MAY 28, 2020

OPEN ACCESS

DOI:
dx.doi.org/10.17504/protocols.io.bd46i8ze

Protocol Citation: Joachim Nwezeobi, Onyeyirichi Onyegbule, Chukwuemeka Nkere, Joseph Onyeka, Sharon van Brunschot, Susan Seal, John Colvin 2020. Genetic network and data analysis. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.bd46i8ze>

License: This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

Protocol status: Working

Created: Mar 23, 2020

Last Modified: May 28, 2020

PROTOCOL integer ID:
 34686

🌐 Genetic network and data analysis

📁 In 2 collections

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

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