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## Genetic boundary to delineate bacteria into discrete natural clusters

**Le Tang**

Harbin Medical University, China

The current taxonomy classifies bacteria into largely arbitrary species because it is still unclear whether the prokaryotes exist as natural species. Based on our previous findings that bacterial genomes are highly conserved in evolution, we hypothesize that bacteria, like all other life forms, should dwell in nature in discrete biological units, members within each of which should share common genetic and biological traits. The key evidence to support this hypothesis would be the demonstration of clear-cut genetic distinction among even very closely related bacterial lineages. To this end, we carried out systematic genomic comparisons among representative *Salmonella* lineages. Remarkably, we found that *Salmonella*, highly related from one serotype to another, formed distinct phylogenetic clusters separated by various genetic distances; whereas over 90% of the approximately four thousand shared genes had completely identical sequences among strains of the same lineage, the percentages dropped sharply to below 10% across the lineages with rare exceptions, demonstrating the existence of genetic boundaries. Recombination assays supported the genetic boundary hypothesis, showing that genetic barriers had been formed between bacteria of even very closely related lineages. We found similar situations also in other bacteria, such as *Yersinia* and *Staphylococcus*. We concluded that bacteria are genetically isolated into discrete clusters equivalent to natural species.

### Biography

Le Tang is currently a Postdoctoral Fellow at University of Calgary. She has received her MD and PhD degrees from Harbin Medical University, one of the top medical schools in China. She has won multiple national and provincial awards and scholarships from China and Canada in the past three years, including the National Natural Science Foundation of China; Alberta Innovates Health Solutions Postdoctoral Fellow of Canada; Heilongjiang Provincial Innovation Endowment Award for graduate studies and the Heilongjiang Provincial Endowment Award for International Academic Exchanges. Her research focuses on understanding how benign bacteria evolve into human pathogens. Her research work has been published in international core journals, along with book chapters in prestigious references like *Molecular Medical Microbiology* and *Encyclopedia of Genetics*.

le.tang@ucalgary.ca

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