

Unexpectedly small effects of mutations in bacteria bring new perspectives

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Most mutations in the genes of the *Salmonella* bacterium have a surprisingly small negative impact on bacterial fitness. And this is the case regardless whether they lead to changes in the bacterial proteins or not. This is shown by Uppsala University scientists in an article being published today in the prestigious journal *Science*.

The researchers have examined the impact of [mutations](#) on the rate of growth of the *Salmonella* bacterium and show that most mutations have generally very small effects. Moreover the negative effects are of the similar magnitude for changes that lead to substitution of amino acids in proteins (so-called non-synonymous mutations) as for mutations that do not change the protein sequence (so-called synonymous mutations).

"The findings open an entirely new chapter for experimental studies of mutations and show that we need to change our view of how mutations lead to negative effects," says Professor Dan Andersson, lead author of the study.

A central question in [evolutionary biology](#), medical genetics, species-conservation biology, and animal breeding is how and why mutations affect an organism's capacity to survive. Usually these questions are studied in DNA sequence analyses from which conclusions have been drawn about what mutations are most common and have become established in the DNA of the organism.

The Uppsala scientists have used another -- experimental -- method

whereby they can use various genetic tricks to introduce random individual mutations into any chosen gene, a method that has previously been used primarily in viruses. Two genes that code for proteins that are included in ribosomes were mutated, and using extremely sensitive growth measurements, doctoral candidate Peter Lind showed that most mutations reduced the rate of growth of bacteria by only 0.500 percent. No mutations completely disabled the function of the proteins, and very few had no impact at all.

Even more surprising was the fact that mutations that do not change the [protein](#) sequence had negative effects similar to those of mutations that led to substitution of [amino acids](#). A possible explanation is that most mutations may have their negative effect by altering mRNA structure, not proteins, as is commonly assumed.

Provided by Uppsala University

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