Magnetic charm in the genes

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New research on magnetic bacteria suggests that their protein function could be regulated by some strange choices made due to the DNA code written for these proteins. A team from Indian Institute of Technology in New Delhi has proposed that even though some proteins in such bacteria might speak the same primary language, it’s the dialect — the DNA code — that actually affects their eventual function. The findings could have far reaching implication in evolutionary biology as well as in utilizing recombinant biotechnology for production of biomaterials.

“We have named it the Functional Control by Codon Bias (FCCB) hypothesis,” says lead researcher Aditya Mittal. Magnetic bacteria are special bacteria found in nature that eat up iron and mysteriously make nano-magnets in their cells. While producing bacterial nano-magnets, the researchers made two interesting observations about the magnetic bacteria Magnetospirillum magnetotacticum. Firstly, they found that with half the number of nano-propellers on their surface and nearly twice the body size of the common bacterium E. coli, magnetic-bacteria swam about twice as fast as E. coli.

Secondly, despite the same primary sequences in the iron transport proteins as in other biological systems, iron transport into the magnetic-bacterial cells resulted in production of intracellular nano-magnets. This is a trait absent in other systems.

“We wondered how magnetic-bacteria programme their protein sequences to do special functions despite having the same raw material as other biological systems,” he says. While primary sequences of the respective proteins in magnetic-bacteria were found to be identical to other well-studied systems, these bacteria had a strong preference towards a specific DNA code (called ‘codon-bias’). Codon-bias, the team proposes, is directly correlated to functions of proteins that are specific to magnetic-bacteria. Again, this codon-bias is absent in “housekeeping” proteins whose functions are common to all biological systems.

Trying to express the DNA code from such bacteria in their cousins from other species could help make a functional difference in the resulting proteins either in terms of efficiency of carrying out similar functions or in specific biological roles. “FCCB is still a hypothesis since it needs to be tested either experimentally or on larger data sets, or both,” Mittal adds.

References