

Hybrid Event

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The *Staphylococcus aureus* strains WH9628 and WH3018 recovered from patients in Wuhan, China, were found to carry in their genomes specifically some horse and mouse genetic loci

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The gene flow from eukaryotes to prokaryotes has been rarely documented. Here, we provide strong evidence for the presence of multiple eukaryotic genetic loci across the genomes of two *Staphylococcus aureus* strains (WH9628 and WH3018) recovered from patients in Wuhan, China. For the analysis, the genome sequences of these isolates (GenBank ID: CP033086.1 and CP033085.1 respectively) were retrieved from the National Center for Biotechnology Information (NCBI) database (<https://www.ncbi.nlm.nih.gov/>). The Basic Local Alignment Search Tool (BLAST) with the megablast algorithm was used to analyze the above genomes in the blastn database, searching for their homologous genetic loci across eukaryotic genomes (taxid: 2759). The BLAST analysis revealed some genomic regions of WH9628 (coordinates: 1824194-1825284; 2314137-2315140; 2371864-2374095; 2375255-2375737; 2412402-2414300; 2426281-2428460; 2440327-2440672) that shared 91.91%-100% of the DNA identity with specific chromosomal loci of *Equus caballus* (KY753876.1 and MH341179.1) and *Mus musculus* (MN537869.1). Similarly, specific genomic regions of WH3018 (coordinates: 2067827-2069293; 2266722-2267786; 2656308-2658513; 2683607-2685428; 2721525-2723219) were found to share 96.77%-100% of the DNA identity with these or other genetic loci of the same eukaryotic species. The above BLAST-hit results were accompanied by strong E-values varying from 0.0 to 8e-132 (with 98%-100% of query coverage). While some of these genomic regions of the *S. aureus* strains WH9628 and WH3018 were determined to be identical/highly homologous (91.91%-99.79%) to the KCNQ1 gene loci in *E. caballus*, others were identical/very highly homologous to the small subunit ribosomal RNA gene loci (100%), the gene encoding for the eukaryotic translation elongation factor 1 alpha 1 (99.94%), or the Gene H19 locus (100%) in *M. musculus*. It remains unclear and needs to be determined whether the acquired eukaryotic genetic loci have any effect on metabolic plasticity, virulence, and pathogenicity in these strains, and/or on their adaptation to new environments.

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Biography

Mamuka Kotetishvili's main expertise lies in the areas of molecular epidemiology and evolution of infectious agents including foodborne and zoonotic pathogens. Currently, his primary occupation is a leading of the biomedical research, working in a capacity of Deputy Director of Science and Foreign Relations, at the G. Natadze Scientific-Research Institute of Sanitary, Hygiene, and Medical Ecology (GNHI), Tbilisi, Georgia. He has pioneered his research on the molecular typing of some important foodborne and other pathogens, including, but not limited to, *Salmonella enteritidis*, *Listeria monocytogenes*, *Vibrio Cholerae*, and the species of *Yersinia*. His most recent studies have provided some important insights into the evolution of bacteriophages and antimicrobial resistance. He has served as an Editorial Board Member and/or an Ad-hoc Reviewer for various internationally well-respected scientific journals including Journal of *Clinical Microbiology*, Journal of Bacteriology, and Journal of Virology.

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