

Getting a step ahead of pathogens

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A recent article in the journal *Chaos* examines the possibility of using epistasis to predict the outcome of the evolutionary processes, especially when the evolving units are pathogens such as viruses.

In biology and genetics, the concept of epistasis is what gives rise to the whole being more (or less) than the sum of its parts. The quantitative effect of a given mutation upon the traits of an organism has the potential to depend strongly upon the gene versions present in other parts of the [genome](#), or even other mutations co-occurring in that gene.

These genetic interactions, termed epistasis, can impact all aspects of organisms and play a pivotal role in the manifestation of sex, ploidy, modularity, robustness, [reproductive isolation](#) and the origin of species, the rate of adaptation, and the emergence of [genetic mutations](#) within individuals and populations.

A recent article in the journal *Chaos*, published by the American Institute of Physics, examines the possibility of using epistasis to predict the outcome of the [evolutionary processes](#), especially when the evolving units are pathogens such as viruses.

The article looks at three topics: empirical evidence from the RNA virus world, mathematical tools, and the application of these tools to particular problems. Santiago Elena and colleagues at Instituto de Biología Molecular y Celular de Plantas have surveyed past work in this field and concluded that even though RNA viruses have small genomes composed of few genes that encode a limited number of proteins, epistasis is

abundant and conditions their evolution.

The next steps may range from characterizing the statistical distributions of epistasis across hosts, which has tremendous relevance for the emergence of new viruses, to drawing the most likely evolutionary paths a virus may follow in response to treatments with [antiviral drugs](#).

While this research is still in the early stages, Elena sees great potential.

"By increasing our ability to predict the most likely evolutionary paths a virus may follow in response to clinical treatments, we could get a step ahead of them and, perhaps, create new and more durable antiviral therapies," he says.

More information: The article, "Simple genomes, complex interactions: Epistasis in RNA virus" by Santiago F. Elena,² Ricard V. Solé, and Josep Sardanyés was published online in the journal Chaos on June 30, 2010. See: link.aip.org/link/CHAOEH/v20/i2/p026106/s1

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