Jiabo Wang

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Education

2014-2018 **Northeast Agricultural University** **Ph.D.**

- will graduate in July 2018, the major study is Statistic Genetic, force on analysis DNA sequencing data, develop new method of GWAS and Genomic Prediction and Coding Genetic tool software.
- First Author paper：Incubating a BLUP Alphabet for Genomic Prediction Adaptable to the Genetic Architectures of Complex Traits, Heredity, Accept (3.96).
- Second Author paper：GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction, Plant Genome,2016 9-2(3.59)
- Develop GAPIT 3rd version, which is popular software to analysis Genome Association Study.
- Create GbyE model to detect interaction effect between Genotype and Environment, this software is coded by C language. The major functions are to distinguish additive and interactive genetic effect and solve big data with genotype and multi-environments.

2007-2010 **Northeast Agricultural University** **M.S.**

- Forced on the functions and association study with GSTM2 and TGF-β1 gene.
- Join in cattle nuclear transfer project of HAAS, and got 2nd Prize.

Experience

2019- **Southwest Minzu University** **Assistant Professor**

2017-2018 **America Washington State University** **Visiting Scholar**

- Forced on Statistic Genetic and develop new analysis software.
- In 2017, attend PAG meeting of American San Diego, give a presentation "New Integrate Association Software-GAPIT3"
- In 2018, attend PAG meeting of American San Diego, give a presentation "GbyE: detect interaction between Genetic and Environment"
- Through network, join in the e-Maize Challenge of Huazhong Agricultural University, got 2nd Prize in preliminary contest.

2010- **Heilongjiang Academy of Agricultural Science** **assistant researcher**

- Forced on analysis data of Genetics
- Join in 2 Nation projects and 13 Provincial projects
- Public 16 Chinese papers

ARTICLES

[1] Wang J, Chai Z, Deng L, et al. Detection and Integrated Analysis of lncRNA and mRNA Relevant to Plateau Adaptation of Yak. Reproduction in Domestic Animals.2020;4:1461-1469

[2] Jiabo Wang, Zhengkui Zhou, Zhe Zhang, Hui Li, Di Liu, Qin Zhang, Peter Bradbury, Edward Buckler and Zhiwu Zhang. Expanding the BLUP Alphabet for Genomic Prediction Adaptable to the Genetic Architectures of Complex Traits. Heredity, 2018,0(0). https://doi.org/10.1038/s41437-018-0075-0

[3] You Tang, Xiaolei Liu, Jiabo Wang, Meng Li, Qishan Wang, Feng Tian, Zhongbin Su, Yuchun Pan, Di Liu, Alexander E. Lipka, Edward S. Buckler and Zhiwu Zhang. GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. Plant Genome，2016，9(2):1-9. doi:10.3835/plantgenome2015.11.0120.