Evolutionary 'selection of the fittest' measured for the first time

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A difference of one hundredth of a percent in fitness is sufficient to select between winners and losers in evolution. For the first time researchers have quantified the tiny selective forces that shape bacterial genomes. The story is published today in the prestigious journal *PLoS Genetics*.

Darwin's Theory of Evolution introduced the concept of 'survival of the fittest'. At each generation the 'fittest' individuals are selected and this is a major force shaping the biological world we see today. Selection can explain why a cheetah runs fast - cheetah's that run fast catch the food to feed their cubs. Those that don't run fast get less food, and fewer cubs survive. Over time [evolution](#) selects against cheetahs that cannot run fast enough. But, how fast is fast enough, and big does the difference have to be before selection is effective? This question was asked by two researchers at Uppsala University, graduate student Gerrit Brandis and Professor Diarmaid Hughes.

Brandis and Hughes used *Salmonella* (a bacterium that causes infections in humans and animals) to measure the power of selection to choose the fittest individuals. *Salmonella* is similar to animals like cheetahs in the sense that it competes for food and is under intense selection to use that food to grow as fast or faster than any other individuals in the same environment. Evolution selects for the fittest variants.

To grow, bacteria, like all living organisms, must translate their [genetic code](#) into [amino acids](#) that are joined together to make proteins. The

speed of translation determines how fast *Salmonella* can grow. Translation is one of the most ancient processes in biology and has been under selection for billions of years on earth.

The genetic code has 'redundancy', meaning that there are several different 'codons' that can be translated into any one amino acid. For some amino acids up to 6 different codons can be used. Brandis and Hughes asked whether it mattered which particular codons were used to make EF-Tu, one of the most important proteins in *Salmonella*.

Brandis and Hughes changed many different codons and showed that changing even a single codon in the gene for this protein into any one of the alternative 'synonymous' codons reduced the 'fitness' of *Salmonella*. The codons that are actually used by *Salmonella* are the very best, and any change reduces the fitness of the bacteria.

Brandis and Hughes quantified the fitness cost of changing codons in this gene. On average, changing a single codon reduced the fitness of the bacteria, by 0.01 procent per generation. This tiny change in fitness is big enough for evolution to select the 'fittest' DNA sequence and causes what is called 'codon usage bias' - the widespread use of particular codons to make highly expressed proteins. Codon usage bias is found in nearly all fast-growing organisms, including bacteria and yeasts that cause infections in humans. Evolution has shaped their translation machinery so that they can grow as rapidly and efficiently as possible - not necessarily good for us, but good for the survival of bacteria and yeast.

"The message is that evolution, working over very long time scales (hundreds of millions of years), can select tiny differences in relative fitness, as small or smaller than 0.01procent per generation for *Salmonella*," says Diarmaid Hughes.

More information: The Selective Advantage of Synonymous Codon Usage Bias in Salmonella. *PLoS Genetics*, DOI: 10.1371/journal.pgen.1005926