# Comparison of genomic signatures among genomic elements within bacterial strains:

Main chromosome *vs*. plasmids and second chromosomes

The aim of this experiment was to demonstrate the tendency of the genomic signatures of elements other than the main chromosome within a bacterium to be similar to the genomic signature of the main chromosome.

METHOD:

- The sequenced bacteria containing one or more plasmids and the sequenced bacteria containing two or more chromosomes were selected from NCBI.
- Genomic Signature distance for hexanucleotides was computed for:
    - 922 pairs of main chromosomes and corresponding plasmids (see appendix A), and
    - 124 pairs of main chromosomes and second chromosomes (see appendix B).
- Distances were represented in Graph 1. Other methods for computing distances yielded similar results (not shown).
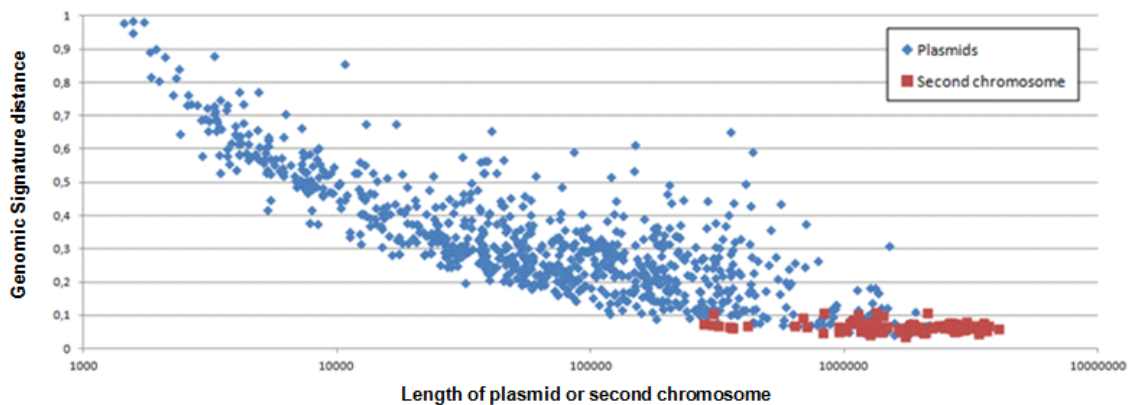
Graph 1: Representation of hexanucleotide based Genomic Signature distances between main chromosomes of bacteria and the plasmids (blue) or second chromosomes (red) present in the cell.

RESULTS AND DISCUSION

The existence of an adaptation process of genomic sequence acquired by Horizontal Gene Transfer to the characteristics of genes in the host is a widely accepted idea in evolution research. So, assuming a genomic environment that influences the oligonucleotide composition of the main chromosome exists, it can be argued that the same environmental factors influence the genomic signature of all genomic elements within the cell in the same direction.

This experiment clearly demonstrates that genomic signatures are similar in main chromosomes and second chromosomes. Similar oligonucleotide composition of main chromosome and second chromosome is logical, as they share the same constant genomic environment.

Concerning plasmids, the distance to main chromosomes are shorter for longer plasmids. It must also be pointed out that the computed distances are expected to be higher when one of the genomic elements compared is short, as for example a small plasmid (total number of oligonucleotides accounted is also small, and it influences the accuracy of the computed distance). But, it is unlikely that all the reductions in distance among plasmids and main chromosomes when size of plasmids increases can be explained by the size issue alone.

http://gscompare.ehu.eus