CURRICULLLUM VITAE

Full names	Muleke Everlyne M'mbone
Nationality	Kenyan
Gender	Female
Current address	Department of Crops Horticulture and Soil Sciences P.O. Box 536 – 20115, Egerton University
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SUMMARY OF QUALIFICATIONS AND EXPERIENCES

- Earned Ph.D. in Horticulture with specialization in horticultural plant biotechnology, molecular biology, bioinformatics, and crop molecular breeding and genetics.
- Ph.D. research centered on horticultural plant biotechnology, molecular biology and bioinformatic techniques.
- 6- years, university teaching experience as a part time lecturer- CHS- Egerton University.
- Published twenty (20) peer reviewed journal papers in Horticulture with cumulative publication points of26.66**.** see –

  https://www.researchgate.net/profile/Mmbone_Everlyne/publications
- 2- years of research experience at KALRO.
- Registered with “Horticultural Association of Kenya”, and a life member of the “International Society of Extension Education.
- Computer literate with extensive skills in the use of MS-word; Access; Excel; PowerPoint; R-programme, SPSS; SAS; and Bioinformatics tools.

EDUCATION BACKGROUND		
QUALIFICATION	**INSTITUTION**	**YEARS ATTENDED**
Doctor of Philosophy (Ph.D.)- (Horticulture/Olericulture)	Nanjing Agricultural University	2014 - 2017
Master of Science (M.Sc.) - Horticulture	Egerton University	2010 - 2013
Bachelor of Science (B.Sc.) - Horticulture	Egerton University	2007 - 2010
Diploma - Horticulture	Egerton University	2002 - 2006

UNIVERSITY TEACHING EXPERIENCE

YEAR	POSITION	INSTITUTION	DUTIES AND RESPONSIBILITIES
2018 -2021	**Part Time Lecturer and Technologist**	Department of Crops, Horticulture and Soil Sciences (CHS), Faculty of Agriculture, Egerton University, Njoro Campus.	➢ Teaching various horticultural courses to Diploma and B.Sc. students namely: • Crop Protection (*Hort 313*) • General Vegetable Production (*HORT 331, HORT 0232*) • Horticultural Seed Production (*Hort 321*) • Horticultural Crop Protection (*Hort 0213)* • Soil Nutrition and Fertility (*SOIL 320*) • Agricultural Experimentation and Statistics (HORT *371, HORT 0371*) • Horticultural Biotechnology (Hort 322).
2010 -2014	**Part Time Lecturer and Technologist**	Department of Crops, Horticulture and Soil Sciences (CHS), Faculty of Agriculture, Egerton University, Njoro Campus.	➢ Teaching various horticultural courses to Diploma and B.Sc. students namely: • Crop Protection (*Hort 313*), • General Vegetable Production (*HORT 331, HORT 0232*) • Seed Production (*Hort 321*) • Soil Nutrition and Fertility (*SOIL 320*) • Agricultural Experimentation and Statistics (HORT *371, HORT 0371*) • Agricultural Experimentation and Statistics (*HORT 0371*)

2019 to 2021	**Research Assistant**	Pest Control Products Board of Kenya (PCPB) P.O. Box 13794-00800, Nairobi.	❖ Designing trials for bio-pesticides and bio-fertilizers, implementing them and overseeing their management. ❖ Data collection. ❖ Analyzing data using statistical packages such as ‘R’, interpretation and presentation of the data. ❖ Preparation and presentation of progress reports.
2020 to Present	**Research Assistant**	Korea Africa Food and Agriculture Collaborative Initiative (KAFACI) project based at Kenya Agricultural and Livestock Research Organisation, (KALRO) – Njoro.	➢ Diversity analysis using SSRmarkers to screen for superior traits in food oil crops canola/sunflower/castor/soya bean ➢ Sample collection for diagnostics and molecular analysis.
	Research Assistant	KCSAP Cassava Value Chain Project	➢ Undertaking cassava ecotype germplasm collection and bulking them utilizing tissue culture
	Research Assistant	KCSAP Banana Value Chain Project	➢ Molecular characterization of the *fusarium oxysporum* fungus affecting bananas in Kenya
2006-2007	**Production Supervisor**	Magana Flowers, Kenya	❖ Cultural production practices of rose flowering greenhouses ❖ Disease scouting, monitoring and ensure adherence to GAP ❖ Rose flower harvesting, pre-cooling and packaging

REFERRED JOURNAL PAPERS			
S/ NO	**JOURNAL PAPERS**	**No. of Authors**	**Publication Points**
1	**Muleke, E. M**., Yan, Wang, Zhang, W. T., Liang, X. U., Ying, J. L., Karanja, B. K., LIU, L. W. (2021). Genome-wide identification and expression profiling of MYB transcription factor genes in radish (*Raphanussativus* L.). *Journal of Integrative Agriculture*, 20 (1), 120-131. **DOI: 10.1016/S2095-3119(20)63308-1**	10	0.8
2	Xie, Y., Ying, J., Xu, L., Wang, Y., Dong, J., Chen, Y.,**Muleke, E. M.**, Liu, L. (2020). Genome-wide sRNA and mRNA transcriptomic profiling insights into dynamic regulation of taproot thickening in radish (*Raphanussativus* L.). *BMC Plant Biology*, 20(1), 1-14. **https://DOI.org/10.1186/s12870-020-02585-z**	8	1
3	Karanja, B. K., Xu, L., Wang, Y., Tang, M., **Muleke, E. M**., Dong, J., Liu, L. (2019). Genome-wide characterization of the AP2/ERF gene family in radish (*Raphanussativus* L.): Unveiling evolution and patterns in response to abiotic stresses. *Gene*, 718, 144048 **https://DOI.org/10.1016/j.gene.2019.144048**	7	1.14
4	**Muleke, E.M.,**Wanwan C., Xu, L., Wang, Y., Karanja, B.K., Zhu, X., Cao, Y., Liwang, L., Identification and transcript analysis of MATE genes involved in anthocyanin transport in radish (*Raphanussativus* L) *ScientiaHorticulturae* (2018) 238, 195-203. **https://DOI.org/10.1016/j.scienta.2018.04.029**	8	1
5	**Muleke, E**., Fan, L., Wang, Y., Xu, L., Zhu, X., Zhang, W., Liu, L. (2017). Coordinated regulation of anthocyanin biosynthesis genes confers varied phenotypic and spatial-temporal anthocyanin accumulation in radish (*Raphanussativus L*.). *Frontiers in Plant Science*, 8, 1243 **DOI: 10.3389/fpls.2017.01243**	7	1.14
6	SaidiMwanarusi, **MulekeEverlyne M**. (2017).Evaluation of Agronet Covers to Reduce Pesticide Application for Yield Improvement and Profitability for Small Scale Cabbage (*Brassica oleraceae var. capitata*) Growers. *International Journal of Plant & Soil Science*, , 17:1. **DOI: 10.9734/IJPSS/2017/33585**	2	4
7	Karanja, B. K., Xu, L., Wang, Y.,**Muleke, E. M**., Jabir, B. M., Xie, Y., Liu, L. Genome-Wide Characterization and Expression Profiling of NAC Transcription Factor Genes Under Abiotic Stresses in Radish (*Raphanussativus* L.). *Peer Journal* (**2017**) 5, e4172 **DOI 10.7717/peerj.4172**	7	1.14
8	Wang, Y., Song, Z., Zhang, W., Xu, L., Su, X., **Muleke, E. M.** , Liu, L. (**2017**). Identification and characterization of expressed TIR-and non-TIR-NBS-LRR resistance gene analogous sequences from radish (*Raphanussativus* L.) de novo transcriptome. *ScientiaHorticulturae*, 216, 284-292.	7	1.14

	http://dx.DOI.org/10.1016/j.scienta.2016.12.019		
9	Feng, H., Xu, L., Wang, Y., Tang, M., Zhu, X., Zhang, W.,**Muleke, E. M.,**Liu, L. **(2017**). Identification of critical genes associated with lignin biosynthesis in radish (*Raphanussativus* L.) by de novo transcriptome sequencing. *Molecular Genetics and Genomics*, 292 (5), 1151-1163.**DOI 10.1007/s00438-017-1338-9**	8	1
10	Karanja, B. K., Fan, L., Xu, L., Wang, Y., Zhu, X., Tang, M.,**Muleke, E. M.,**Liu, L. (2017). Genome-wide characterization of the WRKY gene family in radish (Raphanussativus L.) reveals its critical functions under different abiotic stresses. *Plant Cell Reports*, 36 (11), 1757-1773.**DOI 10.1007/s00299-017-2190-4**	7	1.14
11	Jabir, O., Mohammed, B., BenardKinuthia, K., AlmahadiFaroug, M., NureldinAwad, F.,**Muleke, E. M.,**Liu, L. (**2017**). Effects of Gibberellin and Gibberellin Biosynthesis Inhibitor (Paclobutrazol) Applications on Radish (*Raphanussativus*) Taproot Expansion and the Presence of Authentic Hormones. *International Journal of Agriculture & Biology*, 19 (4).**doi: 10.3389/fpls.2016.01054**	7	1.14
12	Zhang, W., Xie, Y., Xu, L., Wang, Y., Zhu, X., Wang, R.,**Muleke, E. M.,**Liu, L. (**2016**). Identification of microRNAs and their target genes explores miRNA-mediated regulatory network of cytoplasmic male sterility occurrence during another development in radish (*Raphanussativus* L.). *Frontiers in Plant Science*, 7, 1054. **DOI: 10.17957/IJAB/15.0359**	7	1.14
13	Nie S., Li C., Xu L., Wang Y., Huang D.,**Muleke E. M.,**Sun X., Xie Y.,Liwang L. (**2016**). De Novo Transcriptome Analysis in Radish (RaphanusSativus L) and Identification of Critical Genes Involved in Bolting and Flowering. *BMC Genomics*. **DOI 10.1186/s12864-016-2633-2**	8	1
14	Xie, Y., Zhang, W., Wang, Y., Xu, L., Zhu, X.,**Muleke, E. M.,** Liu, L. **(2016**). Comprehensive transcriptome-based characterization of differentially expressed genes involved in microsporogenesis of radish CMS line and its maintainer. *Functional & Integrative Genomics*, 16 (5), 529-543. **DOI 10.1007/s10142-016-0504-1**	7	1.14
15	Zhai, L., Xu, L., Wang, Y., Zhu, X., Feng, H., Li, C., **Muleke, E. M.,** Liu, L. (**2016**). Transcriptional identification and characterization of differentially expressed genes associated with embryogenesis in radish (*Raphanussativus* L.). *Scientific Reports*, 6 (1), 1-13. **DOI: 10.1038/srep21652**	8	1
16	Luo, X. B., Liu, Z., Xu, L., Wang, Y., Zhu, X. W., Zhang, W.,**Muleke, E. M.,**Liu, L. (**2016**). Characterization of RsMYB28 and RsMYB29 transcription factor genes in radish (*Raphanussativus*L.). *Genetics and Molecular*	11	0.73

	Research: GMR, 15 (3). **DOI http://dx.doi.org/10.4238/gmr.15038381**		
17	Nie, S., Xu, L., Wang, Y., Huang, D., **Muleke, E. M.,** Sun, X.Liu, L. **(2015**). Identification of Bolting-Related Micrornas and their Targets Reveals Complex Mirna-Mediated Flowering-Time Regulatory Networks in Radish (*Raphanussativus* L.). *Scientific Reports*, 5. **DOi: 10.1038/srep14034**	7	1.14
18	**Muleke, Everlyne M.**, Saidi, M.; Itulya, F.M.; Martin, T.; Ngouajio, M. **(2014).** Enhancing Cabbage (*Brassica oleraceae*Varcapitata) Yields and Quality through Microclimate Modification and Physiological Improvement Using Agronet Covers. *Sustainable Agriculture Research*, 2(1), 1-5. **DOI:10.5539/sar.v3n2p24**	5	1.6
19	Digo, C. A., Koros, D.,**Muleke, E. M.**, **(2014**). Household Food Security among Women in Groups in Kaiti Division, Kenya. Asian *Journal of Agricultural Sciences*, 6(1), 1-5. **ISSN: 2041-3882; e-ISSN: 2041-3890**	3	2.67
20	**Muleke, Everlyne M.,**Saidi, M.; Itulya, F.M.; Martin, T.; Ngouajio, M .(**2013).**The Assessment of the Use of Eco-Friendly Nets to Ensure Sustainable Cabbage Seedling Production in Africa. *Agronomy*, 3, 1-12. **DOI:10.3390/agronomy3010001**	5	1.6
	TOTAL PUBLICATION POINTS		**26.66**

RESEARCH EXPERIENCE

Year	Research Work	Skills Acquired	Key Findings
2020- Present	**Volunteer Researcher/Research Assistant** **Institution:** Biotechnology Department, Kenya Agricultural and Livestock Research Organization (KALRO) – Njoro.	▪ DNA extraction ▪ Polymerase Chain Reaction Technique (PCR) ▪ Scoring for markers ▪ Marker assisted selection ▪ Tissue culture of cassava ▪ Molecular characterization of microbes	➢ Diversity in canola, soybean, safflower, sunflower, linseed and castor plant. ➢ Clean planting materials
2014-2017	**Doctor of Philosophy (Ph.D.) in Horticulture-Vegetable Science.** **Institution**: Department of Horticulture, National State Key Laboratory. Nanjing Agricultural	▪ Genetic engineering, horticultural plant biotechnology, molecular biology and bioinformatic techniques. ▪ Illumina DNA sequencing ▪ RT-qPCR	➢ Phenotypic and spatial temporal anthocyanin accumulation is due coordinated gene expression. ➢ Anthocyanin biosynthesis pathway

	University Nanjing-Jiangsu Province P. R. of China **Thesis Title**: *Molecular Mechanisms Underlying Differential Anthocyanin Accumulation in Radish.*	▪ Genomic DNA, total RNA extraction and reverse transcription ▪ Primer design ▪ Gene cloning and in silico sequence analysis ▪ Anthocyanin quantification ▪ Spectroscopy &fluorescent microscopy ▪ Bioinformatics ▪ Scientific publishing ▪ Ph.D. thesis writing	switchesoffinthe non- colored radish at *RsCHS* gene. ➢ MATE genes were cloned and characterized and their roles in flavonoid transport predicted through transcript analysis. ➢ Discovered 187 MYB genes in radish and that the genes are spatially, temporally and phenotypically modulated. ➢ 21 gene sequences cloned and deposited in NCBI.
2011 to 2014	**Master of Science (M.Sc.) in Horticulture** Egerton University **Thesis Title**: *Evaluation of Bio-agronets on Micro-Climate Modification, Insect Pest Control and Cabbage (Brassica Oleracea Var. Capitata) Crop Performance*	❖ Field trial designand management. ❖ Insect pest identification, scouting, evaluation and monitoring ❖ Sample collection ❖ Physiological data collection. ❖ Microclimate data collection using specware. ❖ Biomas determination ❖ Data analysis using SAS ❖ Scientific publication	➢ Bio agronets technology was found to be affordable and could modify the microclimate for enhanced crop performance. ➢ Use of Bio agronets technology reduced the use of pesticide and insectpests.

MEMBERSHIP TO PROFESSIONAL BODIES

1	Member - Horticultural Association of Kenya
2	Life member - International Society ofExtension Education

CONFERENCES AND SHORT COURSES ATTENDED

Date	Name of host institution	Theme of Seminar
Jan. 19th - 21st, 2013	Acharya NG Ranga Agricultural University- India	Futuristic Agricultural Extension for Livelihood Improvement and sustainable Development
Sept., 26th- 28th, 2013	Egerton University-Kenya	Research and Development for advancement of Humanity
Oct., 14th -18th , 2014	Nanjing AgriculturalUniversity- China	The 2014 International Horticulture ResearchConference.

HONORS AND AWARDS

DATE	AWARD	AWARDING BODY
2017	Excellent student	Nanjing Agricultural University, P.R. China
2014 - 2017	PhD Scholarship	China Scholarship Council
2010 - 2012	Research Grant	USAID-HortCRSP

NOVEL GENE SEQUENCES DEPOSITEDAT GENBANK(NCBI)

1. **Muleke,E.M.,**andLiuL.(2017):*RaphanusSativusChalconeSynthase*(*CHS-RL-1*)gene,partialcds,depositedat GenBank**Accession No.MF182893.**
2. **Muleke,E.M**.,andLiu,L.(2017):*Raphanussativuschalconeflavanoneisomerase*(*CHI-RL-1*)gene,completecds. GenBank**Accession No.MF182892.**
3. **Muleke,E.M**., and Liu, L. (2017) :*Raphanus sativus Flavanone 3-hydroxylase* (*F3H-RL-1*) gene, complete cds. **AccessionMF182895**.
4. **Muleke, E.M**., and Liu, L. (2017) : Raphanus sativus *Flavonoid 3'-hydroxylase* (*F3'H-RL-1*) gene, complete cds. **Accession No.MF182896.**
5. **Muleke, E.M**., and Liu, L. (2017): *Raphanus sativus Anthocyanidin synthase* (*ANS-RL-1*) gene, complete cds. **Accession No.MF182899**.
6. **Muleke, E.M**., and Liu, L. (2017): *Raphanus sativus Anthocyanidin reductase* (*ANR-RL-1*) gene, completecds.**Accession No. MF182891**.
7. **Muleke,E.M**.,andLiu,L.(2017):*RaphanussativusUDP-glycosyl transferase 78D2* (*UGT78D2-RL-1*) gene,partialcds. MF183115 **Accession No.MF182891.**
8. **Muleke,E.M**.,andLiu,L.(2017):*Raphanussativustransparenttesta12*(*TT12-RL-1*)gene,partialcds.MF182901 **Accession No.MF182891.**
9. **Muleke,E.M**.,andLiu,L.(2017):*RaphanussativusglutathioneS-transferaseU5*(*GSTU5-RL-1*)gene,completecds. **AccessionNo.MF182897:**
10. **Muleke, E.M**., and Liu,L (2017): *Raphanus sativus glutathione S-transferase U17* (*GSTU17-RL-1*) gene, complete cds. **Accession NoMF182898.**
11. **Muleke, E.M**., and Liu, L. (2017): *Raphanus sativus phenylalanine ammonia lyase*(*PAL*) gene, partial cds. **Accession No.MF285801**.
12. **Muleke, E.M**., and Liu, L. (2017): *Raphanus sativus 4-coumarate--CoA ligase* (*4CL-RL*-1) gene, partial cds. **Accession No.MF285800.**
13. **Muleke, E.M**., and Liu, L. (2017): *Raphanus sativus MATE1-1 protein (MATE1-1) mRNA, complete cds.* **No. MF360947.1**

14. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE2-1 protein (MATE2-1) mRNA, complete cds*. **Accession No. MF360948.1.**
15. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE3-1 protein (MATE3-1) mRNA, complete cds.* **Accession No.*MF360949.1*.**
16. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE4-1 protein (MATE4-1) mRNA, complete cds.* **Accession No.*MF360950.1*.**
17. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE5-1 protein (MATE5-1) mRNA, complete cds.* **Accession No.*MF360951.1*.**
18. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE6-1 protein (MATE6-1) mRNA, complete cds.* **Accession No.*MF360952.1*.**
19. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE7-1 protein (MATE7-1) mRNA, partial cds.* **Accession No.*MF360953.1*.**
20. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus MATE8-1 protein (MATE8-1) mRNA, complete cds.* **Accession No.*MF360954.1*.**
21. **Muleke, E.M.**, and Liu, L. (2017): *Raphanus sativus transparent testa 12 (TT12-RL-1) gene, partial cds.* **Accession No.*MF182901.1*.**

ACADEMIC REFEREES:

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Date: 3rd May, 2021