



Genetic network and data analysis

In 1 collection

Joachim Nwezeobi¹, Onyeyirichi Onyegbule², Chukwuemeka Nkere², Joseph Onyeka², Sharon van Brunschot³, Susan Seal³, John Colvin³

¹National Institute of Agricultural Botany, Cambridge, United Kingdom,

²National Root Crops Research Institute, Umudike, Umuahia, Abia State, Nigeria,

³Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent, United Kingdom

1 Works for me dx.doi.org/10.17504/protocols.io.bd46i8ze

Joachim Nwezeobi

- 1 The alignment file (.nex) obtained from Geneious was used to build the minimum spanning tree using PhyloViz [51], to identify the relationships and mutational distances between the different haplotypes.
- 2 After the random selection and testing of two whitefly samples per field, a two-sided Fisher test and the chi-square test were carried out on the number of different populations identified in the two samples to ascertain whether or not more sampling was needed to capture the entire diversity of the genetic groups present in the survey collections.
- 3