

SHARED DNA-DODECAMERS STRUCTURE INCIDENCE AS STUDY OBJECTS IN EXTREME HALOPHILIC ENVIRONMENTS AND EARLY LIFE

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The DNA of halophilic archaeobacteria is exposed to different ions. Using the completely sequenced genomes, we have looked for motifs that are common to this group of organisms to denote elements with structural shared likeness. Dodecamers common to six species have been recognized, this will allow us to recognize biological compatible elements that can interact with saline environments that they may be common in primitive land environments of 3.8 Ga.

DNA structure was studied by dimer presence, periodicity and pattern to recognize changes in double helix, by its modifications in the axis inclination, its twisting and changes in orientation with the major groove.

Combining two previous works (Nussinuv 1984; Quintana et al. 1992) we assumed that any prokaryotic genome could be analyzed by DNA geometry. We selected genomes from Halobacteria because its DNA may interact with ions, according with their *salt-in* strategy, and the increase in KCl in the inner cell to avoid osmotic stress.

Using the Quintana values, it was possible to recognize four different structure values related with particular dimers in the genome: V, L, H and I, these last two variables are related into the widest space between dimers and a modification into the angle of the main axis. These two variables were analyzed in dodecamer tandem repeats (DTR).

We propose, based on the work of Kassai-Jagger et al. (2008) that we can recognize sequence patterns with a stable repetition number in DTR structure for Halobacteria.

We used the software TRF, designed by Benson (Benson 1999) to identify DTR. We used the program in 43 Halobacterial genomes, eight halophilic bacteria genomes and two genomes used to compare as non halophilic species (*Escherichia coli* and *Archaeoglobus fulgidus*) as control.

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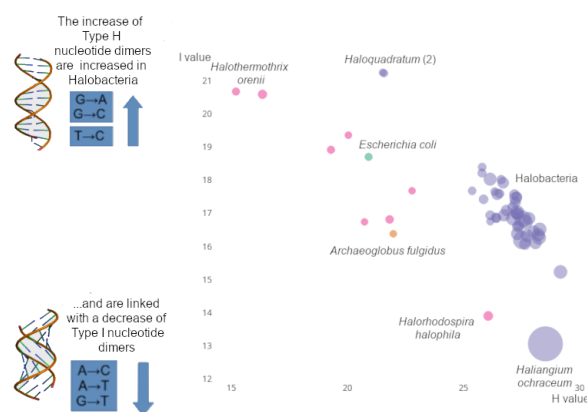


Fig. 1. XY dispersion for two structural values for the halophilic prokaryotes, the cluster sampled has a Pearson correlation value ($P > 0.9$). We can recognize all the Halobacterial species in purple, green and orange are both controls, Bacteria and Archaea respectively

We recognized that the DNA regions maintain an average value of 2.5 repeats in all the DTR along the genomes, however the number of these elements have an increased value in the archaeal genomes compared with the other eight analyzed halophilic bacterial genomes and our control. This is shown in the graphic in **Figure 1**.

It was possible to identify the particular structure in almost all the Halobacteria species with a particular cluster for H and I values, with the exceptions of two Haloquadratum representatives, one Halarchaeum species and Haliangium ochraceum. This last genome, due its genome size, and change in the GC amount could evidence a derivative behavior.

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