

2024-03-06

# Review of Sources of Uncertainty and Techniques Used in Uncertainty Quantification and Sensitivity Analysis to Estimate Greenhouse Gas Emissions from Ruminants

Kimei, Erica

MDPI

---

<https://doi.org/10.3390/su16052219>

*Provided with love from The Nelson Mandela African Institution of Science and Technology*

# Molecular assessment of genetic diversity of Tanzanian and aflatoxin-resistant maize (*Zea mays*. L) accessions

Gregory F. Bundala, Marco Mng'ong'o, Arnold A. Mushongi, Pavithravani B. Venkataramana

To download the complete text, click that link

<https://doi.org/10.3920/WMJ2016.2130>

## Abstracts

Genetic distance information for various maize accessions is important for germplasm improvement and breeding program. However, this information is limited in most of the developing countries such as Tanzania. The present study was conducted to analyze the genetic diversity between Tanzanian maize accessions and the International Maize and Wheat Improvement Center (CIMMYT) lines as a strategy to create heterotic groups for maize breeding. Thirty Tanzanian maize accessions (14 inbred lines, 8 open-pollinated varieties, and 8 landraces) and 10 tester lines from CIMMYT were studied to estimate the molecular genetic variability using Euclidean distance determined by simple sequence repeat (SSR) markers. Fifteen SSR markers, resulting in general maize alleles, were used to determine genetic diversity, where 13 markers were amplified with an average PIC of 0.73. Where a moderate genetic distance between Tanzanian maize accessions and resistant lines, ranging from 0.13 to 0.57, was determined. The 40 maize genotypes (testers and accessions) were studied by using SSR markers classified into three major groups and further divided into 5 subgroups, which were later used to create the heterotic groups. The heterotic groups drawn and determined in phylogenetic tree showed distinct variations among studied genotypes. The study concludes that there is significant ( $P < 0.001$ ) genetic diversity among the maize genotypes, which are essential breeding materials for producing superior maize hybrids with high combining ability and high heritability of traits of interest, such as high yielding and resistance to aflatoxin contamination. Thus, Tanzanian maize breeders can utilize the available maize genotypes to develop hybrids with high yield and resistance to aflatoxin contamination.

