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Molecular characterization of sugarcane streak mosaic virus in Côte d'Ivoire

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S1-P6

Since its development in the 1970s, the cultivation of sugarcane has played an important role in Côte d'Ivoire's economy, but the domestic demand is only 80% satisfied. Production stagnates mainly due to biological constraints (pests and diseases). Sugarcane mosaic disease affects the photosynthesis and growth of sugarcane, leading to a significant decrease in cane yield and sucrose content, and thus serious economic losses. It can be caused by sugarcane mosaic virus (SCMV), sorghum mosaic virus (SrMV), and/or sugarcane streak mosaic virus (SCSMV). SCMV and SrMV are distributed worldwide and SCSMV mainly exists in Asia (1). More recently, the virus has also been reported in Côte d'Ivoire in West Africa (2,3) where it appears responsible of increasing yield losses. In order to characterize the impact and genetic diversity of SCSMV in two of the three production areas, Borotou-Koro (North-West) and Zuénoula (Center), an intensive sampling campaign took place from September to October 2020. For each site, 22 plots (from 1 to 35 ha) were assessed. For each plot, five 100m² micro-plots were defined in which four randomly selected plants were sampled. A partial sequence encompassing the N-terminal variable part of the coat protein was obtained for 470 isolates. Mixed infections were observed for 157 isolates, 49 from Borotou-Koro (10% of sequenced samples) and 108 from Zuénoula (23% of sequenced samples). The remaining sequences presented a high molecular diversity, including isolates of the two major molecular groups described at the global level (4) as well as a specific group of unknown origin, observed so far only in Côte d'Ivoire.

References

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