

Bacterial genome and genomics: a perspective

Keywords: Bacteria; Genome; Classification; Genomic analysis; Bioinformatics

Introduction

Detection and identification of bacterial pathogenesis, drug resistance and sensitivity, antigenicity etc is possible with more validity by scientific attention to their genetic and genomics. Moreover, classification and identifying the bacterial species with attention to their genetics and genomes character will clarify deep and very important details about each of the bacterial species or even an exact bacteria position in prokaryote Kingdom. Obviously these details will be very important and beneficial for application and decision making about both pure scientific purposes and applied fields for bacteriologist and clinicians.

Materials and methods

By comparing the results of bacterial genome projects (Genomics & Metagenomics) and using bioinformatics software to analyze bacteria gene numbers and size, chromosomes size, each gene function, each genes character and position, genes copy numbers and ... modern scientific understandings of the classification and systematic of bacteria and even prokaryotes will be different from the traditional imagination of prokaryotic Kingdom. It is also notable that, there are wide and deep scientific aspects in this field of medical sciences.

Results

The genome size of two isolated strains of *H. pylori* from USA and UK is 1.67Mb and 1.64Mb respectively. The American isolate has 1552 while the englican strain has 1495 genes. 1406 genes are common between both strains. The Chromosome size non-pathogenic of *E. coli* K12 is 4.64Mb while the chromosome of pathogenic 0157:H7 is 5.53Mb. Beside these differences 0157:H7 has 1378 genes on the O-island that do not exist on the K12 but K12 has a genomic motif on the K-island including 528 genes. Thus, 0157:H7 and K12 have 26% and 12% of their own specific genes in their own genomes. The basic and main question here is: Does the difference in pathogenesis between these two strains depend on these genes?

Discussion

12.8% of K12 genome (059Mb) have been transferred to this strain from other species of bacteria with lateral gene transfer. Also 451 genes out of 1877 genes of Thermofilter maritime have been transferred from *Archeobacteria* to this bacteria during evolution periods according to bioinformatically genomic analysis. Normally, there are 950 genes in one Mb of chromosomes in bacterial genomes in free life bacteria while in the one Mb of *Mycoplasma genitalium*

Volume 2 Issue 6 - 2016

Abdolhassan Kazemi,¹ Mostafa kazemi²

¹Tabriz University of Medical Sciences, Iran

²Tabriz Islamic Azad University, Iran

Correspondence: Abdolhassan Kazemi, Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran, Tel +98 (0)411 33373745, Email kazemi1338@Gmail.com

Received: November 05, 2016 | **Published:** November 07, 2016

(with 0.58Mb genome size) there are only 470 genes. It is notable that *M. genitalium* has only one specific gene for biosynthesis of cofactors while *E. coli* has 131 genes for amino acids synthesis and 103 specific genes for cofactors biosynthesis. According to genomic and metagenomic analysis, at least existence of 265-350 genes are necessary for a living bacterial cell but there is no clear idea of how many genes are necessary to identify the two different bacterial species from each other. For example, *Bacillus subtilis* has 120 specific genes of itself and 350 similar genes with *M. genitalium* but can we conclude that: *M. genitalium* has been identified as *M. genitalium* based only on it's 120 specific genes.

Conclusion

Scientifically, it seems that in this stage of medical sciences and bacteriology scientists have to be careful about misunderstandings and should use deep metagenomics fields of pure and applied bioinformatics analysis. This field of scientific investigation should be followed by Transcriptomics, Proteomics, Metabolomics because scientists could not obtain any clear idea by the identification of 120 specific genes of *M. genitalium* and their vital or biological functions about *M. genitalium* cause its unique identity and dignity. In other words, with this kind of information scientists could not obtain any clear and scientific idea why this bacteria (or any other bacteria) is not identified as another bacteria and why it must be considered (and identified) uniquely as Mycoplasma.

Acknowledgements

None.

Conflict of interest

The author declares no conflict of interest.