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Curriculum Vitae

Education

- 2016 – 2019 Ph.D. in Crop Genetics and Breeding, Graduate School of Chinese Academy of Agricultural Science (GSCAAS), China
- 2010 – 2014 Masters in Botany - Plant Ecophysiology, Maseno University, Kenya
- 2005 – 2009 BEd (Science) First Class Hons, Maseno University, Kenya

Professional Career

- 2020 – Present Associate Director, Directorate of Research, Innovation and Partnership, Jaramogi Oginga Odinga University of Science and Technology
- 2019 – Present Lecturer, Jaramogi Oginga Odinga University of Science and Technology
- 2014 – 2016 Part time lecturer, Jaramogi Oginga Odinga University of Science and Technology
- 2014 – 2016 Examiner, Kenya National Examination Council (KNEC)
- 2012 – 2016 Graduate Teacher (Biology and Chemistry), Teachers Service Commission
- 2010 – 2012 Research Assistant, Rice Research Project

Fellowships, Awards, and Honours

- 2022 – 2031 VLIR-Institutional University Cooperation (IUC) Program research grant for Strengthening Climate Change Resilience among Communities and Ecosystems in the Lake Victoria Basin
- 2020 National Research funds - South Africa: Towards COVID-19 Containment: Serological, Faecal and Wastewater Epidemiological Surveillance of SARS-CoV-2 in Support of Home-Based Isolation and Care in Kenya.
- 2019 Most outstanding international PhD. student
(<http://cri.caas.cn/en/newsroom/192701.htm>)
- 2018 Nominated as the most outstanding international student for excellent research skills and outstanding in terms of scientific research publications.
- 2015 Evaluation of upland rice germplasms response to different soil types under drought conditions funds awarded by the National Council of Science and Technology (NACOSTI), Kenya.

Professional Activities

2015 – Present Reviewer, Board Member for the following international journals: Journal of BMC Genomics; Journal of PeerJ; Frontiers in Plant Sciences; Scientific Report; Cleaner Materials Journal; PeerJ; BMC Plant Biology; and Agronomy

Research Interests

Plant genomics, Smart Agriculture, Abio-biotic plant stress evaluation; plant germplasm evaluation; key research activities includes:

- a) Sericulture: Mass production of mulberry plants with an aim of producing silk fibres from silkworms (Ongoing)
- b) Rainfed rice: Due to erratic rainfall pattern, coupled with food insecurity, JOOUST with fundings from NRF, are collaborating on how to scale up the adoption of rainfed type of rice within the lowland areas of Kisumu, Budalangi and other major rice growing areas
- c) Upland cotton, cotton industry has drastically declined, and to boost cotton production, active research is critical.
- d) FAO and JOOUST have partnered to upscale the rearing of black soldier flies (BSF)

Publications (in chronological order)

1. Shiraku ML, **Magwanga RO** (2022). Late embryogenesis abundant gene LEA3 (Gh_A08G0694) enhances drought and salt stress tolerance in cotton. *Int. J. Biol. Macromol.* [doi: 10.1016/j.ijbiomac.2022.03.110](https://doi.org/10.1016/j.ijbiomac.2022.03.110)
2. Shiraku ML, **Magwanga RO** (2021) Knockdown of 60S ribosomal protein L14-2 reveals their potential regulatory roles to enhance drought and salt tolerance in cotton. *J. Cotton Res.* [doi: 10.1186/s42397-021-00102-7](https://doi.org/10.1186/s42397-021-00102-7)
3. Mehari TG, Xu Y, **Magwanga RO** (2021). Genome wide identification and characterization of light-harvesting Chloro a/b binding (LHC) genes reveals their potential role in enhancing drought tolerance in *Gossypium hirsutum*. *J. Cotton Res.* [doi: 10.1186/s42397-021-00090-8](https://doi.org/10.1186/s42397-021-00090-8)
4. Shiraku ML, **Magwanga RO** (2021). Functional Characterization of GhACX3 gene reveals its significant role in enhancing drought and salt stress tolerance in cotton. *Front. Plant Sci.* [doi: 10.3389/fpls.2021.658755](https://doi.org/10.3389/fpls.2021.658755).
5. Mehari TG, Xu Y, **Magwanga RO** (2021) Identification and functional characterization of Gh_D01G0514 (GhNAC072) transcription factor in response to drought stress tolerance in cotton. *Plant Physiol. Biochem.* 166:361–375. [doi: 10.1016/j.plaphy.2021.05.050](https://doi.org/10.1016/j.plaphy.2021.05.050).
6. Jiangna Liu, Richard Odongo Magwanga, Yanchao Xu, Tingting Wei, Joy Nyangasi Kirungu, Jie Zheng, Yuqing Hou, Yuhong Wang, Stephen Gaya Agong, Erick Okuto, Kunbo Wang, Zhongli Zhou, Xiaoyan Cai, Fang Liu (2021). Functional Characterization of Cotton C-Repeat Binding Factor Genes Reveal Their Potential Role in Cold Stress Tolerance. *Front. Plant Sci.* [doi:10.3389/fpls.2021.766130](https://doi.org/10.3389/fpls.2021.766130)
7. **Magwanga RO** (2020) Genotyping by Sequencing (GBS) in the mapping of drought tolerance traits and functional characterization of key genes mined within the QTL regions in upland cotton. *J. Cotton Res.* [doi: 10.1186/s42397-020-0043-0](https://doi.org/10.1186/s42397-020-0043-0)
8. KIRUNGU, J.N., **MAGWANGA, R.O.**, SHIRAKU, M.L. et al. Genetic map construction and functional characterization of genes within the segregation distortion regions (SDRs) in the F2:3 populations derived from wild cotton species of the D genome. *J Cotton Res* 3, 32 (2020). <https://doi.org/10.1186/s42397-020-00072-2>
9. Lu H, Cui X, Zhao Y, **Magwanga RO**, Li P, Cai X, Zhou Z, Wang X, Liu Y, Xu Y, Hou Y, Peng R, Wang K, Liu F. 2020. Identification of a genome-specific repetitive element in the *Gossypium D*

genome. *PeerJ* 8:e8344 <https://doi.org/10.7717/peerj.8344>

10. Zhao H, Wang J, Qu Y, Peng R, **Magwanga RO**, Liu F, Huang J. Transcriptomic and proteomic analyses of a new cytoplasmic male sterile line with a wild *Gossypium bickii* genetic background. *BMC Genomics*. 2020 Dec 2;21(1):859. doi: 10.1186/s12864-020-07261-y.
11. Kirungu JN, **Magwanga RO** (2020) Knockdown of Gh_A05G1554 (GhDHN_03) and Gh_D05G1729 (GhDHN_04) dehydrin genes, reveals their potential role in enhancing drought and salt tolerance in cotton. *Genomics*. doi: 10.1016/j.ygeno.2019.11.003
12. Xu Y, **Magwanga RO** (2020) Genetic regulatory networks for salt-alkali stress in *Gossypium hirsutum* with differing morphological characteristics. *BMC Genomics*. 1–19. doi: 10.1186/s12864-019-6375-9
13. **Magwanga RO** (2019) Knockdown of cytochrome P450 Genes Gh_D07G1197 and Gh_A13G2057 on chromosomes D07 and a13 reveals their putative role in enhancing drought and salt stress tolerance in *G. hirsutum*. *Genes* 10(3):226. doi: 10.3390/genes10030226.
14. **Magwanga RO**, Lu P, Kirungu JN (2019) VIGS of Gh_A01G0884 (ghAlba_4) and Gh_D01G0922 (ghAlba_5) proteins in cotton inhibits root growth and increases Sensitivity to Drought and Salt Stresses. *Front. Plant Sci*. doi: 10.3389/fpls.2019.01292
15. **Magwanga, R. O.**, Joy Nyangasi K. (2019). Physiological and Developmental Response of Selected Upland Rice Genotypes to Water and Nutrient Stress Condition. *Int J Plant Sci Hor*. 1: 22-39.
16. Xu, Y.; **Magwanga, R.O.**; Cai, X.; Zhou, Z.; Wang, X.; Wang, Y.; Zhang, Z.; Jin, D.; Guo, X.; Wei, Y.; Li, Z.; Wang, K.; Liu, F. (2019) Deep Transcriptome Analysis Reveals Reactive Oxygen Species (ROS) Network Evolution, Response to Abiotic Stress, and Regulation of Fiber Development in Cotton. *Int. J. Mol. Sci*. 2019, 20,1863.
17. **Magwanga, R. O.**, Kirungu, J. N., Pu, L., Xiu, Y., Dong, Q., Cai, X., ... Liu, F. (2019). Genomewide identification of the trihelix transcription factors and overexpression of *Gh_A05G2067 (GT-2)*, a novel gene contributing to increased drought and salt stresses tolerance in cotton. *Physiologia Plantarum*, 2067. <https://Doi.org/10.1111/ppl.12920>.
18. Dong, Q., **Magwanga, R.**, Cai, X., Lu, P., Nyangasi Kirungu, J., Zhou, Z., ... Liu, F. (2019). RNA-Sequencing, Physiological and RNAi Analyses Provide Insights into the Response Mechanism of the ABC-Mediated Resistance to *Verticillium dahliae* Infection in Cotton. *Genes*, 10.(2),110. <https://Doi.org/10.3390/genes10020110>.
19. Lu, P., **Magwanga, R. O.**, Kirungu, J. N., Hu, Y., Dong, Q., Cai, X., ... Liu, F. (2019). Overexpression of Cotton a *DTX/MATE* Gene Enhances Drought, Salt and Cold Stress Tolerance in Transgenic Arabidopsis *Frontiers in plant sciences* 10 (March), 1–26. <https://Doi.org/10.3389/fpls.2019.00299>.
20. Salih H, Gong W, He S, Xia W, Odongo MR, Du X. Long non-coding RNAs and their potential functions in Ligon-lintless-1 mutant cotton during fiber development. *BMC Genomics*. 2019 Aug 19;20(1):661. doi: 10.1186/s12864-019-5978-5.
21. Yang X, Kirungu JN, **Magwanga RO**, Xu Y, Pu L, Zhou Z, Hou Y, Cai X, Wang K, Liu F. Knockdown of GhIQD31 and GhIQD32 increases drought and salt stress sensitivity in *Gossypium hirsutum*. *Plant Physiol Biochem*. 2019 Nov;144:166-177. doi: 10.1016/j.plaphy.2019.09.027. zinc
22. Cai X, Magwanga RO, Xu Y, Zhou Z, Wang X, Hou Y, Wang Y, Zhang Y, Liu F, Wang K. Comparative transcriptome, physiological and biochemical analyses reveal response mechanism mediated by CBF4 and ICE2 in enhancing cold stress tolerance in *Gossypium thurberi*. *AoB Plants*. 2019 Aug 9;11(6):plz045. doi: 10.1093/aobpla/plz045.
23. Dong Qi, **Magwanga, R. O.**, Lu, P., Cai, X., Zhou, Z., Xingfen, W., Wang, X., Xu, Y., Hou Y., Wang, Y., Kunbo, W., Fang, L., Zhiying, M. (2019). Expression Analysis in Three D Genome Cotton and Identification of Resistance to *Verticillium* Wilt of *Bet v 1* Gene. *Cotton Science*
24. Kirungu, J. N., **Magwanga, R. O.**, Lu, P., Cai, X., Zhou, Z., Wang, X., Peng, R., Wang, K and Liu, F. (2019): Functional Characterization of *Gh_A08G1120 (GH3.5)*, A Novel *GH3* Gene Reveal Their Significant Role in Enhancing Drought and Salt Stress Tolerance in Cotton. *BMC genetics*,

<https://doi.org/10.1186/s12863-019-0756-6>

25. Haron Salih, **Magwanga, R.O.**, Wenfang Gong, Shoupu He, Xiongming Du (2019). Genome-wide analysis of cotton C₂H₂-zinc finger transcription factors family and their expression analysis during fiber development. *BMC genomics*, <https://doi.org/10.1186/s12870-019-2003-8>
26. Lu, P., **Magwanga, R. O.**, Cai, X., Zhou, Z., Wang, X., Xu, Y., Hou, Y., Kirungu, J. N., Hu, Y., Dong, Q., Wang, K. and Liu, F. (2019): *Gh_A07G0747 (GhTOM1)*, A Novel Cotton GPCR Gene Enhances Drought and Cold Stress Tolerance by Promoting Root Growth in Plants. *BMC Genomics*; <https://doi.org/10.1186/s12864-019-5972-y>
27. **Magwanga, R. O.**, Kirungu, J. N., Lu, P., Cai, X., Zhou, Z., Wang, X., Xu, Y., Hou, Y., Hu, Y., Dong, Q., Wang, K. and Liu, F. (2019): Map-Based Functional Analysis of the *GhNLP* Genes Reveals Their Roles in Enhancing Tolerance to N-Deficiency in Cotton. *Int. J. Mol. Sci.* 2019, 20(19), 4953; <https://doi.org/10.3390/ijms20194953>
28. YANG Xiu, XU Yanchao, YANG Fangfang, **Richard Odongo Magwanga**, CAI Xiaoyan, WANG Xingxing, WANG Yuhong, HOU Yuqing, WANG Kunbo, LIU Fang and ZHOU Zhongli (2019). Genome-Wide Identification of *OSCA* Gene Family and Their Potential Function in the Regulation of Dehydration and Salt Stress in *Gossypium hirsutum*. *Journal of cotton research(JCR)*, <https://doi.org/10.1186/s42397-019-0028-z>
29. Haron Salih, Wenfang Gong, Shoupu He, Wang Xiao, **Magwanga, R.O.**, Wang Xia, Xiongming Du (2019). Long non-coding RNAs and their potential functions in Ligon-lintless-1 mutant cotton during fiber development. *BMC Plant Biology*, <https://doi.org/10.1186/s12864-019-5978-5>
30. Yang Xu, **Magwanga, R.O.**, Kirungu, J. N., Cai, X., Zhou, Z., Wang, X., Xu, Y., Yuqing Hou, Hu, Y., Qi Dong, Wang, K. and Liu, F. (2019): Knockdown of *IQD* genes in upland cotton compromises their ability to tolerate drought and salt stresses. *Journal of Plant Physiology and Biochemistry*, <https://doi.org/10.1016/j.plaphy.2019.09.027>
31. **Magwanga, R. O.**, Pu L., Hejun L., Kirungu, J. N., Diouf L., Wang X., Cai X., Zhou Z., Wang K. and Liu F. (2019): Identification of QTLs and candidate genes for physiological traits associated with drought tolerance in cotton. *J Cotton Res* 3, 3 (2020). <https://doi.org/10.1186/s42397-020-0043-0>
32. **Magwanga, R.O.**, Lu, P., Kirungu, J.N., Lu, H., Wang, X., Cai, X., Zhou, Z., Zhang, Z., Salih, H., Wang, K., Liu, F., (2018). Characterization of the late embryogenesis abundant (LEA) protein family and their role in drought stress tolerance in upland cotton. *BMC Genet.* 19. <https://doi.org/10.1186/s12863-017-0596-1>.
33. **Magwanga, R. O.**, Lu, P., Kirungu, J., Cai, X., Zhou, Z., Wang, X., ... Liu, F. (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. *International Journal of Molecular Sciences*, 19 (9), 2625. <https://doi.org/10.3390/ijms19092625>.
34. **Magwanga, R. O.**, Lu, P., Kirungu, J., Diouf, L., Dong, Q., Hu, Y., ... Liu, F. (2018). GBS Mapping and Analysis of Genes Conserved between *G. tomentosum* and *G. hirsutum* Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC₂F₂ Generation. *International Journal of Molecular Sciences*, 19 (6), 1614. <https://doi.org/10.3390/ijms19061614>.
35. Lu, P., **Magwanga, R. O.**, Guo, X., Kirungu, J. N., Lu, H., Cai, X., ... Liu, F. (2018). Genome-Wide Analysis of Multidrug and Toxic Compound Extrusion (MATE) Family in Diploid Cotton, *G. raimondii* and *G. arboreum* and Its Expression Analysis Under Salt, Cadmium and Drought Stress. *G3; Genes Genomes Genetics*, (July), g3.200232.2018. <https://doi.org/10.1534/g3.118.200232>.
36. Diouf, L., **Magwanga, R.**, Gong, W., He, S., Pan, Z., Jia, Y., ... Du, X. (2018). QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS). *International Journal of Molecular Sciences*, 19 (2), 441. <https://doi.org/10.3390/ijms19020441>
37. Kirungu, J. N., Deng, Y., Cai, X., **Magwanga, R. O.**, Zhou, Z., Wang, X., ... Liu, F. (2018). Simple sequence repeat (SSR) genetic linkage map of D genome diploid cotton derived from an interspecific cross between *Gossypium davidsonii* and *Gossypium klotzschianum*. *International Journal of Molecular Sciences*, 19 (1). <https://doi.org/10.3390/ijms19010204>.

38. Lu, P., **Magwanga, R. O.**, Lu, H., Kirungu, J. N., Wei, Y., Dong, Q., ... Liu, F. (2018). A novel G-protein-coupled receptors gene from upland cotton enhances salt stress tolerance in transgenic *Arabidopsis*. *Genes*, *9*(4). <https://doi.org/10.3390/genes9040209>
39. **Magwanga, R. O.**, Lu, P., Kirungu, J. N., Dong, Q., Hu, Y., Zhou, Z., ... Liu, F. (2018). Cotton Late Embryogenesis Abundant (LEA2) Genes Promote Root Growth and Confer Drought Stress Tolerance in Transgenic *A. thaliana*. *G3*, *g3.200423.2018*. <https://doi.org/10.1534/g3.118.200423>.
40. Li, P., Kirungu, J. N., Lu, H., **Magwanga, R. O.**, Lu, P., Cai, X., ... Liu, F. (2018). SSR-Linkage map of interspecific populations derived from *G. trilobum* and *G. thurberi* and determination of genes harbored within the segregating distortion regions. *PLoS One*, *13*(11), e0207271. <https://doi.org/10.1371/journal.pone.0207271>.
41. Tchister Morrel EBISSA, Bo Yang, Yuanqing Guan, Bingchang Tan, Peizhen Chen, Lili Wang, **Richard Odongo Magwanga** and Xiangqun Zheng: A Comparison of Nitrogen Transfer and Transformation in Traditional Farming and the Rice–Duck Farming System by ¹⁵N Tracer Method. *Agronomy* 2018, *8*(12), 289; doi:10.3390/agronomy8120289.
42. Diouf, L., Pan, Z., He, S.-P., Gong, W.-F., Jia, Y. H., **Magwanga, R. O.**, ... Du, X. (2017). 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 Sciences*, *18*(12). <https://doi.org/10.3390/ijms18122622>.
43. Mustafa, N. S., Liu, F., **Magwanga, R. O.**, Wang, X., Cai, X., Zhang, Z., & Wang, K. (2017). Effects of Colchicine Treatments on Chromosome Doubling in three Diploid Cotton Species. *Journal of Multidisciplinary Engineering Science and Technology*, *4*(4), 2458–9403. Retrieved from www.jmest.org.
44. Diouf, L., Pan, Z., He, S.-P., Gong, W.-F., **Magwanga, R. O.**, & Du, X. (2017). QTL Mapping For Salt Tolerance In An Intra-Specific Upland Cotton At Seedling Stage Using SSR Markers. *J. Plant Breed. Genet*, *5*(2), 57–73. Retrieved from <http://www.esajournals.net/JPBG>.