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Eukaryotic Genes in the Genome of Mycobacterium Tuberculosis Play a Role in Immunomodulation

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Abstract – The sequencing of bacterial genomes has opened new points of view for distinguishing proof of focuses for treatment of irresistible ailments. We have distinguished an arrangement of novel harmfulness related qualities (vag qualities) by contrasting the genome successions of six human pathogens that are known to cause tenacious or interminable contaminations in people: Yersinia pestis, Neisseria gonorrhoeae, Helicobacter pylori, Borrelia burgdorferi, Streptococcus pneumoniae, and Treponema pallidum. This correlation was constrained to qualities explained as theoretical in the T. pallidum genome extend. Seventeen qualities with obscure capacities were observed to be saved among these pathogens. Insertional inactivation of 14 of these qualities created nine mutants that were constricted for harmfulness in a mouse disease show. Out of these nine qualities, five were observed to be particularly connected with harmfulness in mice as shown by disease with Yersinia pseudo tuberculosis in-outline cancellation mutants. What are more, these five vag qualities were fundamental just in vivo, since every one of the mutants could develop in vitro. These qualities are extensively moderated among microscopic organisms. Hence, we recommend that the relating vag quality items may constitute novel focuses for antimicrobial treatment and that some vag mutants could fill in as bearer strains for live immunizations.

Keywords: Immunomodulation, Eukaryotic Genes, Mycobacterium Tuberculosis.

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INTRODUCTION

Gigantic sequencing uncovered that bacterial genomes have experienced a mosaic advancement, joining variable extents of vertically procured DNA from past eras and on a level plane obtained DNA from different living beings display in their condition . In this way, the development of bacterial genomes can't be spoken to by trees alone yet rather should be spoken to buy more intricate structures, for example, rhizomes outlining the different, various wellsprings of DNA that have been joined in one specific bacterial animal categories . Along these lines, to a specific degree, a bacterial genome reveals insight into the specific condition in which that bacterium's precursors used to live and on the measure of DNA trade with neighbor living beings . As needs be, genome sequencing uncovered that as opposed to past guess, current Mycobacterium creatures are the outcome, to a limited extent, of level hereditary exchange from unidentified Eukarya and from ecological alpha-and gamma-Proteobacteria and Actinobacteria, as shown for Mycobacterium tuberculosis. In any case, the spots in whichMycobacterium progenitors interacted with different living beings for these hereditary exchange occasions stayed obscure. Late investigations have demonstrated that free-living protozoa, amoebae specifically, are to be sure places in which even hereditary exchange happens. Free-living amoebae have various single adaptable cell safe microbes, organisms, goliath DNA infections and virophages , all of which live in sympatry in the free-living protozoa. Besides, free-living protozoa are "mixtures" in which microorganisms trade DNA including qualities by even quality exchange (HGT) , as delineated for Rickettsia bellii , Candidatus Amoebophilus asiaticus and the as of late discovered exchange of an Acanthamoeba polyphaga Mimivirus protein to Legionella pneumophila . DNA can likewise be exchanged from the protozoa themselves to the microorganisms, as in the instances of the A. polyphagaMimivirus , Legionella drancourtii and Chloroflexus aurantiacus. Hereditary exchanges can likewise happen in the turnaround bearing, from the microorganisms to free-living protozoa, as on account of Tetrahymena thermophila, which obtained bacterial qualities required in the catabolism of complex starches, contributing to a great extent to its ability to colonize

the rumen . There have likewise been archived exchanges from microscopic organisms to creatures. Non-tuberculous mycobacteria share oceanic and earthbound natural specialties with free-living protozoa including ciliates, whips and amoebae. Co-culture explores additionally demonstrated that non-tuberculous mycobacteria could be phagocytosed by the ciliate Tetrahymena pyriformis , the social single adaptable cell Dictyostelium discoideum and the free-living one-celled critter (FLA) Acanthamoeba polyphaga and additionally dwell in amoebal pimples, which go about as a "Trojan steed" for such one-celled critter safe mycobacteria . M. tuberculosis complex life forms can likewise be phagocytosed by amoebae , and it was as of late watched that, with the exception of Mycobacterium canetti, M. tuberculosis complex individuals can likewise live inside amoebal pimples . We estimated that free-living protozoa may have been puts in which quality moves into mycobacteria happened. We performed broad bioinformatics examinations of accessible mycobacteria genomes with those of single adaptable cell safe microscopic organisms and free-living protozoa to test this hypo, and we utilized co-culture test to affirm its natural pertinence. Mycobacteriu tuberculosis is a gram–positive bacterium that causes around three million passings yearly and contaminates an expected 33% of the total populace, making it the best human pathogen. The essential site of contamination is the lung, where it is at first ingested by pneumonic macrophages in the lower projections and experiences intracellular augmentation. The logical perceptions on the development of life forms made by Charles Darwin (1809 1882) in the nineteenth century are not just valid for eukaryotic creatures; they additionally appear to be legitimate for prokaryotes. The key procedures of Darwinian development can be portrayed by four distinct ends: hereditary inconstancy, phenotype arrangement, selection and separation. There is most likely the changeless advancement of new hereditary variations speaks to the primary essential for the improvement of life. The same number of hereditary modifications (changes) doesn't prompt new pheno-sorts it is significant to bring up that exclusive the adjustments that do deliver new phenotypes are conclusive for development. New phenotypic variations are quickly subject to selection by natural and non-organic powers. As officially depicted by Darwin, the geological segregation of specific species or gatherings of creatures might be valuable for evolutionary advancement. What's more, a hereditary detachment because of exchange hindrances, solid limitation alteration frameworks or changes in the codon use may likewise add to the speed of evolutionary improvement. The principal smaller scale living beings showed up on Earth more than three billion years prior. As people have created in the last 1.5 million years, entirely human pathogens can be considered as exceptionally youthful organisms. By and by, transformative improvement is likewise found in these organisms. A developmental procedure that happens inside a more extended timeframe and that prompts the arrangement of new species or subspecies is considered as macroevolution. As indicated by Ernst Mayr, macroevolution is the key formative process for the development of life. Interestingly, procedures of microevolution take days or weeks. As an outcome of microevolution, new variations of a specific animal groups or subspecies are produced. Amid advancement, 'fluctuation generators', for example, addition succession (IS) components, exchanging DNA pieces or transposons have showed up, which assume a key part in microevolution. Microevolution is critical for the pathogenesis of irresistible maladies. The expression or non-articulation of specific qualities (stage variety) or the change of microbial structures, particularly surface structures, for example, pili or external film proteins (antigenic variety) in vivo speak to standards of miniaturized scale development. Likewise, these procedures are harmfulness instruments, critical in numerous irresistible ailments. In this article we will initially portray the general hereditary components required in the advancement of microorganisms. Specific consideration, in any case, will be given to pathogenic microorganisms. It is our view that pathogens create numerous destructiveness or pathogenicity variables, which straightforwardly or in a roundabout way add to the improvement of an irresistible malady. These variables and the hidden quality groups are of specific significance for the advancement of pathogens. What's more, pathogenic miniaturized scale creatures express resistance variables, which render the life forms impervious to antimicrobial medications. The hereditary premise of antimicrobial sedate resistance is additionally a case for 'advancement under the magnifying instrument'.

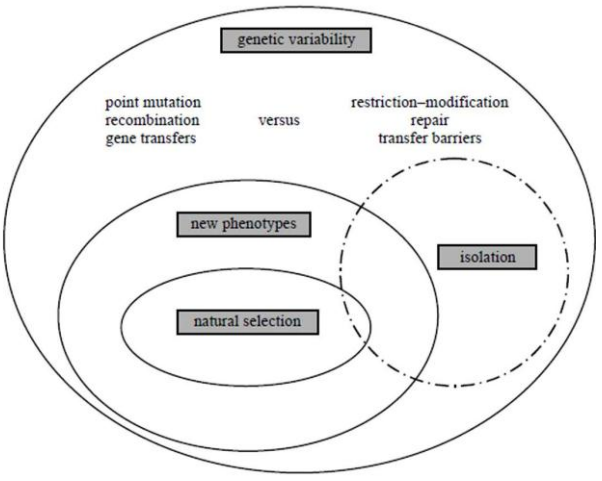

Figure: Darwinian principles of evolution

Transformation is a vital stratagem for here and now adjustment of microorganisms to unfriendly

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conditions and fast versatile advancement has been connected to various capacities related with destructiveness (Metzgar and Willis 2000). In harmful microorganisms, these changes can empower a pathogen to enter as well as make due in a harmfulness specialty and have been alluded to as pathoadaptive transformations (Sokurenko et al. 1999). Since numerous versatile changes may adjust the first capacity of a quality, they can be relied upon to be unfavorable to the bacterium in its hereditary specialty, and will be chosen against in the genealogical living space; it is conceivable that a few clones will advance a way to exist in both specialties. Then again, if these bacterial pathogens by one means or another gain a system to translocate straightforwardly starting with one host then onto the next, the reliance on the hereditary specialty would be enormously decreased, or as on account of commit intracellular bacterial pathogens, lost totally. While quality procurement and quality change through point transformation are altogether different developmental components, they can be corresponding. Basically, a particular destructiveness quality situated in a pathogenicity island could transform to wind up plainly more powerful at creating the pathogenic phenotype in a particular host, or a pathoadaptive transformation could be exchanged among clones by recombination (Sokurenko et al. 1999).

Wellsprings of changes: Point transformations happen pretty much haphazardly all through the genome and are created by replication blunders or wrong repair following DNA harm. ITiey can be quiet; for instance, when they are brought into the coding grouping of a quality without modifying the amino-corrosive succession of" the quality item. In any case, if the muta¬tion brings about an amino-corrosive trade, an adjusted protein will be the result. On the other hand, such muta¬tions may likewise happen in administrative districts, in this manner influencing the expression example of" the particular gene(s). Single point transformations more often than not influence one particular quality that may give leverage in an evolving situation (Musser 1995). This can produce new variations of a clone inside moderately brief times of" time (small scale advancement), on a bigger scale, i.e. the era of" new species, advancement by amassing of" point transformations is a moderate procedure. This is particularly valid for transformations in fundamental species-particular housekeeping qualities, e.g. loci encoding ribosomal RNAs, specific catalysts (for instance ATPases) or strucmral proteins. The hereditary variables required in DNA replication and repair may themselves be liable to change, determination and versatile advancement (Wang et al. 1999), demonstrating that creatures may advance components that advance their transformation rates under particular natural conditions. Determination following up on mutator loci, and, thus delivers invaluable changes in other loci vital for survival, has been named second-arrange choice (Weber 1996) by which life forms 'develop to advance'. The hereditary elements that expansion a living being's transformation rate can be isolated into 'worldwide mutators' and 'possibility loci', where the previous causes a vast change in sorts and rates of change while the last influences particular loci (Field et al. 1999).

Worldwide mutators are related with the DNA crisscross repair pathways and hereditary changes influencing these variables can be heritable or transient (Rosenberg et al. 1998). In Mycoplasma pneumoniae, for instance, the whole methyl-coordinated jumble repair (MMR) framework is missing and the life form demonstrates expansive lifted rates of transformation when contrasted with firmly related nonpathogenic species (Woese 1984). Essentially, the most destructive strains of Yersinia spp. inherently have the most astounding rates of transformation (Najdenski 1995, Iteman 1995) and it has been accounted for that some characteristic detaches of pathogenic E. coli and Salmonella spp. are confound repair inadequate, suggesting a choice for changeability in the host specialty (LeClerc 1996). Similarly, normally happening mutator strains of Pseudomonas aeruginosa have been shown to be in charge of expanded anti-microbial resistance in lung contaminations of cystic fibrosis patients (Oliver et al. 2000). Hypermutable subpopulations have been exhibited to exist inside coli laboratory cultures during the stationary growth-stage (Torkelson et al. 1997) and it has been recommended that crisscross repair movement is not kept up at a consistent level. Or maybe, a transient downregulation happens because of ecological signs, which builds far reaching change rates (Radman 1999, Wang et al. 1999), which improves the chances of acquiring worthwhile transformations, without bargaining the wellness of who and what is to come. Mistake inclined DNA polymerases IV and V, related with the SOS framework in E. coli, which has useful parts like that of the MMR framework, have been appeared to be inducible under unpleasant conditions and seem to bring blunders into DNA (Wagner et al. 1999). Besides E. coli strains that are actually more variable have been appeared to outcompete low changing strains in vitro (Chao and Cox 1983).

Possibility loci are extends of dreary succession, either basic rehashes or microsatellites, inside particular qualities that are included in delivering a particular harmfulness stage state or antigenic phenotype in pathogenic bacteria (Moxon 1994). These repetitive tracts are to a great degree inclined to transformation, because of their expanded inclination for causing "slippages" amid replication. These loci enable qualities to be exchanged "on" in one round of replication and "off" in another because of casing shifts (Levinson and Gutman 1987, Direnzo et al. 1994). While coordinate

determination follows up on the quality items changed by strand-slippage transformations, backhanded second-arrange choice follows up on the grouping attributes of the possibility rehashes themselves. In this examination, techniques for recognizing qualities that have experienced versatile determination through the impacts of worldwide mutators, as opposed to possibility loci, were explored with the point of distinguishing novel destructiveness related qualities. Pathoadaptation in Helicobacter pylori : Helicobacter pylori (H. pylori) is a human-particular gastric pathogen which is in charge of a range of ailments extending from shallow gastritis to gastric and duodenal ulceration, and which is likewise profoundly connected with gastric malignancy. The pathogenesis of extreme gastric issue caused by H. pylori is multifactorial and includes complex connections between the organism and the gastric mucosa. H. pylori ex presses a few grip proteins. These atoms have essential parts in the foundation of constant disease and perpetual aggravation, which cause tissue harm. The point of this was to consider the connection of this bacterium to human gastric epithelium, intervened by blood assemble antigens in both wellbeing and ailment. One of the best-described H. pylori adhesins is the histo-blood aggregate antigen restricting adhesin (BabA). which ties particularly to the Lewis b antigen (Leb) in the gastric mucosa. A defensive bodily fluid layer lines the stomach. The mucosal glycosylation designs (GPs) vaiy between various cell heredities, diverse areas along the gastrointestinal (GI) tract and distinctive formative stages. What's more. GPs experience changes amid threatening change. MUC5AC is a mucin atom created by the surface epithelium. Three unmistakably unique sorts of human gastrointestinal tissue were considered by bacterial adherence examination in situ. MUC5AC is the most essential transporter of Leb and the new outcomes show that it shapes real receptors for H. pylori adherence. By investigating a H. pylori baM-cancellation mutant, a novel adhesin-receptor restricting mode was found. Shockingly, the mutant bound proficiently to both human gastric mucosa and to gastric mucosa of Leb transgenic mice. The sialylated and fucosylated blood assemble antigen. sialyl-dimeric-Lewis x (sdiLex). was fundamentally recognized as the new receptor. A positive relationship was found between adherence of H. pylori to sialyl-Lewis x (sLex) and lifted levels of irritation reaction in the human gastric mucosa. These outcomes were bolstered by point by point examination of sialylated and fucosylated blood gather antigen glycosylation designs and. also, in situ bacterial adherence to gastric mucosa of tentatively tested Rhesus monkey. The related sialic corrosive restricting adhesin (SabA) was decontaminated by the retagging system, and the comparing saM-quality was recognized. H. pylori lipopolysaccharide (LPS) contains different Lewis blood aggregate antigens, for example, Lewis x (Lex) and Lewis y (Ley). Extra bacterial adherence modes, which are free of the BabA as well as SabA adhesins. could be intervened by Lex cooperations. Adherence of a dinical confine and its comparing Lex mutant to human gastric mucosa with different gastric pathologies was considered in situ. The outcomes recommend that H. pylori LPS plays an unmistakable yet minor part in advancement of bacterial attachment. Taken together, the outcomes propose systems for consistent choice of H. pylori strains, including ability to adjust to changes in the nearby condition, for example, moves in cell separation and related glycosylation designs. Adherence of H. pylori is subject to both the BabA and the SabA adhesin. Multi-step subordinate connection systems may guide the microorganisms to unmistakable biological specialties amid steady contaminations, driving the constant aggravation forms promote toward the improvement of peptic ulcer malady and additionally threatening change.

3. BACTERIAL GENOMES AND GENOME SEQUENCING

➢ Bacterial Genomes

The genome of a living being alludes to its whole supplement of qualities contained in the DNA of its chromosome (s). The bacterial genome is typically contained in a roundabout DNA particle which is supercoiled and restricted inside the nucleoid of the phone. There are exemptions, as a few microbes have at least two chromosomes and a few chromosomes might be direct. Among therapeutically vital microorganisms, Vibrio, Burkholderia, Leptospira and Brucella species are those with at least two chromosomes, while Borrelia burgdorferi has its genome in a straight chromosome. Most bacterial genomes are under 5 MB, in spite of the fact that a couple of, for example, Bacillus megaterium, might be as extensive as 30 MB. The real example in bacterial genome estimate is that, all things considered, free-living species have bigger genomes than parasitic species which thusly have bigger genomes than commit pathogens. Bacterial genomes differ significantly between species regarding nucleotide piece: The G+C (guanosine-cytosine) substance may change locally inside a genome, yet it is generally uniform inside a bacterial variety or animal types, going from around 25% in Mycoplasma spp. to around 75% in some Micrococcus species. On the normal, a run of the mill bacterial genome has around 2,500 qualities, which are kept up in a specific genomic design through particular weight, instead of through an arbitrary progression of qualities. The genome of microbes encodes all the biochemical capacities that are essential for survival. Moreover, pathogenic microscopic organisms may convey hereditary components required for destructiveness, while non-coding areas are likewise situated in the bacterial genome. Distinctively, bacterial qualities might be composed into operons, which allude to a

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gathering of qualities found neighboring each other, and are practically related. A case of an operon is the lactose operon in Escherichia coli, which contains three qualities required in the transformation of lactose, a disaccharide into monosaacharide units-glucose and galactose. Bacterial genomes are dynamic, and are presented to different hereditary occasions, including, transformations, duplications, reversals, transpositions, recombination, addition, and cancellations. Quality securing through even quality exchange is likely the system having the best effect on the life form's way of life by giving a novel metabolic limit, for example, procurement of anti-microbial resistance qualities and harmfulness elements. In some bacterial cells, aside from the genome, there might be additional chromosomal DNA particles alluded to as plasmids. In some cases, the refinement between a megaplasmid and a moment chromosome may not be clear. By and large, plasmids are roundabout and twofold stranded, and reproduce autonomously of the bacterial chromosome. Plasmids encourage even quality exchange inside a microbial populace of microorganisms and ordinarily give a particular preferred standpoint under a given ominous natural state.

- **Standards of Genome Sequencing**

DNA and protein sequencing begun in the 1970s when the infection Lambda (50,000 nucleotides) was sequenced by Sanger et al.. Around this time DNA sequencing was done for little genomes, for example, infections and organelles, and finish sequencing of a bacterium, was not attainable due to monetary and specialized impediments. In any case, later on, sequencing of the human genome, and changes in sequencing advances encouraged entire genome sequencing of microbes. In this technique, a conjugate of DNA polymerase and DNA layout are joined to 50 vast wells. Utilizing nucleotide fluorescently named with γ-phosphate, the DNA polymerase do second strand DNA combination. Fuse of bases amid DNA union is recognized by methods for a particular beat of fluorescence. ITPGM utilizes innovative advances in semi-conductor science and non-touchy transistors to succession DNA. This technique contrasts from other cutting edge sequencing strategies as polymerisation occasions are identified by pH changes as opposed to light. DNA pieces conveying particular connector arrangements are connected to a dot and after that clonally enhanced by emulsion PCR. The templated dots are stacked onto a chip which has proton-detecting wells that are manufactured on a silicon wafer, and sequencing is prepared from a foreordained area in the connector grouping. As bases are fused amid the sequencing procedure, protons are discharged and a flag is distinguished corresponding to the quantity of bases fused. Correlation of key elements of the different sequencing techniques portrayed above, and their points of interest and disservices are abridged in Table 1. Additionally propels in genome sequencing are normal soon as the alleged third era advances are being created to additionally build throughput, diminish cost, and lessen an opportunity to acquiring comes about. One intriguing region of such sequencing strategies includes microscopy based procedures, for example, nuclear drive microscopy that are utilized to distinguish the areas of nucleotides inside long DNA parts.

- **Streptococcus Pneumoniae TIGR4 Genome: An Example of a Sequenced Genome**

TIGR4 is a harmful S. pneumoniae strain (serotype 4, ST 205) disengaged from the blood of a 30-year old male patient in Norway. As per Tettlin et al. the genome of this strain is a solitary round chromosome containing 2,160,837 base sets and 2,236 putative qualities, the lion's share (64%) of which have been allocated a natural capacity. The genome has a GC substance of 39.7%, and about portion of the anticipated proteins are most like proteins from other low-GC Gram-positive species. Examination uncovered that 5% of the genome is made out of rehashes including inclusion, BOX, and RUPS components that may encourage joining of remote DNA into the S. pneumoniae chromosome and add to reworking its structure. The genome encodes numerous ATP-subordinate transporters and 30% of transporters are included in sugar transport, which may mirror its natural adjustment to sugar-related conditions, for example, the oral depression. Extracellular chemical frameworks for sugar digestion give carbon and nitrogen to the life form and encourage colonization in have pathogen association. Iron and phosphate transporters and a 13-quality bunch required in capsular biosynthesis may likewise add to harmfulness. Sixty-nine proteins are anticipated to be communicated on the bacterial surface and a putative flag peptide theme distinguished is conceivably required in focusing on these proteins to the surface of the cell.

- **Genome Sequencing and Insights into Bacterial Pathogenesis**

One of the essential uses of pathogenic genome investigation is the recognizable proof of destructiveness qualities, which can give bits of knowledge into pathogenesis of bacterial pathogens. Harmfulness qualities are found in particular districts of the chromosomes of microscopic organisms, shaping the supposed pathogenicity islands (PAIs). These locales are up to 200 kb in estimate, regularly have particular addition arrangements at their finishes which encourage their translocation and inclusion between microorganisms. There are a few methods for recognizing PAIs or destructiveness qualities. One approach known as the genome structure approach includes scanning for areas with DNA marks that

are unmistakable from different parts of the genome. Identified with this are hints, for example, couples rehashes of basic arrangements found in or close to certain harmfulness qualities called possibility qualities.

➢ **Genome Sequencing and Insights into Development of Antibiotics**

Another imperative use of genome arrangement information is the revelation of anti-infection focuses for improvement of novel anti-infection agents. This critical application can't be overemphasized, considering the present pattern of expanding anti-toxin resistance, particularly different medication resistance of superbugs. Cutting edge sequencing stages, for example, PacBio can give methylation information, which could be helpful in planning anti-infection agents and understanding anti-microbial resistance. For instance, sequencing of Stapylococcus aureus detaches gathered from over the globe gave uncommon bits of knowledge into anti-toxin resistance of this superbug, including resistance components, microevolution and sub-atomic the study of disease transmission. Resistance will probably happen when recently composed anti-microbials are artificially like past ones as of now rendered ineffectual. In this way in a perfect world, new anti-microbials ought to have novel instruments of activity, which is a definitive objective of the genome sequencing way to deal with find novel antimicrobials.

CONCLUSION:

In fossil science, the impact of a hypothesis of macroevolutionary patterns affected by flat quality exchanges will probably be significant. A great part of the fossil record is described by broad parallelisms. At the pious devotee of the most recent century, numerous scientistss concentrated on these perceptions and developed speculations to oblige them. These prompted "orthogenetic" hypotheses (see ref. 24, for a verifiable record). With the predominance of neoDarwiman hypotheses, the thoughts of orthogenesis have been generally scrutinized as teleological or even as vitalistic. These reactions are. generally, ridiculous smce numerous orthogenetic speculations were offered as genuine logical theories. Be that as it may, in light of the fact that components to oblige parallel varieties were not known, the speculations slipped by. Presently, with known instruments, these old hypotheses ought to be reanalyzed m another light—a procedure that has as of now started by scientistss.

REFERENCES:

Heritable matadors in adaptive evolution in the lab and in nature.

Sokurenko E.V., Hasty D.L., Dykhuizen D.E. (1999). Pathoadaptive mutations: gene loss and variation in bacterial pathogens.

Stephens R.S. et. al. (1998). Genome Sequence of an Obligate Intracellular Pathogen of Humans:

Wagner J., Gruz P., Kim S., Yamada M., Matsui K., Fuchs R.P.P., Nohmi T. (1999). The dinB gene encodes a novel E. coli DNA polymerase,

Waldor KM, Mekalanos J.J. (1996). Lysogenic conversion by a filamentous phage encoding cholera toxin.

Wang G., Humayun M.Z., Taylor D.E. (1999). Mutation as the origin of genetic variability in Helicobacter pylori.

Weber M. (1996) Evolutionary plasticity in prokaryotes: a pan-glossian view.

Weber M. (1996). Evolutionary plasticity in prokaryotes: A Panglossian view.

Woese C. (1998). The Universal Ancestor.

Wolf YI et. al. (1999). Rickettsiae and Chlamydiae, evidence of horizontal gene transfer and gene exchange.

Wolf Y.I. et. al. (2000). Interkingom gene fusions. Genome Biology

Yang Z. (1998). Likelihood ratio tests for detecting positive selection and application to primate lysozyme evolution.

Altschul S.F. et. al. (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs.

De Luanoit Y. et. al. (1999). Unique multifunctional HSDb4 gene product: 17-hydroxysteroid dehydrogenase and D-3-hydroxyacyl coenzyme A dehydrogenase/hydratase involved in Zellweger syndrome.

Felsenstein J. (1996). Inferring phylogenies from protein sequences by parsimony, distance and likelyhood methods.

Hacker J. et al. (2000). Pathogenicity islands and the evolution of microbes.

Hernandez-Pando R. et. al. (1998). The effects of and rostenediol and dehydroepiandosterone on the course and profile of tuberculosis in BALB/c mice. Immunology.

Morschhauser J. (2000). Evolution of microbial pathogens.

Ochman H. et. al. (2000). Lateral gene transfer and the nature of bacterial innovation. .

Ochman H. et. al. (2001). Genes lost and genes found: evolution of bacterial pathogenesis and symbiosis.

Rook, G.A. et al. (1994). T cell helper types and endocrines in the regulation of tissue-damaging mechanisms in tuberculosis. .

Shirai M. et al. (1995). The influence of ovarian hormones on the granulomatous inflammatory process in the rat lung.

Thompson, J. D. et al. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position- specific gap penalties and weight matrix choice..

Tsyuguchi K. et al. (2001). Effect of oestrogen on Mycobacterium avium complex pulmonary infection in mice. .

Wolf Y.I. et al. (1999). Rickettsiae and Chlamydiae, evidence of horizontal gene transfer and gene exchange.

Wolf Y.I. et. al. (2000). Interkingom gene fusions. Genome Biology

Ziebuhr W. et. al. (1999). Evolution of bacterial pathogenesis.

Bhatt, A. H. M. Kicscr. R. E. Melton, and T. Kicscr (2002). Plasmid transfer from *Strepiomyces* to *Mycobacterium smegmatis* by spontaneous transformation. Mol. Microbiol.

Boddinghaus. B., T. Rogall. T. Flohr. H. Blockcr. and E. C. Bottger (1990). Detection and identification of mycobacteria by amplification of rRNA.

Brosch. R-. S. V. Cordon. M. Marmiesse. P. Brodin. C. Buchricscr. K. Eiglmeier. T. Garnier. C. Gutierrez. G. Hewinson. K. Krcmcr. L. M. Parsons. A. S. Pym. S. Samper. I), van Soolingcn. and S. T. Cole. (2002). A new evolutionary scenario for the *Mycobacterium tuberculosis* complex.

Craig. N. L, R. Craigie. M. Gellert, and A. M. Lambowitz (2002). Mobile DNA II. ASM Press. Washington. DC.

Derbyshire. K. M., and S. Bardarov (2000). DNA transfer in mycobacteria: conjugation and transduction.

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