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Role of Horizontal Gene Transfer in Bacteria

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Abstract
This paper documents an overview on the current knowledge of gene transfer in bacteria with emphasis on the role of horizontal gene transfer**,** in contrast to the numerous gaps in our understanding of Bacterial gene expression. Horizontal gene transfer is the genetic exchange in bacteria that is different from a parent-offspring relationship. Horizontal gene transfer is the transfer of genetic material from unrelated taxa. This type of gene transfer is important in bacteria because it transfers the gene from another group of bacteria with drug resistance, virulence and pathogenicity genes to bacteria's, which lacks these type of genes. Not all type of gene on bacteria are equally likely to be transferred. genes taking part in replication, interpretation, and interpretation (educational qualities) are less inclined to be on a level plane exchanged than operational. Plasmids are the circular genetic materials in bacteria that encode the resistance genes; that is important to bacterial virulence and are mostly transferred from one bacterium to another. Bacteria use different methods to transfer these types of genes from one bacterium to another and horizontal gene transfer can be affected by the mechanism of genetic transfer, system of gene integration and by ecology. Therefore, it is important to control the rapid horizontal gene transfer in bacteria.
Keywords: Bacteria; bacteriophages; Horizontal Gene Transfer; plasmid

1. INTRODUCTION

Bacterial gene transfer is to transfer a gene from one DNA molecule to another DNA molecule by the horizontal and vertical way. Vertical gene (binary fission) is a simple process; a cell merely needs to grow to twice its size and then split in two (Esther, 2005). Horizontal gene transfer (HGT) is the phenomenon in which genetic material is transmitted laterally between organisms or between genomes within organisms, rather than vertically through sexual reproduction (Bock, 2010; Renner and Bellot, 2012). This process can occur irrespective of the relatedness of the organisms and occurs frequently between prokaryotes and eukaryotes (Keeling and Palmer 2008; Bock 2010).

It also refers to the movement of genetic material between organisms that do not follow the normal pathway of vertical transmission from parent to offspring (Methot, 2016). Avery *et al.* (1944) demonstrated that deoxyribonucleic acid (DNA) was the transforming substance and is known as a responsible molecule for gene transfer. In 1952, Hershey and Chase demonstrated that DNA was the main material exchanged amid bacteriophage disease, which recommended that the DNA is the hereditary material. Level hereditary exchange was then depicted in Seattle in 1951, in a paper exhibiting that the exchange of a viral quality into Corynebacterium diphtheria made a harmful strain from a non-destructive (Di Rita, 2016). And this giving the first example for the relevance of the lysogenic cycle(is one of two cycles of viral reproduction and is characterized by the integration of the bacteriophage nucleic acid into the host bacterium's genome or arrangements of a round replicon in the bacterial cytoplasm) (Racine and Valerie, 2014). Between bacterial gene, an exchange was first portrayed in Japan in 1959 that exhibited the exchange of antimicrobial resistance between various types of microscopic organisms (Gebre-Yohannes and Drasar, 1988).

As indicated by Rivera *et al*., (2004) investigations of gene and genomes are demonstrating that impressive level exchange has happened between prokaryotes"(Rivera et al., 2004).According to Rivera *et al*., (2004). The wonder seems to have had some hugeness for unicellular eukaryotes also. As Bapteste *et al*. (2005) watch, extra proof proposes that gene transfer might also be an important mechanism in bacterial evolution" (Bapteste *et al*., 2005).

Flat gene move made conceivable in substantial part by the presence of portable hereditary components, for example, plasmids (additional chromosomal hereditary material), transposons ("bouncing qualities"), and microscopic organisms tainting infections (bacteriophages). These mobile genetic elements transferred to other microorganisms by different mechanisms such as transformation, conjugation, and transduction. All three methods have served as elegant tools in the development of genetic methods for bacteria's and have played a major role in bacterial evolution and drug resistance (Gyles and Boerlin, 2014).

In this time, molecular hereditary genetic and genome examination gave broad confirmation that quality misfortune and obtaining are probably going to be the essential systems by which bacterial populations hereditarily adjust to novel or changing environments and by which bacterial populations diverge and form separate, evolutionary distinct species. Three systems of gene exchange have been recognized in microorganisms: transformation, conjugation, and transduction, yet our insight concerning even quality move in the earth was still is extremely constrained. Creature gut, specifically the rumen possibly support flat gene

exchange with conjugation and transduction, because of expansive, assorted and thick bacterial and bacteriophage populaces, in any case, there is the scarcity of reviewed documents regarding the role of horizontal gene transfer in bacteria.

Therefore, the objectives of this Seminar Paper are-

- ✓ To review compiled information on the role of horizontal gene transfer in bacteria.
- ✓ To discuss factors that affect (either favors or hinders) horizontal gene transfer in bacteria.
- ✓ To highlight the mechanisms of horizontal gene transfer in bacteria

2. HORIZONTAL GENE TRANSFER IN BACTERIA

Level gene exchange (LGT) or horizontal gene exchange (HGT) is the development of hereditary material amongst unicellular and additionally multicellular life forms (Keeling, 2008; Robinson, 2013). It is the transfer of DNA between organisms, which allows acquisition of novel traits unique from those inherited. The advent of large-scale genome sequencing has greatly improved our understanding of the importance of HGT, particularly among Eubacteria. For example, the phylogenetic analysis of 144 prokaryotic genomes has indicated that, although most genetic information flows vertically, genes are also frequently transferring horizontally between closely related taxa and between bacteria inhabiting the same environment (Beiko *et al*., 2005). HGT in Eubacteria has implicated in the acquisition and evolution of many traits including antibiotic resistance, pathogenesis, and bioremediation (Boucher *et al*., 2003).

Schwartz and Dayhoff (1978) first addressed the evolutionary and phylogenetic importance of gene transfer through it quickly dismissed as an irrelevant phenomenon; lately, as gene sequences started to accumulate and the purity of genomes became more dubious. Doolittle (1998, 1999) proposed HGT could be an important process that may account for the current conformation of the genomes and, in extreme cases, may actually preclude us from reconstructing a "Universal Tree of Life". This is of course debated and not all the parties involved in the discussion agreed on the importance of HGT in its evolutionary long-term effects. HGT is an important factor in the evolution of many organisms (Gyles and Boerlin, 2014) and plays an important role in the evolution of bacteria that can degrade novel compounds such as human-created pesticides (McGowan, 1998) and in the evolution, maintenance, and transmission of virulence (Keen, 2012). It often involves temperate bacteriophages and plasmids (Naik, 1994; Varg, 2012) and is the primary mechanism for the spread of antibiotic resistance in bacteria, (Kay *et al*., 2002; Koonin *et al*., 2001).

The great amount of genomic information that began to accumulate during the decades of the 1980s and 1990s, made it possible to find an increasing number of examples of transferred genes either individually or by the group even between different kingdoms. There are, however, several difficulties to positively detect (Suárez Díaz and Anaya-Muñoz, 2008). Horizontal gene transfer can safely assumed if a gene shows a lower similarity with an orthologue in a closely related organism than with a probable homolog from an organism in a distant taxon, usually producing unexpected tree topologies, another signature of lateral gene transfer when gene synteny is conserved between distant lines (Koonin, 2001 and Koonin 2002).

2.1. Horizontal Gene Transfers in Rumen

Bacteria are present in large populations (10^{10} cells ml^{-1}) in the rumen fluid and they can find attached to the substrate particles and the rumen wall. An extensive populace of bacteriophages saw in the rumen liquid and few examinations played out, the bacteriophages coordinated with ruminal bacterial genomes likewise found. This indicates necessary requirements for conjugation and transduction are fulfilled. Natural transformation, on the other hand, seems less likely, because of nucleolytic activity of the ruminal fluid (Peterka *et al.,* 2000). Although these micro floras have importance on the supply of volatile fatty acid (Wanapat *et al*., 2012), most members are potential donors of various genes as done by Scott and Flint in 1995 on *E. coli.* Bacteria's from these strains isolated from the rumen can successfully exchange their plasmids by conjugation in anaerobic conditions in a medium that included whole rumen fluid. This process can continue on related and phylogenetically distant bacteria's inhabiting in the rumen (Scott and Flint, 1995).

According to Mercer *et al.* (1999), the predominant form of gene transfer in rumen could function via mobile chromosomal elements similar to those found in the human colonic *Bacteroides* species (Mercer *et al*., 1999). In this manner, horizontal gene exchange can happen between species and additionally inside a populace. This can wind up tricky if harmful bacteria that artificially chose for anti-infection opposition happen to be in the colon, where bacteria can exchange the resistance gene to different species of bacteria (Gerding, 1991).

3. MECHANISMS THAT FAVOR HORIZONTAL GENETIC EXCHANGE IN BACTERIA

Bacteria avail themselves by a variety of efficient mechanisms for the transfer of advantageous genes to other organisms and other species (Courvalin, 1994). The bacterial genome consists of chromosomal DNA, which encodes for general cellular characteristics and metabolic repair pathways, and smaller circular DNA elements known as plasmids that encode for supplemental bacterial activities such as virulence factors and resistance

genes. However, the presence of transposons made it possible to exchange genes from chromosome and plasmid in either direction by simple recombination. Transposons are small, mobile DNA elements capable of mediating transfer of DNA by removing and inserting themselves into host chromosomal and plasmid DNA and include Insertion Sequences, Transposons, and integrons. If these elements become associated with either transmissible or mobilizable plasmids, increased chances of transfer to other organisms. Numerous resistance genes, for example, plasmid-intervened beta-lactamase, tetracycline-resistance genes, and aminoglycosides-changing catalysts are sorted out on transposons, which can shift extraordinarily in size and complexity. Transposons may have a broader host range than their parent plasmids and which is important in the dissemination of resistance genes among species (Courvalin, 1994).

Advantageous genes in bacteria can be lost unless they have the selective advantage. These genes maintained in bacteria by vertical or horizontal means of transfer. For example, resistance genes in the chromosome are transmitted by clonal dissemination and resistance determinants on plasmids transferred vertically. HGT mechanisms are mainly classified as transduction (mediated by phages), conjugation (mediated by plasmids), and transformation (mediated by uptake of naked DNA) (McDaniel *et al*., 2010)

3.1. Common Ways that Favor Horizontal Gene Transfer in Bacteria

3.1.1. Transduction

Transduction is the procedure of gene exchange whereby a bacteriophage erroneously bundles a portion of the host DNA in the capsid and exchanges it to another bacterium upon subsequent infection (John and Parkinson, 2016). It can be a generalized mechanism, any bacterial gene can be transferred (Masters, 1996), or specialized where only genes located near the site of prophage integration are transferred (Weisberg, 1987). Traditionally, phage-host interaction is believed to be quite specific (Peterka, *et al.*, 2000). However, it can occur across wide taxonomic boundaries, at least in the hot spring environments (Chiura *et al*., 1998). Bacteriophages are viruses infecting bacteria, which are common and stable in most environments (Jiang and Paul, 1998; Wichels *et al*., 1998). There are different phages for the number of different bacteria (Kokjohn, 1989). This indicates that pages from a particular environment facilitate transduction in bacteria's that share the same environment with it (Jiang and Paul, 1998).

The bacteriophage-interceded exchange has been recommended to clarify the conveyance of the pyrogenic exotoxin C among various phylogenetic genealogies of Streptococcus pyogenes (Kapur et al., 1992). Bacteriophages coding for Shiga toxin is involved in the pathogenicity of *E. coli* O157: H7. Recent work shows that such phages are common in sewage (Muniesa and Jofre, 1998) and that they may be the source of genetic diversity among Shiga toxin producing *E. coli* (Muniesa *et al*., 1999).

Introduction of DNA by phages needs maintenance of transferred sequences in received bacteria, and then it can be assimilated into the bacterial genome. This received DNA forms an episome to avoid loss. Integration of exogenous DNA can be mediated by bacteriophage integrases or by mobile element transposases. This is the important mechanism of gene transfer in the environment (Stratz *et al*., 1996).

3.1.2. Conjugation

Bacterial conjugation is a plasmid or transposon-encoded gene transfer mechanism that requires physical contact between cells. As Lederburg and Tatum (1946) first seen in *Escherichia coli*, it has been reported for numerous bacterial species. Conjugal gene transfer can occur in a variety of environments such as human and animal gut, rhizosphere, on plant leaves, in seawater and marine sediments and polluted soils, sludge and water (Top *et al.*, 1994).

The classic examples of self-transmissible conjugative plasmids are the F-plasmid and the plasmid RP4 of *E. coli*. Transfer of such plasmids begins when donor cell produce the pilus, which is encoded by the plasmid and contact the potential recipient cell which does not contain the plasmid. Retraction of the pilus brings the cells into close contact and a pore forms in the adjoining cell membranes. Development of the mating pair flags the plasmid to start the exchange from a solitary stranded scratch at oriT. The 5’ end of a single strand of the plasmid is transferred to the recipient through the pore. During the transfer, the plasmid is replicated in the donor, its synthesis being primed at the 3' OH^- end of the *oriT* nick. Replication of the single strand in the recipient proceeds by another mechanism using RNA primers. At the end, when mating pair separates, both cells contain double-stranded plasmids. Conjugative plasmids encode all capacities they requirement for the exchange amongst cells and in some cases they can encourage the exchange of mobilizable plasmid, which encodes a few yet not all of the proteins required for the transfer. Occasionally, conjugative plasmids can integrate into chromosomes, and when such plasmids attempt to transfer (during *Hfr* formation by the F plasmid of *E. coli*), they may take part of the chromosome with them (Snyder and Champness, 1997).

3.1.3. Transformation

Transformation is an active uptake of exogenous DNA by competent cells followed by genomic integration. Normally, transformable species have been recognized in all the major scientific categorizations of Eubacteria and in the Archaea (Kleter *et al*., 2005). For transformation to occur, DNA has to be released from donor cells

and dispersed or maintained in the environment until being encountered by potential recipient cells. There are numerous extracellular DNA of multiple bacterial sources. that can be present in diverse prokaryotic habitats and persist for the considerable time (Nielsen *et al.*, 2007).

In nature, the DNA may come from dead cells that lyse and release their DNA. This condition usually occurs when the recipient bacteria are in the late logarithm phase of their growth. Competent bacteria cells produce a special protein that binds donor DNA fragments at specific sites on the cell surface. Despite existing differences in transformation systems among bacteria, four discrete steps are common to all of them: competence development, DNA binding, DNA uptake, and integration into the chromosome (Stewart, 1989). Although chromosomal DNA can be readily transferred to competent recipient bacteria, plasmid DNA is not easily transferred by ordinary transformation procedure that simply adds DNA to recipient cells. However, special procedures widely used in genetic engineering can be used to accomplish transformation with plasmid DNA. Plasmids can also be transferred to recipient cells via phages (Pelczar *et al*., 1992).

3.2. Common Traits Introduced Through Horizontal Gene Transfer

It is winding up progressively evident that numerous genes inside prokaryotes have been on a level plane gained, yet not all gene are similarly prone to be exchanged. Genes taking part in replication, transcription, and translation (informational genes) are less likely to be horizontally transferred than operational genes (Rivera *et al*., 1998; Jain et *al*., 1999). Ribosomal RNA for example, which is a part of the translation machinery, should be resistant to horizontal gene transfer. Lawrence (1999) inferred that genes encoding the ribosomal RNA (enlightening genes) are probably not going to be exchanged effectively since the beneficiary taxa would as of now bear utilitarian orthologues. Moreover, the corresponding product of native genes have experienced long-term coevolution with the rest of the cellular machinery and are unlikely to be displaced. However, at this time, it is known that even rRNA genes are not immune to horizontal gene transfer. According to Asai *et al*., (1999) 16S rRNA of *E. coli* can be completely replaced by that of *Proteus vulgaris* and that the ribosomal protein L11 binding domain of *E. coli* 23S rRNA can be replaced by the homologous region of yeast 28S rRNA. There are traits that most commonly transferred from one bacterium to another, but most are, antibiotic resistance genes, pathogenicity determinant genes and metabolic property genes (Asai *et al*., 1999)

3.2.1. Antibiotic resistance genes

Nearness of bacterial cells in thickly populated living spaces with microorganisms, for example, animals gut could support the exchange of hereditary material containing anti-infection opposition qualities to potential pathogens. Antibiotic-resistant genes make possible for the bacterium to expand its ecological niche to environments where the noxious compound is present. Because the benefit to the microorganism-derived from an antibiotic, resistance is transient. It is not surprising that antibiotic resistance genes are associated with highly mobile genetic elements (Ochman *et al*., 2000).

3.2.2. Pathogenicity determinants

Unlike the acquisition of antibiotic resistance, adoption of pathogenic determinants usually involves a fundamental change in the recipient's ecology. The virulence plasmids of Yersinia and Shigella are cases of plasmids that make extraordinary phenotypic changes when they are gained (Maurelli *et al*., 1985). Recent studies have discovered that horizontally acquired pathogenicity islands are the major contributors to the virulent nature of many pathogenic bacteria. Pathogenicity islands are chromosomally encoded areas that contain expansive bunches of virulence genes and can upon consolidation; change a kind life form into a pathogen (Hacker *et al*., 1997). Some virulence determinants are encoded by bacteriophages and lysogenization by such phage brings about a pathogenic variation of the strain (Jackson *et al*., 1987).

3.2.3. Metabolic properties

Horizontal gene transfer has also played a significant role in the dissemination of genes involved in physiological processes, which have allowed organisms to explore new environments. Metabolic characteristics are normally mind-boggling, and fruitful preparation of such attributes requires the physical grouping of qualities, with the end goal that every single fundamental quality will be moved in a solitary advance. Therefore, gene bunches and operons, which can be communicated in the beneficiary cell by a host promoter at the inclusion site, will be chosen (Lawrence and Roth, 1996 Genetic mechanisms responsible for metabolic traits dissemination are likely to have been the same as in antibiotic resistance genes or pathogenicity determinants (Romine *et al*., 1999).

4. ROLE OF HORIZONTAL GENE EXCHANGE IN BACTERIA

The hugeness of HGT between bacteria was first perceived when infectious heredity' of numerous infectious from pathogens was watched (Richard and Bruce, 1990). From that point forward, the expected significance of HGT has changed a few times, yet ongoing advances fundamentally in entire genome sequencing of microbes proposed that HGT is a noteworthy, if not the dominant, force in bacterial evolution (Doolittle, *et al.*, 2003). Confirmation for monstrous gene trades in bacterial development was found in totally sequenced genomes by

degenerate piece of procured hereditary components (guanine cytosine content, codon utilization), high closeness of genes to distantly related species, variation of gene content between closely related strains, and incongruent phylogenetic trees (Koonin *et al.*, 2001).

According to Ochman *et al.* (2000), up to 20% of a typical bacterial genome can be acquired from other species. Regularly remainders of plasmid, phage or transposon-related arrangements are discovered contiguous qualities distinguished as on a level plane exchanged, proposing that this versatile hereditary component (MGE) filled in as vectors for HGT" (Ochman *et al.*, 2000). The search of 56 sequenced bacterial genomes for prophage sequences performed was revealed that 40 genomes contained prophage sequences exceeding 10 kb in length, which encoded numerous virulence factors and other adaptive traits (Canchaya *et al.*, 2003)

4.1. Effect of Horizontal Gene Transfer on Bacterial Evolution

The primary branching pattern of the universal tree of life separates bacteria on one side from Archaea and Eukarya on the other. But, evidence supporting gene exchange between bacterial and archaeal domain (Aravid *et al*., 1998; Jain *et al*., 1999) and gene transfer from bacteria and archaea to eukaryotes (Pennisi, 1998) suggest that reticulated tree or a net might more appropriately describe the evolution of life (Doolitle, 1999).

Horizontal gene transfer results in abrupt large-scale alterations in the structure and organization of genomes and is, therefore, capable of generating new variants of bacterial strains by “genetic quantum leaps” (Falkow 1996). It is a potential confounding factor in inferring phylogenetic trees based on the sequence of one gene. There is developing confirmation that HGT may happen crosswise over huge phylogenetic separations, for example, from microscopic organisms to eukaryotes (Doolittle 1998), from creatures to microbes (Wolf et al., 1999), from bacteria to archaea (Nelson *et al.*, 1999) and so on. It appears that some genes have flowed ‘randomly' through the biosphere, almost as if all life forms constituted one global organism. Therefore, HGT may create the high degree of similarity between donor and recipient strain for the analyzed character. Transferred DNA is introduced into a single lineage and because of that, the acquired trait will be limited to descendants of the recipient strain and absent from closely related taxa. The strongest evidence for horizontal gene transfer derives from genetic analysis of the DNA sequences. DNA segments acquired through gene transfer often display restricted phylogenetic distribution among related strains or species. Additionally, horizontally acquired DNA regions display high levels of sequence similarity between strains, which are divergent by other criteria (Doolittle, 1999).

It is indicated that horizontal gene transfer is a major driving force of bacterial and archaeal evolution is not only dramatic but can also be a threat to the phylogenetic classification, which is based on comparative analyses of the nucleotide sequences of genes encoding ribosomal RNAs and some proteins (Woese, 1987).

4.2. Effect of Horizontal Gene Transfer in Drug Resistance

The revelation of the primary anti-toxin, penicillin, in the mid-twentieth century was a milestone therapeutic leap forward that ensured people and their trained animals from bacterial agents. Numerous trusted that this revelation would prompt the disposal of all sicknesses and a general public of basically consummate wellbeing. In any case, none of these expectations was true and slowly the “miracle medicine penicillin” became less effective. With the revelation of DNA being the hereditary code, researchers discovered that a some bacteria were impervious to specific antibiotics because of genes that rendered microbes unaffected by the impacts of a few antibiotics agents. Level quality exchange enables new variations to emerge without a transformation in that variation. In addition to antibiotic resistance increasing from natural selection, bacteria can receive genetic material through the process of horizontal gene transfer. The genetic material is received in two forms: a DNA plasmid or a transposon. A transposon is a hereditary material from one living being that winds up fused into the DNA of another life form, while plasmids don't end up consolidated into the DNA of the host creature. Level quality exchange adds to the spread of anti-microbial resistance through the trading of hereditary material crosswise over genera, which builds the potential for destructive anti-infection safe microorganisms to create (Kaiser *et al*., 2012).

Bacteria can develop resistance to antibiotics by mutating existing genes (vertical evolution) (Martinez *et al.*, 2000) or by acquiring new genes from other strains or species (horizontal gene transfer) (Hegstad *et al*., 2010) and the sharing of genes between bacteria by horizontal gene transfer occurs by many different mechanisms. Mobile genetic elements, including phages, plasmids, and transposons mediate this transfer, and in some circumstances, the presence of low levels of the antibiotic in the environment is the key signal that promotes gene transfer; perhaps ensuring that the whole microbial community is protected from the antibiotic. The revelation of anti-infection agents was one of the best therapeutic advancements in mankind's history, while it's manhandled can prompt the improvement of one of society's most exceedingly awful scourges (Jeters *et al*., 2009).

5. FACTORS AFFECTING HORIZONTAL GENE TRANSFER

5.1. Molecular factors affecting HGT

Molecular factors that affect the horizontal gene transfer in bacteria are the mechanism of genetic exchange in bacteria. These mechanisms are mainly classified as transduction conjugation transformation (McDaniel *et al*., 2010) and mechanism of DNA incorporation that includes homologous recombination (Majewski and Cohan, 1999) and non-homologous recombination (Stoke and Gilings, 2011)

5.1.1. Effect of Mechanisms of Genetic Exchange on HGT

Transduction is a mechanism of genetic exchange in bacteria that contain the bacterial virus (bacteriophage) (John and, Parkinson, 2016). These Phages can infect either specific species (or even strains of a species) or can have a broad-host-range (i.e., different species, genera or even families). (Jensen *et al*., 1998). An example of a broad-range bacteriophage is the ΦOT8 phage that has been shown to successfully transfer genes related to antibiotic resistance between two different species of the Enterobacteriaceae family, *Pantoea agglomerans*, and *Serratia* species, so these type phages are capable of transferring genetic materials between different bacterial species that facilitates HGT (Evans *et al*., 2010)

Bacterial conjugation is the exchange of hereditary material between bacterial cells by guide cell-to-cell contact or by an extension like the association between two cells and offer plasmid between two bacteria (Holmes, 1996). Plasmids can also be categorized based on their host range, similar to phages. Plasmids can be either specific (narrow-host-range) or broad range (broad-host-range). Broad-host-range plasmids can be transferred even across phyla or even kingdoms. The most studied case is the transfer of the tumor-inducing plasmid (PTI) from *Agrobacterium tumefaciens* to a plant cell. (Stachel, and. Nester, 1986) Another case of broad-host-range plasmids is the incompatibility group Q plasmids (inch). These plasmids have been found in a wide variety of environments and have been transferred between gram-positive and gram-negative bacteria i.e. broad host range plasmids facilitate HGT and that of narrow host range plasmids limit HGT (Rawlings and Tietze, 2001)

The components involved in DNA-uptake are not the same for gram-positive and gram-negative bacteria due to the difference in cell wall structure. In gram-positive bacteria, retraction of a pseudo pilus opens a cell wall hole that allows DNA to diffuse from the surface. In gram-negative microorganisms, because of the nearness of an additional layer, DNA take-up requires the nearness of a more mind-boggling channel, mostly framed by discharges (PilQ). In contrast to DNA uptake, DNA translocation across the cell membrane is similar in gram-negative and gram-positive bacteria. Incorporation into the chromosome can be catalyzed by the mechanisms of HR if sufficient sequence identity exists, so in gram-positive bacteria, there is the high chance of transformation, that can facilitate HGT than in gram-negative bacteria, that can hinder back HGT (Meibom *et al*., 2005)

5.1.2. Effects of Mechanisms of Foreign DNA Incorporation in HGT

Recombination can be responsible for horizontal gene transfer, by homologous or non-homologous recombination of the gene occurs in bacteria. Homologous recombination is a kind of hereditary recombination in which nucleotide arrangements are traded between two comparable or indistinguishable particles of DNA. Be that as it may, where all the more indirectly related sequences are traded into bacterial genomes by non-homologous recombination (Alberts *et al*., 2002).

Interestingly, the same process allows the integration of foreign DNA (from the donor cell) to the chromosome of the recipient cell, resulting in the substitution of whole or parts of genes. There are several constraints that affect the frequency of HR happens. For instance, the divergence between recombining sequences has a major (negative) effect on the recombination rates (Majewski and Cohan, 1999). In addition, the type of gene and its locations in the genome also affects HR rates; recent genomic analysis of recombination in *Acinetobacter baylyi* showed that the rates of recombination might vary up to 10,000 fold across the genome, and these differences appear to be related to local gene organization and synteny. The outcome of HR is diverse and depends on multiple factors such as the selection pressure of the environment and the genetic divergence between the donor and the recipient cells. So, this resulting effect of homologous recombination on HGT (Ray *et al*., 2009).

Non-homologous recombination mechanisms incorporate DNA material without the requirement of sequence homology, and therefore, are more frequently responsible for conferring novel metabolic capabilities than HR (Rodriguez-Minguela *et al*., 2009 and Juhas *et al*., 2009). This incorporation is primarily mediated by the integration of sequences through mobile genetic elements (MgE) such as phages, transposases, and integrons. The presence of these MgE on the bacterial gene can simply favor HGT in bacteria. There are many studies showing HGT mediating the acquisition of pathogenicity determinants. Recently, the dynamics of such acquisitions have been confirmed using population genomic approaches (Dimopoulou *et al*., 2007).

5.2. Mechanisms of Immunity-Related System in Bacteria to HGT

Restriction endonucleases recognize specific DNA sequences; these sequences are mostly palindromes of four, six or eight base pairs. A modification enzyme that methylates the recognition sequence (palindrome) in the host

DNA accompanies the endonucleases. The methylation protects the host and allows the identification and degradation of foreign DNA. Therefore, it is expected that bacteria sharing the same restriction-modification system can more effectively exchange and incorporate DNA. Late investigations in Neisseria meningitidis have demonstrated that clade-related confinement adjustment frameworks create a differential obstruction to DNA trade and that this barrier is consistent with the observed population structure and frequency of HR (Budroni *et al*., 2011)

The Clustered Regularly Interspaced Short Palindromic Repeats system (CRISPRs-Cas) is a nucleotide-based immune system mechanism that provides defense against foreign phages or plasmids. The CRISPRs are composed of short repeated sequences (21-48 bp length), separated by a sequence spacer (26-72 bp length). Most of the times, the sequence spacer is derived from phages or plasmids that have previously infected the cell lineage. Examples of acquisition of immunity to M102-like phages have been identified, for instance, in strains of *Streptococcus mutans*. (Van der Ploeg, 2009); however, the process by which a new spacer is integrated into the host genome remains poorly understood. (Bhaya *et al*., 2011). A clear case of how this mechanism can limit HGT has been described for *Staphylococcus epidermidis*. A CRISPR present in *S. epidermis* prevents conjugation and plasmid transformation of known staphylococcal conjugative plasmids by the binding of the spacer RNA to a nickase gene present in almost all staphylococcal conjugative plasmids (Marraffini and Sonthiemer 2008).

5.3. Ecological Factors Affecting HGT

Ecological interactions and preexisting diversity influence the genetic adaptation of populations. Populations capable of HGT can adapt faster than clonal ones, this indicates that genetic diversity of co-occurring organisms in the environment can provide new or advantageous alleles for adaptation through HGT. There is also the higher frequency of HGT between niche-overlapping organisms (Perron *et al*., 2011).

When different bacteria's with different chromosomally-encoded drug resistance mechanisms were living in the same environment, MDR evolved rapidly in strains with an active HR mechanism through shuffling of the preexisting resistance alleles. The multidrug-resistant (MDR) *Staphylococcus aureus* is one interesting example of how preexisting genetic diversity fosters faster adaptation to new antibiotics in clinical settings. Finally, different bacteria's living in the same environment that are having different advantageous genes can adapt the environment quickly than others (Baltrus *et al.*, 2008).

Ecological interactions are protocooperation, commensalism, neutralism, amensalism and competition (Atlas, and Bartha, 1987). Genetic exchange between co-occurring organisms has been observed at different levels of genetic divergence, ranging from same species to different phyla or kingdoms (Beiko *et al.*, 2005). Accordingly, it can be hypothesized that the different ecological interactions among co-occurring species of bacteria can have an important effect on the frequency of encounter and therefore, can facilitate or impede, depending on the type of interaction (Smillie *et al*., 2011).

6. CONCLUSION AND RECOMMENDATION

Gene transfer is to transfer a gene from one DNA molecule to another DNA molecule by the horizontal and vertical way. Level quality exchange (HGT) alludes to the development of hereditary material between organisms that do not take after the ordinary pathway of vertical transmission from parent to posterity. Progressively, investigations of qualities and genomes are showing that extensive even quality exchange has happened between prokaryotes. Bacteria's can simply get a chance to evolve from one strain to another that they get an advantage to drug resistance, environmental adaptation, and pathogenic to the host. Horizontal gene transfer is the primary mechanism for the evolution of bacteria and plays an important role in the spread of antibiotic resistance. Findings indicating that there is also HGT in the rumen of animals. Genes that are mostly transferred from one bacterium to the others are pathogenicity property genes, drug resistance genes, and metabolic property genes. However, this HGT can be affected by molecular factors, immunity, and ecological factors. Therefore, horizontal gene transfer has an important role in the evolution and transfer of drug resistance genes in bacteria. Finally, HGT will suddenly lead to the development of one of society's worst epidemics. Therefore, it is important to control rapid horizontal gene transfer.

Based on the above conclusion the following recommendations are forwarded:

- ✓ Continuous research should be conducted to check HGT in micro floras with respect to drug resistance.
- ✓ Organized and detail study Should be done on the different factors affecting horizontal gene transfer in bacteria
- ✓ Many of the basic components and mechanisms involved in the modulation of Bacterial gene transfer should be characterized.

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