

Intra-species recombination as an additional mechanism in the evolution of *Brucella abortus* populations

Tamar Chkhikvishvili¹, Leila Tabatadze¹, Ekaterine Gabashvili¹, Saba Kobakhidze¹ and Mamuka Kotetishvili^{1, 2}

¹Division of Risk Assessment, Scientific-Research Center of Agriculture, 6 Marshal Gelovani ave. 0159, Tbilisi, Georgia

²G. Natadze Scientific-Research Institute of Sanitation, Hygiene and Medical Ecology, 78 D. Uznadze St. 0102, Tbilisi, Georgia

It has been long believed that genetic recombination plays no role in the evolution of *B. abortus*, which is an important zoonotic agent, reflecting a remarkably conserved genome. Here, we provide strong statistical evidence for genetic recombination of some virulence-associated loci across natural populations of this infectious agent. In the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/>) nucleotide database, using the megablast algorithm, we analyzed the genome shotgun sequences of three *B. abortus* strains (MIJI00000000, MIJN00000000, and MIJM00000000) recovered in Georgia. Intriguingly enough, the BLAST-hit trees, generated from the analyses of separate genome segments of these strains (in a range of 200-800 kilobases), exhibited different evolutionary histories of their genetic relatedness. Bearing in mind that these noncongruences, observed between the constructed trees, could be partially due to horizontal gene transfer (HGT), we applied a large array of the recombination detection algorithms, implemented in the GARD, SplitsTree, and RDP4 software packages, to test the above hypothesis. In these analyses, the GARD-identified recombination breakpoints, SplitsTree-generated robust fit (100) and bootstrap values (>95) being highly supported by the Phi and RDP4 p statistics (≤ 0.0217 and ≤ 0.0233 respectively), provided strong evidence suggesting genetic recombination of specific genetic loci between multiple *B. abortus* strains. These HGT-associated loci were found to be involved in encoding for the autotransporter outer membrane beta-barrel domain-containing protein and the low molecular weight phosphotyrosine protein phosphatase. More in-depth studies are needed to understand whether HGT contributes to the emergence of virulent strains in *B. abortus* global populations.

Biography

Tamar Chkhikvishvili is a veterinarian, who has received her Master Degree at the age of 25 years from the Agricultural University of Georgia, Tbilisi, Georgia. She is Veterinary Specialist in the Risk Assessment Division of the Scientific-Research Center of Agriculture. She conducts risk assessment research in "One Health" areas, mainly focusing on zoonotic bacterial and viral agents. She has been initiating her PhD thesis concerning some important research aspects being related to microbial-host interactions and co-evolution.