

Biography

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Education

2014-2018: Appeared for Ph.D. in Crop Genetics and Breeding- Molecular Genetics, Institute of Cotton Research, Chinese Academy of Agricultural Sciences, Beijing, China.

2006-2009: Engineer degree (Msc), Senegalese National College of Agricultural, ENSA (Thies Polytechnic University-Senegal).

2004-2006: Bachelor of Agronomy, Senegalese National College of Agricultural, ENSA (Thies Polytechnic University-Senegal).

Academic Experience

- PhD Research candidate. Graduate School of Chinese Academy of Agricultural Sciences (CAAS), Beijing, China (2014-2018)
- Agronomist Engineer, Project Manager, Senegalese River Valley Development Agency (SAED), Saint Louis, Senegal (2010-2014)
- Consultant on food security in the northern part of Senegal (Senegalese river valley) funded by United Nations Development Program (UNDP) from Sept to December 2018
- Consultant at PRODAM Senegalese development project for business plan conception from December to January 2019.

Non Academic Experience

- Billiard (pull)
- scrabble
- wrestling
- Soccer
- Volley-ball

Advisor

- Prof Dr. Du Xiongming (from 2014 – to 2018)
- Dr. Saliou Ndiaye (from 2004 – to 2009)

Research Interests & Statement

Awards, Funding, and Other Support

- Outstanding Graduates Students Award: July 2018
- China scholarship council (CSC) award: august 2014

Publications and Scholarly Work

Published papers

- **Latyr Diouf,** Richard Odongo Magwanga, Wen-fang Gong, Shou-Pu He, Zhaoe Pan, Yin Hua Jia, Joy Nyangasi Kirungu, Xiongming Du*. QTL Mapping Of Yield Related and Fiber Quality Traits in an Intra Specific Upland Cotton Using Genotype by Sequencing (GBS**). International Journal of Molecular Science, 2018, *19* (2), 441; doi: 10.3390/ijms19020441,** published on http://www.mdpi.com/1422-0067/19/2/441
- **Latyr Diouf**, Zhaoe Pan, Shou-Pu He, Wen-fang Gong, Yin Hua Jia, Richard Odongo Magwanga, Kimbembe Romesh Eric Romy, Harun or Rashid, Joy Nyangasi Kirungu, Xiongming Du*. High Density Linkage Map Construction and Mapping of Salt Tolerant QTLs at Seedling Stage in Upland Cotton Using Genotyping by Sequencing (GBS**). International Journal of Molecular Science, 2017, 18 (12), 2622; doi: 10.3390/ijms18122622**, published on http://www.mdpi.com/1422-0067/18/12/2622
- **Latyr Diouf**, Zhaoe Pan, Shou-Pu He, Wen-fang Gong, Richard Odongo Magwanga, Xiongming Du*. QTL Mapping for Salt Tolerance in an Intra-Specific Upland Cotton at Seedling Stage Using SSR Markers. **Journal of Plant breeding and genetics, 2017**, published, http://escijournals.net/index.php/JPBG/article/view/2195
- Richard Odongo Magwanga, Pu Lu, Hejun Lu, Joy Nyangasi Kirungu, **Latyr Diouf**, Xingxing Wang, Xiaoyan Cai, Zhongli Zhou, Kunbo Wang, Fang Liu. GBS Mapping and Analysis of Genes Conserved between Gossypium tomentosum and Gossypium hirsutum Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC2F2 Generation, published Int. J. Mol. Sci. 2018, 19, 1614; doi:10.3390/ijms19061614
- Richard Odongo Magwanga, Pu Lu, Hejun Lu, Joy Nyangasi Kirungu, **Latyr Diouf**, Xingxing Wang, Xiaoyan Cai, Zhongli Zhou, Kunbo Wang*, Fang Liu*(2018): Whole Genome Analysis of Cyclin Dependent Kinase (CDK) Gene Family in Cotton and Functional Evaluation of the Role of CDKF4 Gene in Drought and Salt Stress Tolerance in Plants, published Int. J. Mol. Sci. 2018, 19, 2625; doi:10.3390/ijms19092625

Works under Review

- Richard Odongo Magwanga, Pu Lu, Hejun Lu, Joy Nyangasi Kirungu, **Latyr Diouf**, Xingxing Wang, Xiaoyan Cai, Zhongli Zhou, Kunbo Wang, Fang Liu. Genotyping by Sequencing (GBS) in mapping of drought tolerance traits and functional characterization of key genes mined within the QTL regions in upland cotton

  (**Under review in BMC Genomics**)
- Richard Odongo Magwanga, Pu Lu, Hejun Lu, Joy Nyangasi Kirungu, **Latyr Diouf**, Xingxing Wang, Xiaoyan Cai, Zhongli Zhou, Kunbo Wang*, Fang Liu*(2018): Fine mapping of a backcross population

(BC2F2) of a semi wild origin by use of Genotyping by Sequencing (GBS) techniques (**Under review in IJMS**)

Publications (refereed)

- **Diouf, L**.; Magwanga, R.O.; Gong, W.; He, S.; Pan, Z.; Jia, Y.H.; Kirungu, J.N.; Du, X. QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS). *Int. J. Mol. Sci.* **2018**, *19*, 441.
- **Diouf, L**.; Pan, Z.; He, S.-P.; Gong, W.-F.; Jia, Y.H.; Magwanga, R.O.; Romy, K.R.E.; or Rashid, H.; Kirungu, J.N.; Du, X. High-Density Linkage Map Construction and Mapping of Salt-Tolerant QTLs at Seedling Stage in Upland Cotton Using Genotyping by Sequencing (GBS). *Int. J. Mol. Sci.* **2017**, *18*, 2622.
- **Diouf, L**.; Pan, Z.; He, S.-P.; Gong, W.-F.; Jia, Y.H.; Magwanga, R.O.; Du, X QTL Mapping for Salt Tolerance in an Intra-Specific Upland Cotton at Seedling Stage Using SSR Markers. *http://escijournals.net/index.php/JPBG/article/view/2195.*
- Magwanga, R.O.; Lu, P.; Kirungu, J.N.; **Diouf, L**.; Dong, Q.; Hu, Y.; Cai, X.; Xu, Y.; Hou, Y.; Zhou, Z.; Wang, X.; Wang, K.; Liu, F. GBS Mapping and Analysis of Genes Conserved between *Gossypium tomentosum* and *Gossypium hirsutum* Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC_2F_2 Generation. *Int. J. Mol. Sci.* **2018**, *19*, 1614.
- Magwanga, R.O.; Lu, P.; Kirungu, J.N.; Cai, X.; Zhou, Z.; Wang, X.; **Diouf, L**.; Xu, Y.; Hou, Y.; Hu, Y.; Dong, Q.; Wang, K.; Liu, F. Whole Genome Analysis of Cyclin Dependent Kinase (*CDK*) Gene Family in Cotton and Functional Evaluation of the Role of *CDKF4* Gene in Drought and Salt Stress Tolerance in Plants. *Int. J. Mol. Sci.* **2018**, *19*, 2625.

Title:

QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS)

Abstract

Fiber quality and yield improvement are crucial for cotton domestication and breeding. With the transformation in spinning techniques and multiplicity needs, the development of cotton fiber quality and yield is of great importance. A genetic map of 5178 Single Nucleotide Polymorphism (SNP) markers were generated using 277 F2:3 population, from an intra-specific cross between two upland cotton accessions, CCRI35 a high fiber quality as female and Nan Dan Ba Di Da Hua (NH), with good yield properties as male parent. The map spanned 4768.098 cM with an average distance of 0.92 cM. A total of 110 Quantitative Traits Loci (QTLs) were identified for 11 traits, but only 30 QTLs were consistent in at least two environments. The highest percentage of phenotypic variance explained by a single QTL was 15.45%. Two major cluster regions were found, cluster 1 (chromosome17-D03) and cluster 2 (chromosome26-D12). Five candidate genes were identified in the two QTL cluster regions. Based on GO functional annotation, all the genes were highly correlated with fiber development, with functions such as protein kinase and phosphorylation. The five genes were associated with various fiber traits as follows: Gh_D03G0889 linked to qFM-D03_cb, Gh_D12G0093, Gh_D12G0410, Gh_D12G0435 associated with qFS-D12_cb and Gh_D12G0969 linked to qFY-D12_cb. Further structural annotation and fine mapping is needed to determine the specific role played by the five identified genes in fiber quality and yield related pathway.