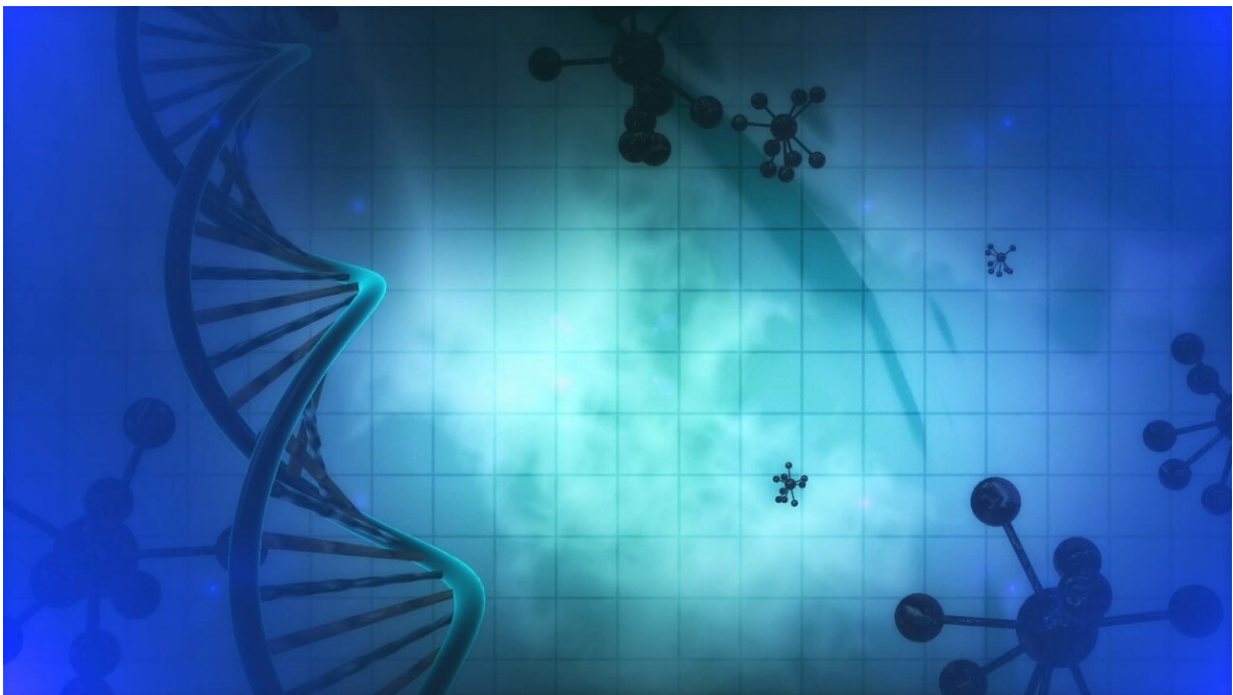


DNA sequence symmetries from maximum entropy: The origin of the Chargaff's second parity rule

May 15 2020, by Cristian Taccioli



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Most living organisms rely on double-stranded DNA to perpetuate their genetic code. This biological information is the main target of evolution.

Chargaff's second parity rule has been a mystery for more than 50 years.

In 1968, the Austrian biochemist Erwin Chargaff discovered that on the single strand of a double-stranded DNA molecule, the adenines count was almost identical to the number of thymines, and in the same way, the number of cytosines was almost equal to the number of guanines. To date, there was no explanation for such a symmetry. In recent years, many research groups have tried to clarify the reason for this biological oddity, but have never obtained valid predictions.

Now, researchers have discovered that the symmetries found within the genome can emerge from the physical peculiarities of the double helix DNA molecule itself and the maximum [entropy](#) principle alone, rather than from biological or evolutionary pressure. Professor Piero Fariselli of the University of Turin in collaboration with professors Cristian Taccioli, Luca Pagani and Amos Maritan of the University of Padua, created a [mathematical model](#) able to explain the origin of Chargaff's second parity rule.

Furthermore, their new theory, named "GCT," is able to formulate extremely precise genomic predictions that have been validated on bacteria, archaea and mammals, including humans; the study will be published in *Briefings in Bioinformatics*.

"By means of a multidisciplinary collaboration that includes biologists, anthropologists and [theoretical physicists](#), we have succeeded in the intent of explaining the origin of Chargaff's second parity rule through the hypothesis that this genomic symmetry emerges from the DNA double helix constraint and the principle of maximum randomness (entropy)," says Cristian Taccioli, professor of molecular biology and bioinformatics at the M.A.P.S Department of the University of Padova.

He concludes: "Moreover, we have been able to describe the evolution of the genome in terms of energy rather than focusing only on natural selection. Our idea is that DNA, like all the other systems in the

universe, follows the stream of entropy, trying to reach an equilibrium and maximizing its stability. In fact, our results show that processes that increase the entropy of a double-stranded DNA molecule are favored during the evolution of [living organisms](#)."

More information: Piero Fariselli et al. DNA sequence symmetries from randomness: the origin of the Chargaff's second parity rule, *Briefings in Bioinformatics* (2020). [DOI: 10.1093/bib/bbaa041](https://doi.org/10.1093/bib/bbaa041)

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