

Genotyping by Sequencing on cassava collections in Indonesia using SNP markers developed by the Alliance of Bioversity International and CIAT

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► Summary

Collection of cassava genetic resources in Indonesia is one of the great potentials that need to be utilized to meet the demand for cassava at the downstream level. The number of genetic resources can reach around 1000-1100 accessions that are maintained in Research Centers / Institutions and Universities, which are 534 accessions at the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRD), 325 accessions at the Indonesian Legumes and Tuber Crops Research Institute (ILETRI), 163 accessions at the Indonesian Institute of Sciences (LIPI), and 72 accessions at the Padjadjaran University (UNPAD) (Figure 1). However, all of these cassava accessions are obtained from local areas in Indonesia and have not been identified at the genetic level, so the possibility of finding duplicates is high, especially as cassava propagation is generally carried out vegetatively. Therefore, the approach through Genotyping by Sequencing (GBS) on all cassava accessions (around 1000 accessions) can overcome this problem for removing duplicates. The GBS will be performed in the Alliance of Bioversity International and CIAT, Colombia, while the isolation of all cassava DNA are carried out at ITB and UNEJ.



Figure 2. FGD for the GBS collection of cassava in Indonesia, attended by ICABIOGRD, ILETRI, LIPI, UNPAD, ITB, and UNEJ.

► Reference

Rabbi, I.Y., Kulakow, P.A., Manu-Aduening, J.A. et al. (2015). Tracking crop varieties using genotyping-by-sequencing markers: a case study using cassava (*Manihot esculenta* Crantz). *BMC Genet* 16, 115

► Methodology

- (1) Testing the quality of DNA with gel electrophoresis and determining the quantity of DNA using a synergy quantifier,
- (2) SNPs genotyping will be carried out by following the protocol for 96 single nucleotide polymorphisms. (SNP) genotyping on cassava with the EP1 system and the type of testing Fluidigm application version 3.1.2.
- (3) Data analysis will be carried out on data that is integrated on the Galaxy Platform (<http://galaxyproject.org/>) and duplicate tests will be done on the Eclipse SDK v. 4.2.2 using the NGSEP Platform. Reference library uses 2500 samples of cassava from genotypes originating from Asia, Africa and Latin America.

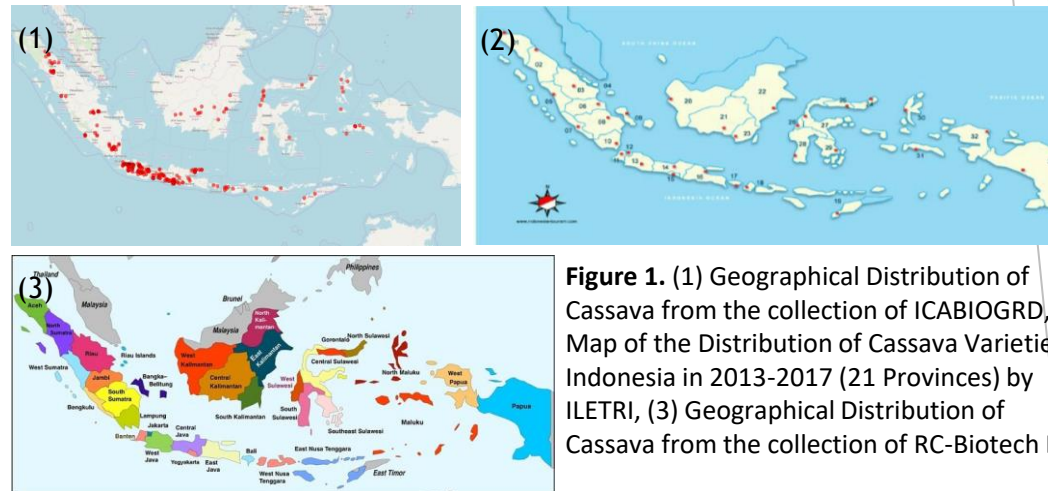


Figure 1. (1) Geographical Distribution of Cassava from the collection of ICABIOGRD, (2) Map of the Distribution of Cassava Varieties in Indonesia in 2013-2017 (21 Provinces) by ILETRI, (3) Geographical Distribution of Cassava from the collection of RC-Biotech LIPI

► Results

1. Focus Group Discussion (Figure 2)
2. Cooperation Agreement between ITB and UNPAD, LIPI, and ICABIOGRD
3. Approval of Material Transfer Agreement (MTA) between Institutions/Universities and the Alliance of Bioversity International and CIAT
4. Licensing from the Center for Plant Variety Protection and Agricultural Licensing (PPVTPP), Ministry of Agriculture RI
5. Implementation of DNA Isolation at ITB and UNEJ (Figure 3)

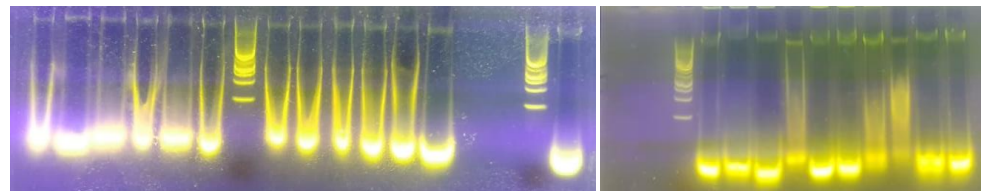


Figure 3. Part of the results of DNA isolation from 43 samples contributed from UNPAD

► Conclusion

Due to the delay of results No. 2-4, the Activities are targeted to be completed in July 2021.

► Acknowledgement

We thank P3MI ITB for supporting financially the GBS program on cassava collection in Indonesia so that it can be carried out well.