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### The presentation of the genes involved in iron or heme transport in *R. anatipestifer* through sequence comparison and analysis

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*Riemerella anatipestifer* (*R. anatipestifer*, RA) is one of the most important bacterial pathogens that cause septicaemia and death in ducklings, and other avian species. It has been shown that *R. anatipestifer* encoded for iron/heme uptake systems and heme can be as an iron source. However, the mechanism of iron/heme uptake of *R. anatipestifer* and the proteins involved in iron/heme uptake have not been systematically studied. Unlike the organization of the iron/heme uptake system in other well studied gram-negative bacteria, the genes involved in iron/heme uptake are not in the same cluster in *R. anatipestifer* and were not been annotated well. Here, we presented and compared the iron/heme utilization related genes in four different *R. anatipestifer* genomes (*RA-ATCC11845*, *RA-CH1*, *RA-CH2* and *RA-GD*), and the proteins functions of them in iron/heme uptake were predicted. Interestingly, we found that there exists a hemophore family protein and one hemophore-like protein (HmuY) in all sequenced *R. anatipestifer* genomes. In addition, we found five putative substrate-specific heme receptors and six siderophore receptors that could be involved in heme/hemoglobin and Fe<sup>3+</sup>-siderophore uptake, respectively. Accordingly, we also found the energy provider, one ExbB-ExbD-TonB, one ExbB-ExbDD-TonB and one TonB family protein to help the receptors transport substrate to periplasm. However, all these putative proteins have low similarity with other well-identified iron/heme transport proteins. Also, we can not find the gene encode for heme degrading protein through sequence analysis. It indicated that *R. anatipestifer* encode for a novel iron/heme uptake systems.

#### Biography

Ma Feng Liu has completed his PhD at the age of 31 years from Paris VI University. He has published more than 12 papers in reputed journals.

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