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## Bioinformatics analysis of MUC13 and differentially expressed genes in regulating piglets' diarrhea

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To understand the mechanism of MUC13 gene regulating piglet diarrhea more deeply and comprehensively, this study established the interaction network of MUC13 and differentially expressed genes in piglets' diarrhea. A total of 33 piglets diarrhea differentially expressed genes were obtained through GEO datasets analysis tools; Based on the interaction network of MUC13 and differentially expressed genes in piglets diarrhea constructed by Cytoscape software, we found the network contained 238 nodes, 505 edges and 6 molecular complexes, and the sixth molecular complexes included 21 genes, one of which is MUC13; Identified by DAVID analysis underlying complexes 6, specific functional annotations terms and biological pathways were founded. Noteworthy is that function annotations of MUC13 and TLR4 gene displayed significantly in the signal peptide, disulfide bond and glycoprotein terms, which indicated the two genes have similar structural characteristics. Moreover, the biological pathways of the sixth molecular complexes are mainly related to the Toll-like receptor signaling pathway. We speculate that the specific structure of the MUC13 determined MUC13 had a specific function in the development process of piglet diarrhea and involved in the regulation of piglet diarrhea occurs through Toll-like signaling pathway together with the TLR4 receptor.

### Biography

Lu Fu-zeng has completed his Ph.D. at the age of 29 years from Nanjing Agricultural University, China, and his major is animal genetics and breeding. Now he is working at Institute of Animal Husbandry Sciences and Veterinary Medicine, Zhejiang Academy of Agricultural Sciences, focus on the study of pig functional and comparative genomics. He has published more than 15 papers in reputed journals.

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