogenicity. Facultative and recently evolved pathogenic bacteria exhibit a smaller genome size than free-living bacteria, yet they have more pseudogenes than any other form of bacteria. Obligate bacterial symbionts or pathogens have the smallest genomes and the fewest number of pseudogenes of the three groups. The relationship between life-styles of bacteria and genome size raises questions as to the mechanisms of bacterial genome evolution.
- Researchers have developed several theories to explain the patterns of genome size evolution amongst bacteria. One theory predicts that bacteria have smaller genomes due to a selective pressure on genome size to ensure faster replication. The theory is based upon the logical premise that smaller bacterial genomes will take less time to replicate. Subsequently, smaller genomes will be selected preferentially due to enhanced fitness.
- Deletional bias selection is but one process involved in evolution. Two other major processes (mutation and genetic drift) can be used to explain the genome sizes of various types of bacteria.
- Evidence of a deletional bias is present in the respective genome sizes of free-living bacteria, facultative and recently derived parasites and obligate parasites and symbionts. Free-living bacteria tend to have large population sizes and are subject to more opportunity for gene transfer. As such, selection can effectively operate on free-living bacteria to remove deleterious sequences resulting in a relatively small number of pseudogenes. Continually, further selective pressure is evident as free-living bacteria must produce all gene-products independent of a host. Given that there is sufficient opportunity for gene transfer to occur and there are selective pressures against even slightly deleterious deletions, it is intuitive that free-living bacteria should have the largest bacterial genomes of all bacteria types. Recently formed parasites undergo severe bottlenecks and can rely on host environments to provide gene products. As such, in recently formed and facultative parasites, there is an accumulation of pseudogenes and transposable elements due to a lack of selective pressure against deletions. The population bottlenecks reduce gene transfer and as such, deletional bias ensures the reduction of genome size in parasitic bacteria.

GENE VERSUS GENOME

| | |
|--|---|
| A gene is a part of a DNA molecule | The genome is the total DNA in a cell |
| Hereditary element of genetic information | All set of nuclear DNA |
| Encodes protein synthesis | Encodes both proteins and regulatory elements for protein synthesis |
| Length is about a few hundreds of bases | Length of the genome of a higher organism is about billion base pairs |
| A higher organism has about thousands of genes | Each organism has only one genome |
| Variations of the gene named alleles can be naturally selected | Horizontal gene transfer & duplication cause large variations in the genome |

A genome is an organism's complete set of DNA, including all of its genes. Each genome contains all of the information needed to build and maintain that organism. In humans, a copy of the entire genome—more than 3 billion DNA base pairs—is contained in all cells that have a nucleus.

Prokaryotic vs. eukaryotic genomes

| Prokaryotic | Eukaryotic |
|--|---|
| No-nonsense genomes – nearly all coding | Lots of noncoding regions (introns, intergenic regions) |
| Frequent horizontal gene transfer (HGT) | Less frequent HGT |
| Circular genome plus plasmids | Distinct linear chromosomes |
| Operons | More dispersed regulation |
| Streamlined genomes, few repetitive elements | Abundant repetitive elements |
| Very rapidly evolving in both sequence and structure | More conservative mode of evolution |
| Very large population sizes (10^9 - 10^{10}) | Smaller population sizes ($\sim 10^3 - 10^4$) |

Microbial genomes encompass all chromosomal and extra chromosomal genetic material. The study of genomes as an entity as opposed to individual genetic components is referred to as genomics. Microbial genomes are widely variable and reflect the enormous diversity of bacteria, archaea and lower eukaryotes.

Genome sequencing is figuring out the order of DNA nucleotides, or bases, in a genome—the order of As, Cs, Gs, and Ts that make up an organism's DNA.

Gene Pool: Gene pool consists of all the genes and their alleles present in all individuals which can hybridize with each other.

Types of gene pool

Primary gene pool (GP1)

- The gene pool in which intermating (crossing) is easy and leads to production of fertile hybrids is known as primary gene pool.
- It includes plants of the same species or of closely related species which produce completely fertile offspring on intermating.

Secondary gene pool (GP2)

- The genetic material that leads to partial fertility on crossing with GP1 is referred to as secondary gene pool.
- Transfer of gene from such material to primary gene pool is possible but difficult.

Tertiary gene pool (GP3)

- The genetic material which leads to production of sterile hybrids on crossing with primary gene pool is termed as tertiary gene pool. It includes material which can be crossed with GP1, but the hybrids are sterile.
- Transfer of genes from such material to primary gene pool is possible with the help of special techniques.

- Genomics reveals surprising variation in gene pool of even a single species
 - Perhaps 75% of *E. coli* genes found in all strains
 - Termed *core genome* of species
 - Remaining make up mobile gene pool
 - Plasmids, transposons, genomic islands, phage DNA

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| TABLE 8.4 The Mobile Gene Pool | | |
|--------------------------------|---|---|
| | Composition | Property |
| Transposons | | |
| Insertion sequences (ISs) | Transposase gene flanked by short repeat sequences | Move to different locations in DNA in same cell |
| Composite transposons | Recognizable gene flanked by insertion sequences | Same as insertion sequences, but encode additional information |
| Plasmids | | |
| | Circular double-stranded DNA replicon; smaller than chromosomes | Generally code only for non-essential genetic information |
| Genomic Islands | | |
| | Large fragment of DNA in a chromosome or plasmid | Code for genes that allow cell to occupy specific environmental locations |
| Phage DNA | | |
| | Phage genome | May encode proteins important to bacteria |

Shinji

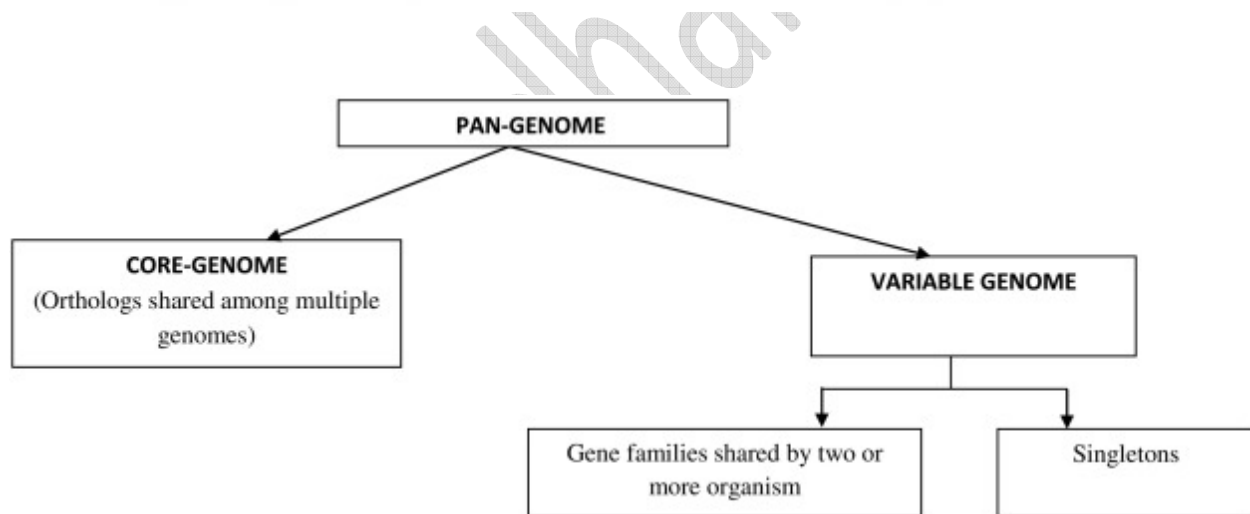
Core and Pan Genomes

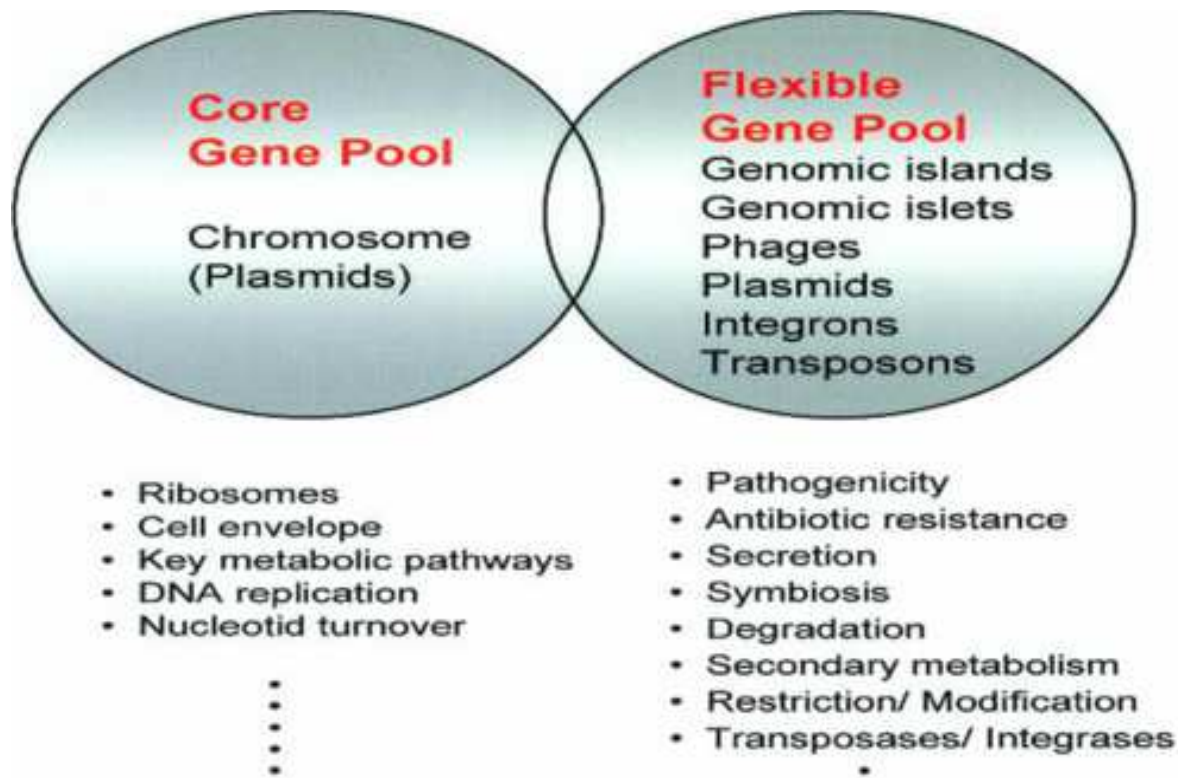
- The **Core Genome** consists of genes shared by all the strains studied and probably encode functions related to the basic biology and phenotypes of the species
- The **Pan-Genome** is the sum of the above core genome and the dispensable genome
 - The dispensable genome contributes to the species' diversity and probably provides functions that are not essential to its basic lifestyle but confer selective advantages including niche adaptation, antibiotic resistance, and the ability to colonize new hosts.
- The Pan-Genome tends to be much much larger than the Core Genome of a prokaryotic “species”

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TERMINOLOGIES:

- ▶ **Core genome**
 - ▶ pool of genes shared by all members of a bacterial species
- ▶ **Accessory or dispensable genome**
 - ▶ pool of genes present in some but not all genomes within the same bacterial species
- ▶ **Pangenome**
 - ▶ global gene repertoire of a bacterial species, comprised of core genome + accessory genome
- ▶ **Metagenome**
 - ▶ global gene repertoire of mixed microbial population





HORIZONTAL GENE TRANSFER

Horizontal gene transfer, also called **lateral gene transfer**, the transmission of DNA (deoxyribonucleic acid) between different genomes. Horizontal gene transfer is known to occur between different species, such as between prokaryotes (organisms whose cells lack a defined nucleus) and eukaryotes (organisms whose cells contain a defined nucleus), and between the three DNA-containing organelles of eukaryotes—the nucleus, the mitochondrion, and the chloroplast. Acquisition of DNA through horizontal gene transfer is distinguished from the transmission of genetic material from parents to offspring during reproduction, which is known as vertical gene transfer.

Horizontal gene transfer is made possible in large part by the existence of mobile genetic elements, such as plasmids (extrachromosomal genetic material), transposons (“jumping genes”), and bacteria-infecting viruses (bacteriophages). These elements are transferred between organisms through different mechanisms, which in prokaryotes include transformation, conjugation, and transduction. In

transformation, prokaryotes take up free fragments of DNA, often in the form of plasmids, found in their environment. In conjugation, genetic material is exchanged during a temporary union between two cells, which may entail the transfer of a plasmid or transposon. In transduction, DNA is transmitted from one cell to another via a bacteriophage.

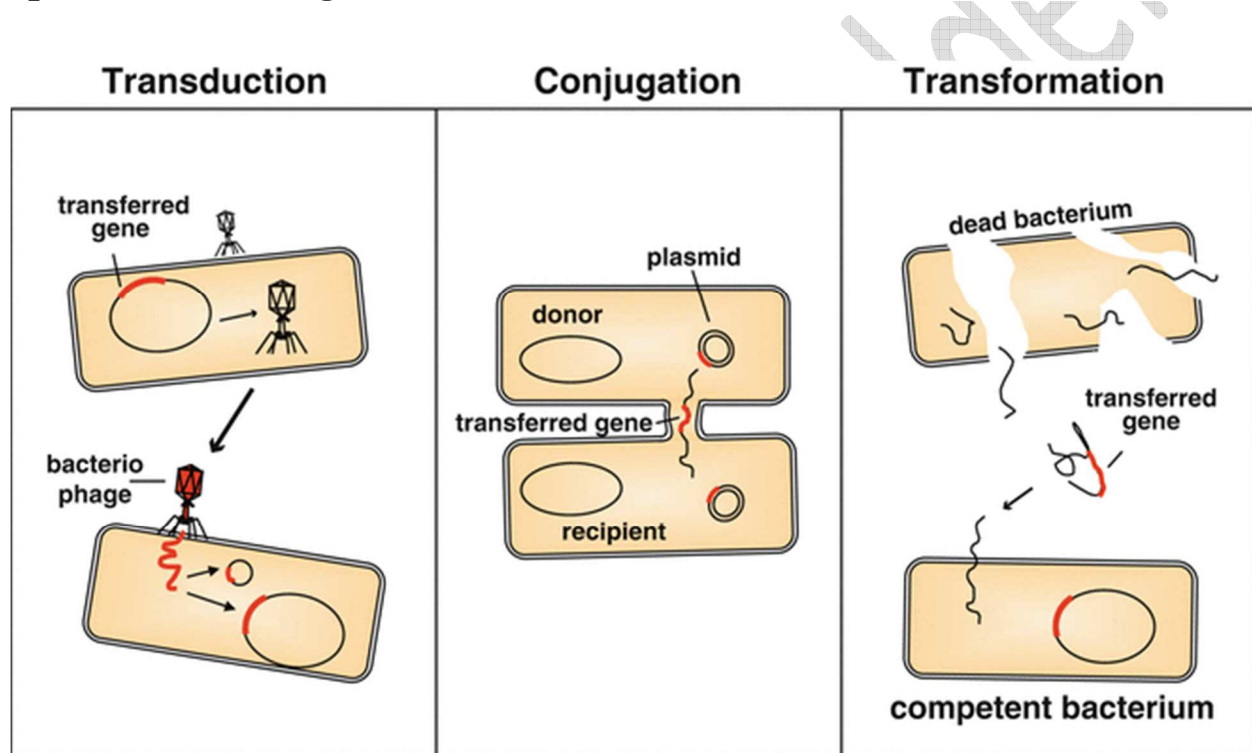
In horizontal gene transfer, newly acquired DNA is incorporated into the genome of the recipient through either recombination or insertion. Recombination essentially is the regrouping of genes, such that native and foreign (new) DNA segments that are homologous are edited and combined. Insertion occurs when the foreign DNA introduced into a cell shares no homology with existing DNA. In this case, the new genetic material is embedded between existing genes in the recipient's genome.

Compared with prokaryotes, the process of horizontal gene transfer in eukaryotes is much more complex, mainly because acquired DNA must pass through both the outer cell membrane and the nuclear membrane to reach the eukaryote's genome. Subcellular sorting and signaling pathways play a central role in the transport of DNA to the genome.

Prokaryotes can exchange DNA with eukaryotes, although the mechanisms behind this process are not well understood. Suspected mechanisms include conjugation and endocytosis, such as when a eukaryotic cell engulfs a prokaryotic cell and gathers it into a special membrane-bound vesicle for degradation. It is thought that in rare instances in endocytosis, genes escape from prokaryotes during degradation and are subsequently incorporated into the eukaryote's genome.

Horizontal gene transfer plays an important role in adaptation and evolution in both prokaryotes and eukaryotes. For example, the transfer of a gene encoding a unique metabolic enzyme from a species of *Pasteurella* bacteria to the protozoan parasite *Trichomonas vaginalis* is suspected to

have facilitated the latter organism's adaptation to its animal hosts. Likewise, the exchange of a gene from a human cell to the bacterium *Neisseria gonorrhoeae*—a transfer that appears to have occurred relatively recently in the bacterium's evolution—may have enabled the organism to adapt and survive in humans. Scientists have proposed too that the recent evolution of the methylaspartate pathway of metabolism in the halophilic (salt-loving) archaean *Haloarcula marismortui* originated with the organism's acquisition of a specialized set of genes via horizontal transfer.



HORIZONTAL GENE TRANSFER IN PROKARYOTES