**Community of Practice Partnership (COPP) for the Application of**

**Genomic-assisted Cassava Breeding**

**General Overview**

Technology innovations are key to increase cassava production on the continent. Genomics has a central role in crop improvement and is increasingly being used owing to the decrease in cost of technologies. Analysis of plant genetic variation is crucial in breeding. Aside the challenge of accessing innovative technologies to generate data, an important constraint encountered by National Agricultural Research Systems (NARS) on the continent is the limited access and the inability to analyze and interpret genomics data.

**Objectives of the CoPP**

The CoPP aims at disseminating, transferring knowledge and technologies and build-up NARS research capabilities.

**Current Members**

The current members include Ghana, Sierra Leone, Zambia, Rwanda, Kenya, Mozambique, DR Congo and Cote D'Ivoire.

**Work Performed and Achievements**

Several meetings were held with CoPP members, including Rwanda, Cote d’Ivoire, Ghana, Sierra Leone, Mozambique, and Kenya to gather information relative to their respective breeding programs, understand their breeding priorities, the challenges encountered, and evaluate the current impact of the support provided by NextGen so far. These will enable us to design a more effective strategy to address potential limitations and ensure that skills acquired are effectively implemented by the members. NextGen has supported and coordinated the genotyping of breeding populations of four of the NARS partners, including NARC-SLARI-Sierra Leone, CSIR-Ghana, CNRA-Côte d'Ivoire, and RAB-Rwanda using 10 trait-linked SNPs for selection of provitamin A, CMD, and DM content, and QC fingerprinting panel of 18 SNPs.

We have provided training to some of the members, including Ghana, Kenya and Rwanda to enable them to process genotypic data. Owing to the COVID-19 pandemic and travel restrictions we organized online training. We recognize that understanding of theoretical concepts is key to facilitate the transition to practice. From this perspective, the first sessions were theoretical. Key concepts were explained. The different type of molecular markers existing, their advantages and limitations were explored. The emphasis was on single nucleotide polymorphisms (SNPs) not only because they are the most abundant type of molecular markers, but also as SNP markers were used to genotype NARS breeding populations. We reviewed the process leading to SNPs discovery, the existing genotyping platforms. We summarized the development process of the QC panels used to genotype NARS breeding populations and highlighted other possible use cases. Since trait markers were also used to genotype NARS samples, we presented the necessary steps leading to trait-marker development. An overview on the genetics and breeding applications of molecular markers was presented. After emphasizing on the theoretical concepts, we reviewed the data analysis process, including data formatting, data quality control, data conversion. The following sections d were demonstration sessions using real data from the members. Some of the challenges encountered was the difficult access to a stable internet connection for some of the participants.

**Conclusion**

Online discussions and trainings Were organized. Considerable progress has been achieved. Expectations of the participants were matched. We are planning follow-up trainings this year. We also plan to extend the training to other members that could not benefit last year due to some logistic issues or because they were not available at the that time.