

Mining Moringa : Climate Change Mitigation Strategy

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1. Background

- Moringa, native to India and parts of South Asia is highly nutritious, fast growing, adaptable and evergreen with great versatility [1][2].
- Increasing Moringa tree cultivation will compensate for huge CO₂ emissions of densely populated cities, as it assimilates 20x CO₂ higher than other vegetation[3] .
- Its a useful tool in preventing global warming; 1,000,000 hectares =5 gigatonnes of CO₂e being sequestered.
- It is underutilised and understudied, its genetic resources have not been adequately studied from the standpoint of utilization ,conservation,breeding potentials & genetic improvement [4].



Fig1: Trees for life .Showing Countries where Moringa grow. Image source: treesforlife.org



Seed (pods):
Quercetin, Benzylamine
Vitamins: C, E
Mineral: Ca



Flowers:
Quercetin, Kaempferol,
Benzylamine
Vitamin: E
Mineral: Ca



Leaves:
Quercetin, Kaempferol,
Benzylamine
Vitamins: A, C, E
Minerals: Fe, Ca, Zn, Mg



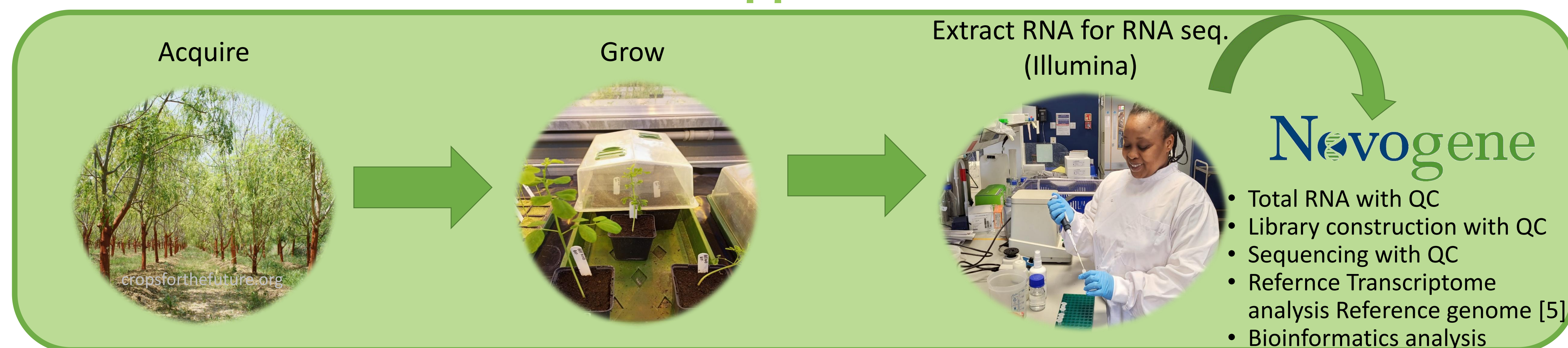
Stem:
Benzylamine
Vitamin: C
Minerals: Fe, Ca



Roots:
Benzylamine, Oleanolic acid,
Ursolic acid,
Morphine,Morginine
Minerals: Fe, Zn,Ca,Mg,Na

1. Key Objective: Perform an in-depth transcriptomic analysis of a diverse selection of *Moringa oleifera*

2. Approach



3. Key Results

7 X Vit C than



4 X Ca⁺ than milk

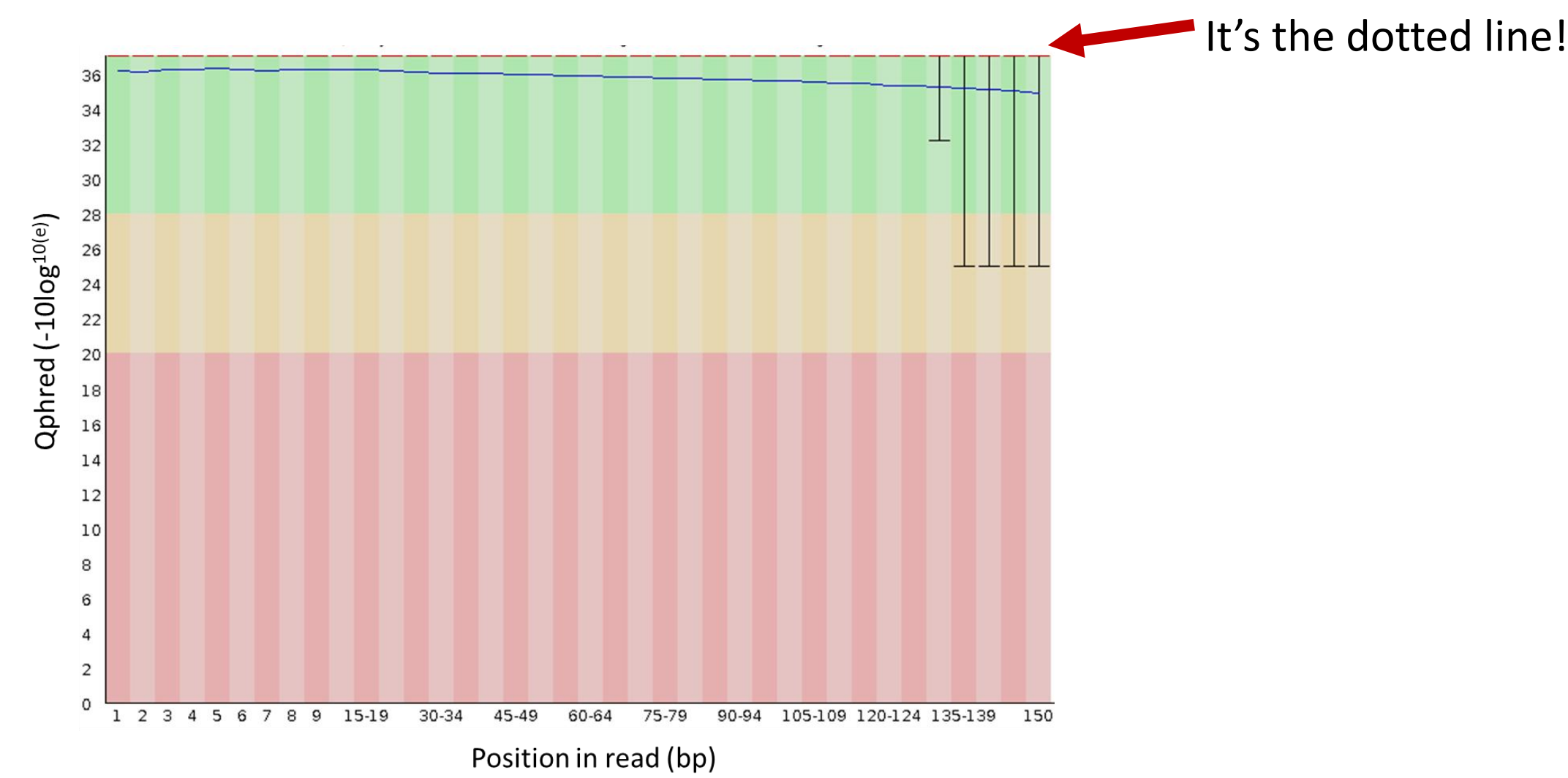


Fig.2: The high quality of the sequences is shown in the quality scores across all bases for 1 plant (red dotted line) bars showing error distribution.

Result 1.
We can trust the quality of the sequences for assembly and further pipeline work (Fig.2).

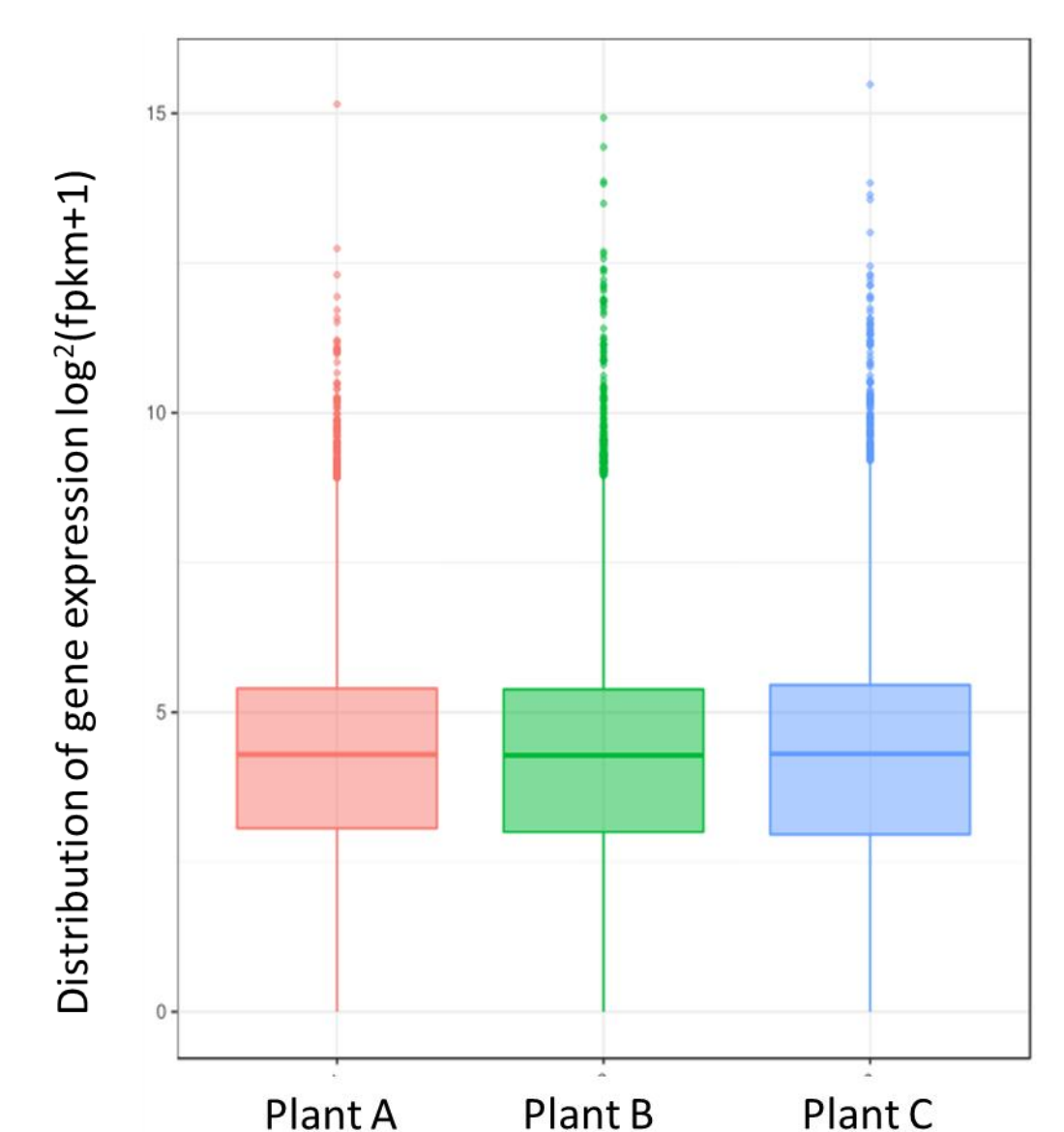


Fig.3: Distribution of gene expression levels in 3 different *Moringa oleifera* plants of different origin for leaf, stem and root tissue.

Result 2.
Across 3 different plants grown in the same condition, distribution of gene expression was highly similar, as expected (Fig.3).

4. Towards using phylogeny to assess population genetic structure in various Moringa communities

- Known nucleotide sequences of *rbcl* were aligned by MUSCLE in CLUSTAL W and PHYLIP format for the Phylogenetic tree construction.
- The Rubisco gene is important in the study of chemoautotrophs hence an indicator of carbon fixation [6]

5. Conclusion.

This work has initiated our ability to deeper understand and potentially harness the much-needed climatic change mitigation benefits Moringa possesses. I will be using whole transcriptome analysis to assess population structure at full genomic levels, that is linking transcriptomic data to genomic data in a wider study of genetic diversity.

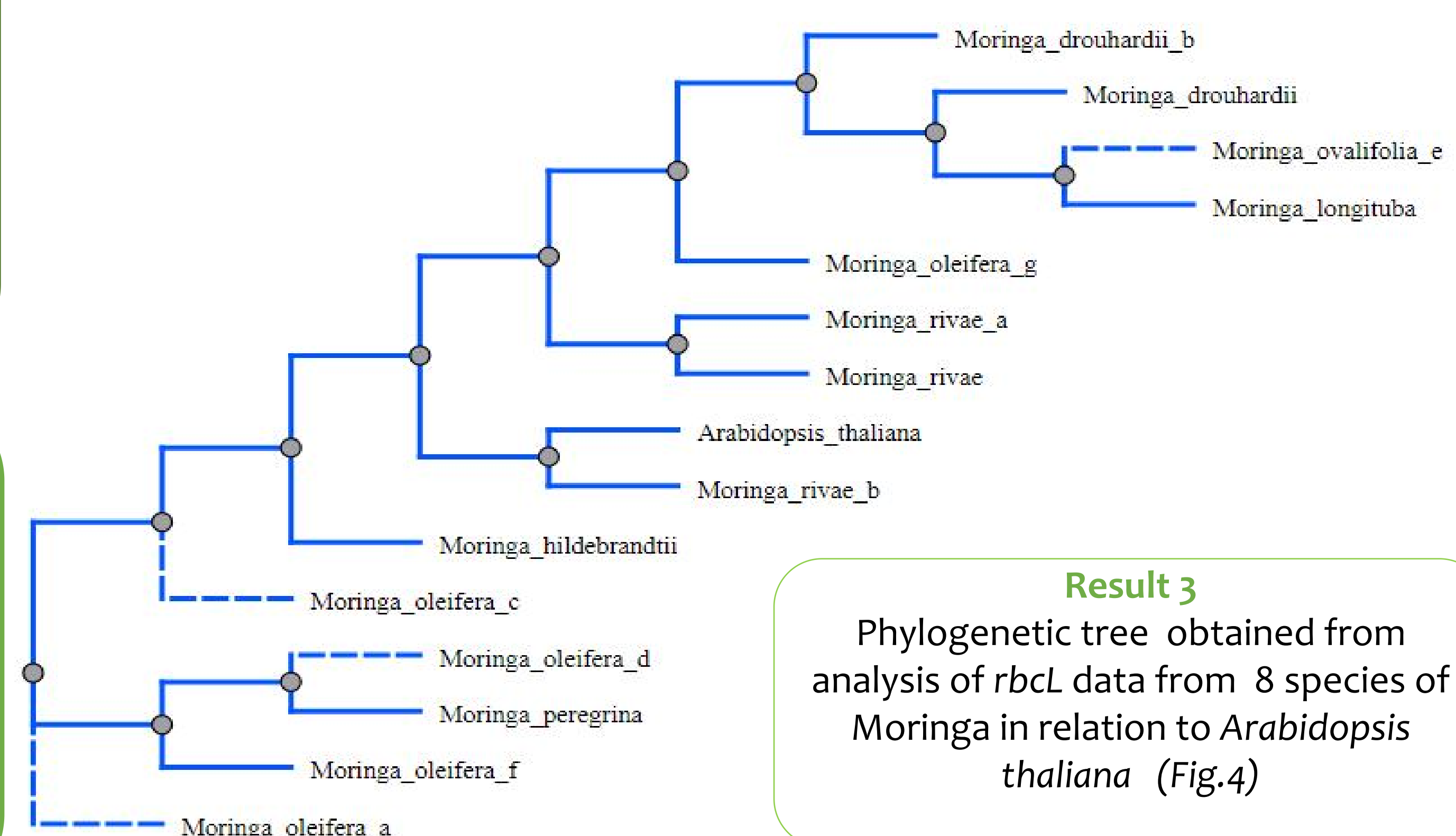


Fig.4: Inferred Phylogenetic tree from *rbcl* gene squences of Moringa spp

Result 3
Phylogenetic tree obtained from analysis of *rbcl* data from 8 species of Moringa in relation to *Arabidopsis thaliana* (Fig.4)

Reference:

- [1] Mallenakuppe, R, et.al., *SSR Inst. Int. J. Life Sci* ; 2019 [2] Pasha S N ,.et al., *Genomics 2020* [3] *Daba,M, J Earth Sci Clim Change* , 2016 [4] Rajalakshmi,R., et.al., *Current Science,2017*, [5] Shafi,M., *Data in Brief,2020* [6] Giri.et.al. *Applied and environmental microbiology,2004*

Acknowledgements

Davis Lab: Mandi Davis, Dr. Sarah Lock, Jessie Downing, Ethan Redmond, Dr. K McCarthy
Harper Lab: Dr. Sara Ortega
UoY Horticulture: Paul Scott,
TF Genomics: Dr. Sally James
Bioinformatics: Dr. Emma Rand, Dr. Sarah Forrester

