African Crop Science Journal, Vol. 31, No. 4, pp. 379 - 390
pISSN 1021-9730/2023
eISSN 2072-6589/2023

DOI: https://dx.doi.org/10.4314/acsj.v31i4.1

CASSAVA MOSAIC DISEASE AND ABUNDANCE OF ITS WHITEFLY VECTOR IN NORTH-WESTERN DEMOCRATIC REPUBLIC OF CONGO

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(*Received 18 August 2023; accepted 24 September 2023*)

ABSTRACT

Cassava mosaic disease (CMD) is rampant in the Democratic Republic of Congo (DRC). The objective of this study was to assess the significance of CMD and abundance of its whitefly (*Bemisia tabaci*) vector, in the North-Western provinces of the DRC. A field study was conducted in three provinces, namely Mongala, North Ubangi, and South Ubangi, of north-western DRC, during February to March 2022. One hundred cassava (*Manihot esculenta* Crantz) fields, aged 3 to 9 months and at intervals of about 10 Km apart, were prospected during an epidemiological survey of cassava mosaic disease. The cassava cropping system (pure culture or intercropped), and the epidemiological parameters of cassava mosaic disease (incidence, severity of CMD, abundance of whiteflies, sources of infection) were assessed. Results showed that the prevalence of CMD and abundance of whitefly vectors in DRC were significantly different among the three provinces. The incidence was low in South-Ubangi (16.49%), medium in Mongala (21.83%), and high in North-Ubangi (44.63%). The severity of the disease in north-western DR Congo is very low and remains below level a value of 3 in all the provinces covered by this study. Whitefly abundance fluctuated between 1.49 (South-Ubangi) to 5.74 (Mongala). Infected cuttings were the main source of CMD infection in all the provinces. Cassava cultivated in monoculture had the highest populations of this victory.

Key Words: *Bemisia tabaci,* incidence, *Manihot esculenta*

RÉSUMÉ

La maladie de la mosaïque du manioc (MMM) sévit en République démocratique du Congo (RDC). L'objectif de cette étude était d'évaluer l'importance du MMM et l'abondance de son vecteur de mouche blanche (*Bemisia tabac*i), dans les provinces du Nord-Ouest de la RDC. Une étude de terrain a été menée dans trois provinces, à savoir la Mongala, le Nord-Ubangi et le Sud-Ubangi, au Nord-Ouest de la RDC, de Février à Mars 2022. Cent champs de manioc (*Manihot esculenta* Crantz), âgés de

3 à 9 mois et à intervalles de distants d'environ 10 Km, ont été prospectés lors d'une enquête épidémiologique sur la mosaïque du manioc. Le système de culture du manioc (culture pure ou culture intercalaire) et les paramètres épidémiologiques de la mosaïque du manioc (incidence, gravité de la MMM, abondance des aleurodes, sources d'infection) ont été évalués. Les résultats ont montré que la prévalence du MMM et l'abondance des vecteurs d'aleurodes en RDC étaient significativement différentes entre les trois provinces. L'incidence était faible au Sud-Oubangui (16,49%), moyenne à la Mongala (21,83%), et élevée au Nord-Oubangui (44,63%). La gravité de la maladie au nord-ouest de la RD Congo est très faible et reste inférieure au niveau 3 dans toutes les provinces couvertes par cette étude. L'abondance des aleurodes a fluctué entre 1,49 (Sud-Oubangui) et 5,74 (Mongala). Les boutures infectées constituaient la principale source d'infection par la MMM dans toutes les provinces. Le manioc cultivé en monoculture avait les populations les plus élevées de cette victoire.

Mots Clés : *Bemisia tabac*i, incidence, *Manihot esculenta*

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is among the most important food and industrial crops in sub-Saharan Africa, where more than 500 million people depend on the crop (Monde *et al*., 2013). It is particularly important for poor farmers because of its role in food security and as a source of income (Mtunguja *et al*., 2019).

In the Democratic Republic of Congo (DRC), cassava is the main source of food and income for the population (Muengula-Manyi *et al*., 2012). In fact, the DRC is ranked the 5th producer of cassava in the world, and 2nd in Africa after Nigeria (Muhindo *et al*., 2020; Casinga *et al*., 2021).

Cassava production in the DRC has been characterised by low yields, attributed largely to the recent outbreak of viral diseases, most especially the cassava mosaic disease (CMD) (Casinga *et al.*, 2021; Biola *et al.,* 2022; Kwibuka et *al.*, 2022). Cassava Mosaic Disease is caused by a diverse group of at least eleven distinct virus species, grouped under the name of Cassava Mosaic Geminivirus (CMG, genus: Begomoviruses; family: Gemiviridae). It has become one of the most serious socio-economic problems in sub-Saharan Africa (Fondong *et al.*, 2000; Fondong and Chen, 2011; De Bruyn *et al*., 2016).

The disease largely spreads through infected cuttings and vectored by the whiteflies, *Bemisia tabaci* (Legg *et al*., 2011). The disease symptoms are usually manifested through strong discolouration, often associated with severe leaf deformation (Tiendrébéogo *et al.*, 2009). In the case of early and severe infection, the development of the entire plant is affected, leading to stunted growth with deformed, discoloured, and small leaves (Zinga *et al*., 2013).

In the DRC, CMD has been reported since 1930 and selection of resistant varieties was initiated in 1932 in the Yangambi Agricultural Research Center (Sapin, 1958; Monde, 2010). This disease hurts several cassava cultivars and has been studied in some regions of the country (Muengula-Manyi *et al.*, 2012; Biola *et al.*, 2022). Its impact depends on factors, including cassava variety, virus strain, and type of infection.

It is more severe on local than improved cultivars (Monde *et al*., 2013; Zinga *et al*., 2016). In the case of early infection, the losses may be significant and vary from 77.5 to 97.3%, compared with 44.9 to 80% in the case of late infection (Bisimwa *et al*., 2015).

There is limited information about the CMD and its whitefly vector in the North-West region of DRC, although CMD continues to ravage all regions where cassava is cultivated. The objective of this study was to assess the significance of cassava mosaic disease and the abundance of its *Bemisia tabaci* vector in the North-western provinces of the Democratic Republic of Congo.

MATERIALS AND METHODS

Study area. The study was conducted in three provinces in North-Western DRC; namely Mongala, North-Ubangi, and South-Ubangi (Fig. 1).

Epidemiological survey. One hundred cassava fields, aged 3 to 9 months, were investigated from February to March 2022. In each field, cassava plants were systematically diagnosed along two diagonals. The cropping system, the incidence and severity of CMD, and the abundance of whitefly vectors were scored using the harmonised protocol of the Central and West African Virus Epidemiology Programme (2022). Field incidence was determined as the percentage of plants showing characteristic symptoms of the CMD out of the total number of plants; while severity was assessed on cassava plants using a severity score scale of 1 to 5 (Fig. 2).

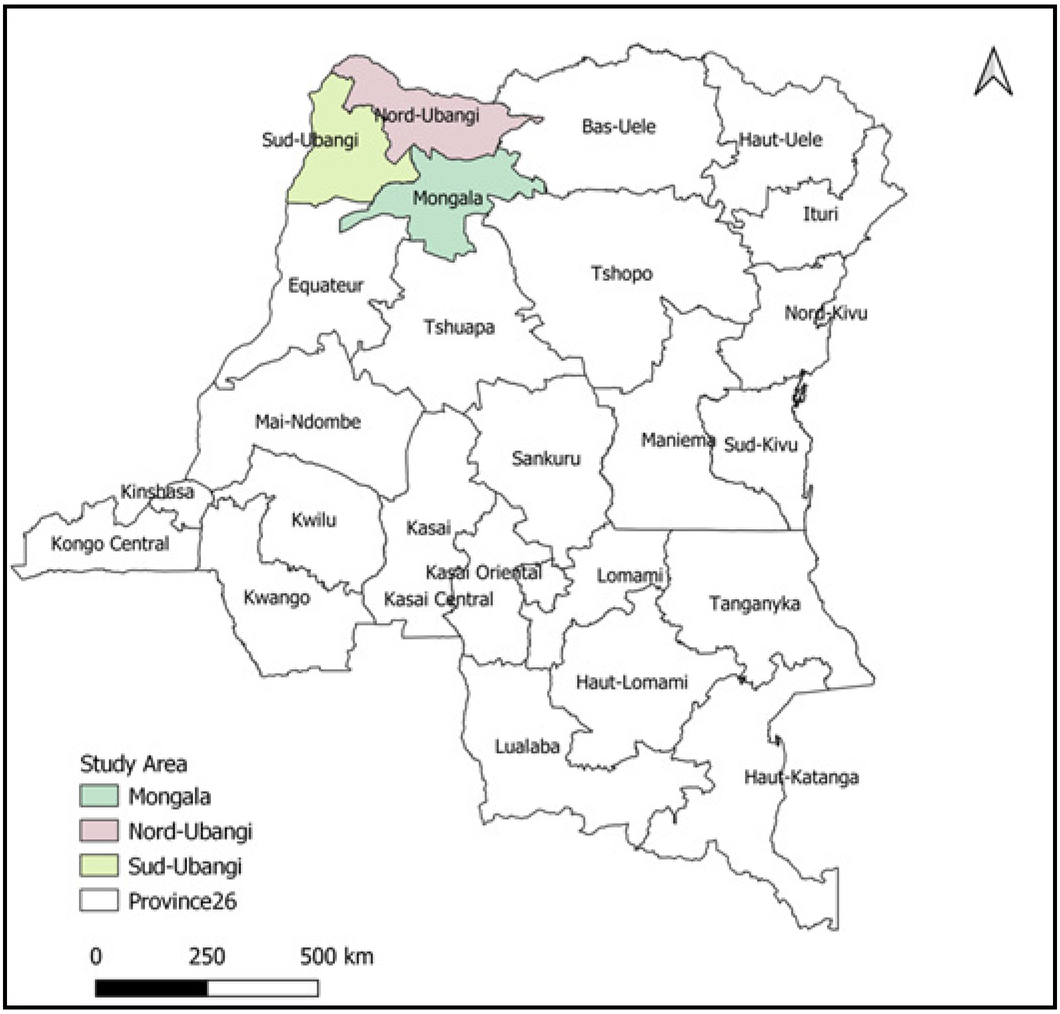

Figure 1. Map showing the provinces surveyed for epidemiology of Cassava Mosaic Disease and abundance of whitefly disease vector in the North-Western Democratic Republic of Congo.

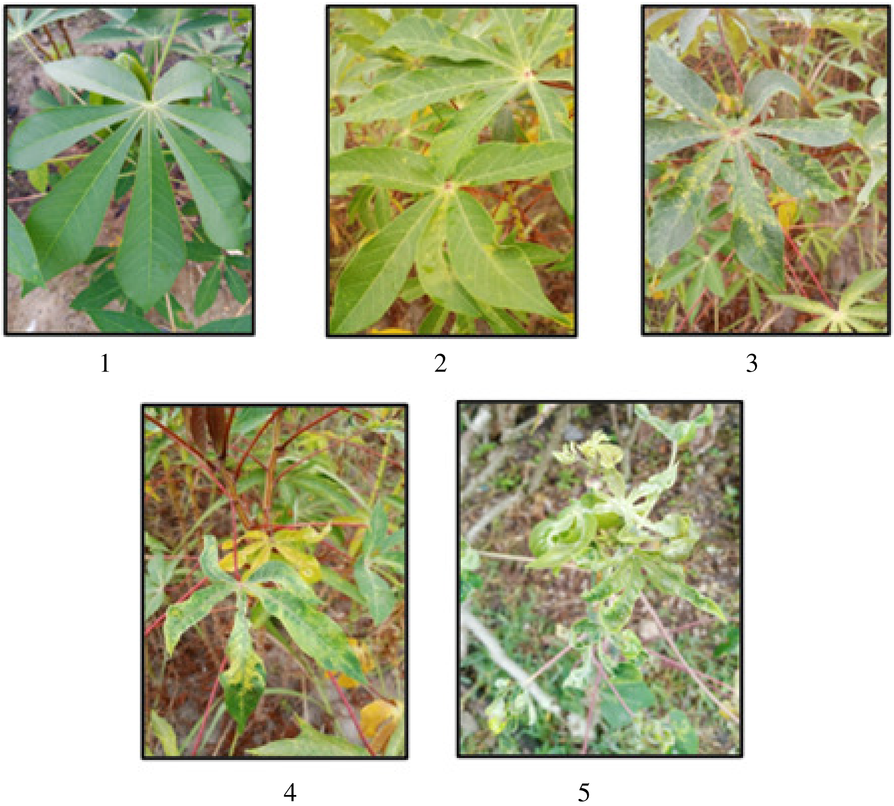

Figure 2. Scoring scale for CMD severity levels on cassava leaves in North-Western Democratic Republic of Congo. 1 = No symptoms on the leaves; 2 = Appearance of slight chlorotic patches on the leaves; 3 = Chlorotic patches on almost all the leaves (2/3 of the plant's leaves) without deformation of the leaf surface; 4 = Chlorotic patches covering most of the leaf, accompanied by deformation (curling) and reduction of the leaf surface; and 5 = Severe mosaic, leaves twisted, deformed and practically reduced to the veins.

The infection source was determined by observing the CMD symptoms on the cassava plants. Symptoms due to transmission of the virus by the whitefly (primary infection) appear on the apical leaves, whereas infection due to cuttings (secondary infection) appears on all the leaves as soon as the cuttings merge (Mallowa *et al*., 2006).

The survey data were recorded by the iForm application, designed by the Scriptoria team, Cambridge University, UK. Statistical analyses were carried out after data processing using MS Excel. These analyses involved a comparison of means using the Student's T-test, the Wilcoxon and Mann-Whitney tests, under R software version 4.2.1.

RESULTS

Incidence of CMD. Cassava mosaic disease remains one of the main constraints of cassava production in several areas in DR Congo (Fig. 3). Results showed that CMD is widespread (Fig. 4) in the study area and that its incidence varies significantly different between the three provinces (χ^2= 6.4547, df = 2, P-value = 0.04). There was greater incidence of the disease in North-Ubangi province (44.63 ± 6.37 %) than in Mongala and South-Ubangi provinces, which recorded incidences of 21.83 ± 9.033 and 16.49 ± 6.38%, respectively.

Data showed the prevalence of CMD in different cassava cropping systems in

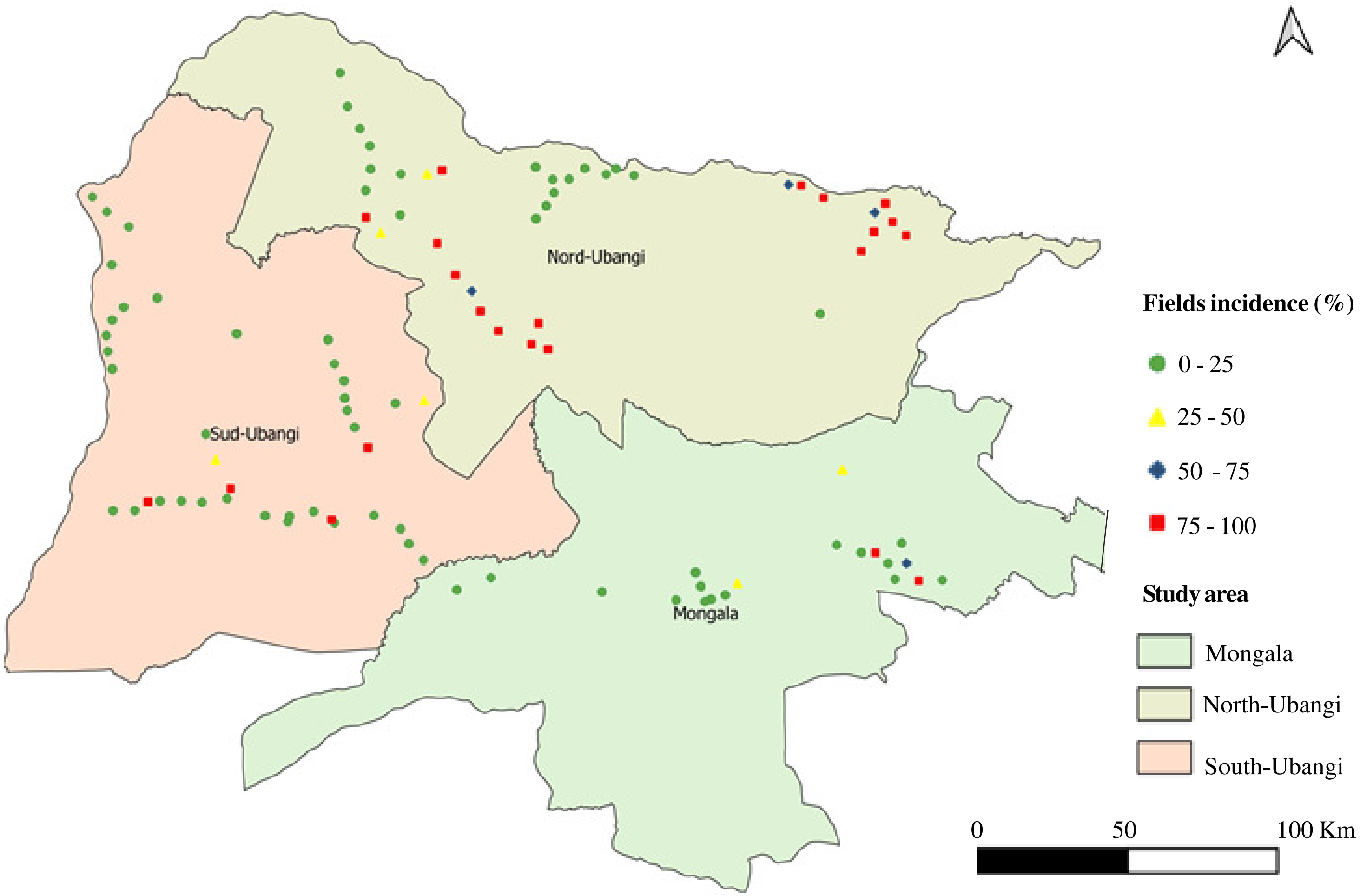

Figure 3. Cassava mosaic disease incidence in the study provinces of the north-western region of the Democratic Republic of Congo.

Northern DRC (Fig. 5). The pure cassava stands were more vulnerable to CMD than in their intercrop counterparts. In fact, in Mongala province, cassava intercrops showed hardly any CMD symptoms.

Severity score of cassava mosaic disease. The severity score of CMD in the study region was less than 3 in the three provinces (Fig. 6). However, North-Ubangi province recorded a higher score (2.31 ± 0.16), followed by South-Ubangi province (1.91 ± 0.16) and finally the province of Mongala (1.80 ± 0.22) (Fig. 6).

Source of infection. The results of the different sources of CMD infection in the study region showed that use of infected

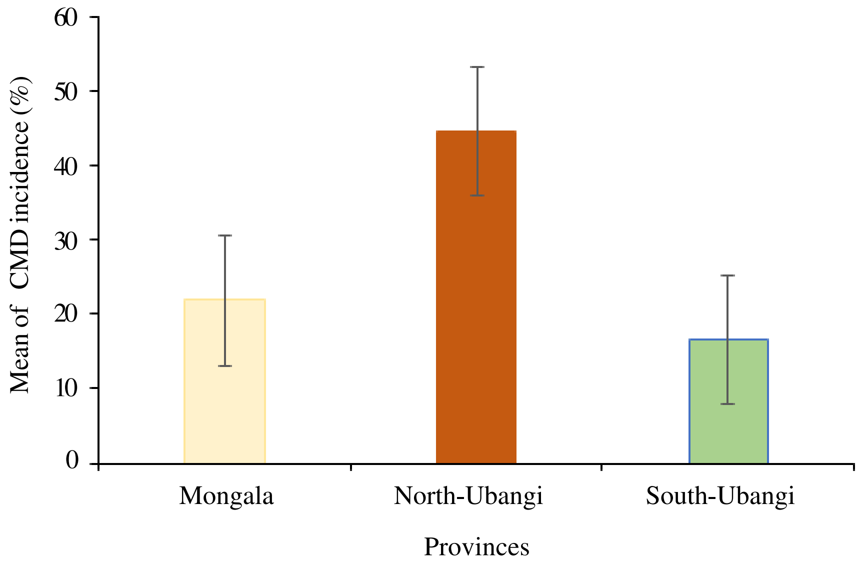

Figure 4. The incidence of CMD across study provinces in North-Western Democratic Republic of Congo.

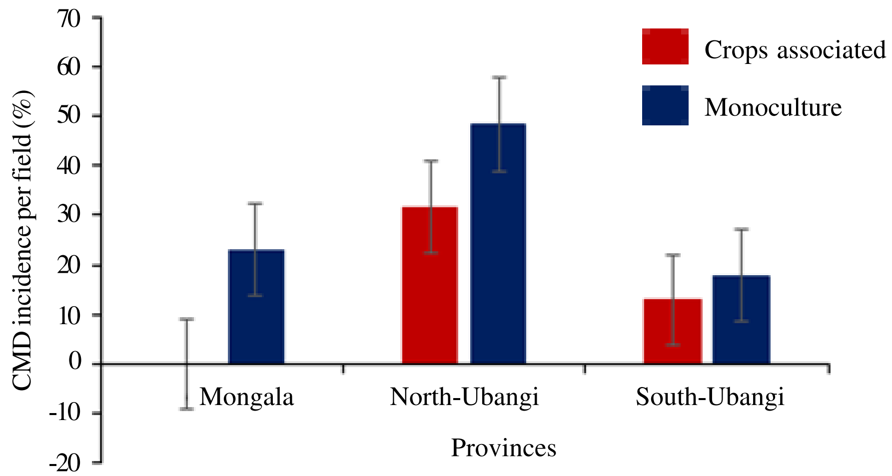

Figure 5. CMD incidence in relation to cropping system of cassava in three provinces in North-Western Democratic Republic of Congo.

cuttings was the most important source of infection (77.09 to 98.42%), compared to whitefly transmission (1.78 to 22.91 %). Mongala Province had a much higher disease infection deriving from whiteflies transmission than in South-Ubangi Province (Fig. 7).

Abundance of whitefly. The abundance of whiteflies, the cassava mosaic virus vector, was greatest in Mongala province (5.74 ±2.6 whiteflies/plant) (Fig. 8). Whiteflies were more abundant in pure cassava stands than in intercropped cassava plots (Fig. 9).

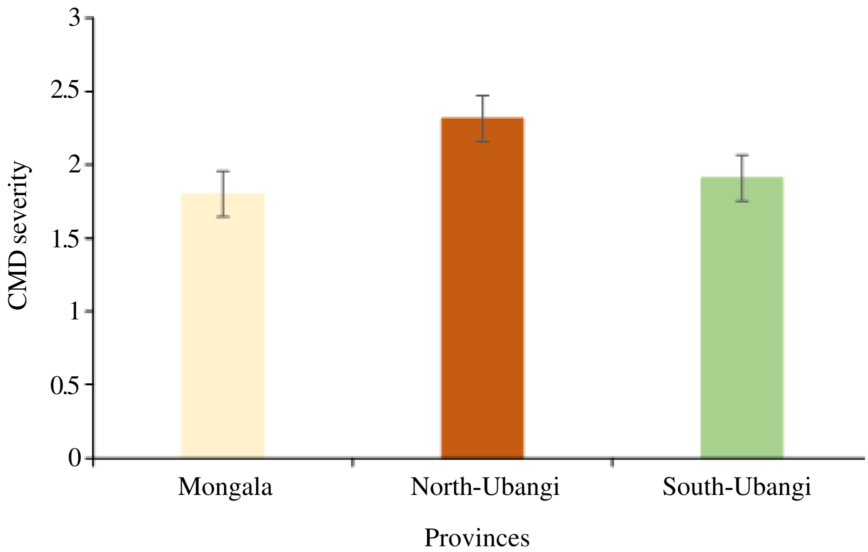

Figure 6. The severity of CMD across study provinces in North-Western Democratic Republic of Congo.

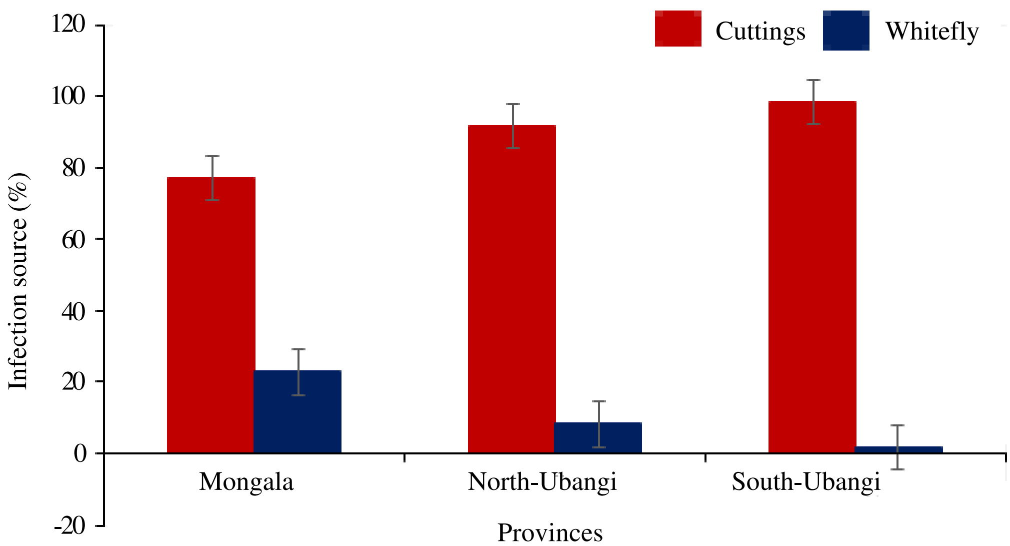

Figure 7. Sources of CMD infection in cassava grown in the North-Western Democratic Republic of Congo.

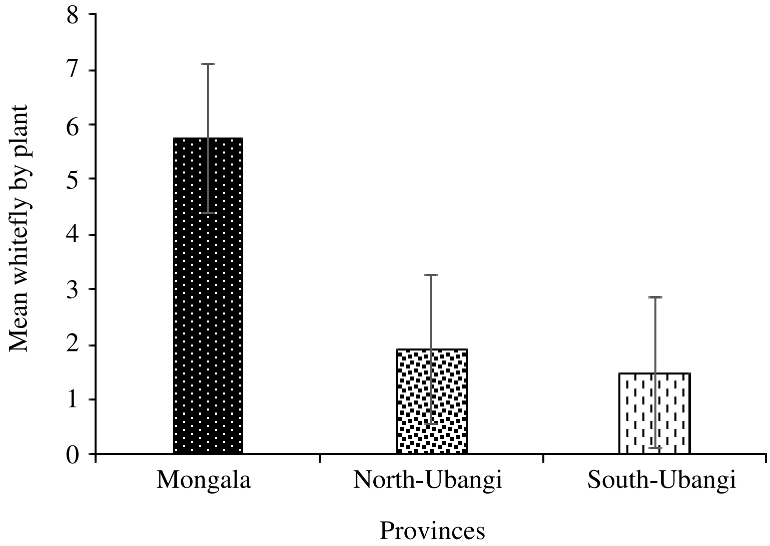

Figure 8. Abundance of *B. tabaci* per cassava plant in the North-Western Democratic Republic of Congo.

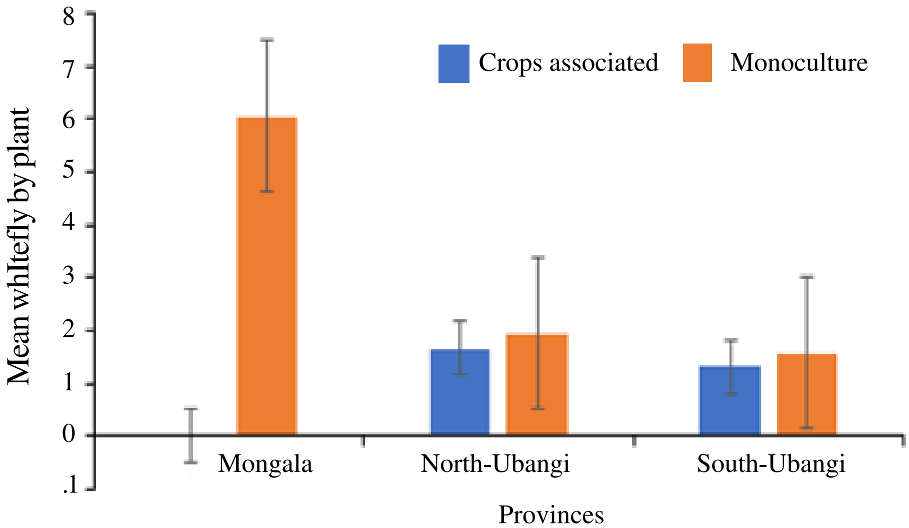

Figure 9. Abundance of whitefly according to pure cassava stand *versus* cassava intercrops in the north-western Democratic Republic of Congo.

DISCUSSION

Incidence of cassava mosaic disease. All the study provinces infected by CMD; with incidences varying from one province to another (Fig. 3) and between pure culture against cassava intercrops (Fig. 4). The high CMD incidence found in North-Ubangi Province (44.63 ± 6.37 %) could be explained by the predominant use of cassava cuttings of local varieties as propagation materials (Fig. 7). The cuttings as a source of CMD inoculants was 92% for the entire study area. The other suspected source of CMD infection was associated with the proximity to the Central African Republic (CAR), where the incidence of the disease is reportedly very high in the country's three agro-climatic zones; namely Forest Guineans (85%), Soudan Guineans (88%) and Soudan Ubangian (79%) (Zinga *et al.*, 2013). The community's close neighbourhood could easily facilitate the unregulated exchange of infected planting materials between the two countries.

The lower disease incidence in Mongala can be explained by use of infected cuttings, its geographical position near the border with Tshopo province, where high CMD incidence was unregistered, and the implication of vectors in the spread of cassava mosaic disease (Monde *et al.*,2010; 2012). The incidence recorded in this province where pure cassava fields, dominated could be also explained by the use of infected cassava cuttings and the spread of *Cassava mosaic begomoviruses* by high whitefly abundance on cassava plants (Fig. 7).

The low prevalence of CMD in South-Ubangi Province (16.08%) can be attributed to resistant cassava varieties supplied by the INERA Boketa Station as part of the maintenance of accessions and varieties from the National Cassava Programme. The National Cassava Programme of INERA (National Institute for Study and Agronomic Research) has the goal of promoting cassava production by improving its productivity and providing farmers with improved varieties and technologies. To achieve this, INERA disseminates new varieties to the farmers around its research centres and stations.

Severity of cassava mosaic disease. The considerably lower severity of CMD in north-western DRC (<level 3) in all study provinces (Fig. 6), than the eastern regions of the country (severity score 3) has been reported (Monde *et al.*, 2010; Bisimwa *et al.*, 2012). This suggests that CMD pressure is more pronounced in the eastern part of the country, the front-line for introduction of cassava mosaic disease from East to West Africa (Legg *et al.*, 2006; 2011).

Sources of cassava infection. It was clear that the north-western of the Democratic Republic of Congo which had the most widespread of *Bemisia tabaci* vector, had cutting symptomatic infection by the disease (Fig. 7). The highest cuttings infected were recorded in South-Ubangi provinces (98.42%), contrasting with the lowest in Mongala province (77.01%) (Fig. 7).

The movement of infected cuttings between regions within the same province and between provinces may be responsible for this proportion, as was the case in East African countries, with historical outbreaks of CMD (Alicai *et al.*, 2007). The use of cuttings as propagation materials explains this high proportion and contributes to the CMD spread over longer distances and regions (Maruthi *et al.*, 2017).

The vector, *Bemisia tabaci*, is involved in the spread of CMD in different parts of the three provinces. It was implicated in the order of 22.91% in Mongala against 1.78% in South-Ubangi. The difference in the level of activity of the vector is linked directly with the abundance of its population (high in Mongala, medium in North-Ubangi, and low in South-Ubangi, Fig. 8).

This is thought to depend on the cassava cropping system; varieties grown and environmental conditions, such as temperature and humidity, and field landscape (proximity of fields to main roads) (Macfadyen *et al.*, 2018; Katono *et al.,* 2021). These factors could influence the abundance of whiteflies and, consequently, their impact on the spread of CMD. In fact, local varieties were largely planted as pure culture in Mongala Province and North-Ubangi; while improved varieties dominated associated fields in South-Ubangi.

Abundance of whitefly. The higher abundance of whiteflies recorded in Mongala province compared with that of the South-

Ubangi (Fig. 8) could be because cassava fields were mostly cultivated in pure culture rather than cassava intercrops. In contrast with the severe CMD pandemics in Uganda, where whitefly outbreaks were a key factor in the spread of the disease, with an average of 7.1 insects/plant (Sseruwagi *et al*., 2004), the results of the present study show that whitefly outbreaks do not seem to be a major factor in the spread of the disease in the study region. The low activity of whiteflies in the spread of CMD in the present study could be explained by their relatively low level of abundance in the study areas (Fig. 7). We observed a significant suppression of colonisation of whitefly by cassava Intercropping (Fig. 9). This is thought to depend on the cassava cropping system, (Macfadyen *et al*., 2018); varieties grown and environmental conditions, such as temperature and humidity, and field landscape (proximity of fields to main roads) (Katono *et al*., 2021). These factors could influence the abundance of whiteflies and, consequently, their impact on the spread of CMD. Local varieties were largely planted as pure culture in Mongala Province and North Ubangi; while improved varieties dominated associated fields in South Ubangi.

CONCLUSION

Casava Mosaic Disease (CMD) is widely spread in the North-Western DRC cassava-growing provinces. Infected cassava cuttings, most likely originating from the CMD hotspots in the neighbouring Central African Republic are the most likely major sources of infection. Similarly, whitefly vector abundance parallels the CMD infection intensity are additional sources. Cassava intercropping has been confirmed to suppress the prevalence of CMD and the abundance of the whitefly vector on cassava plants in the study region. We recommend the use of improved CMD-free cuttings, which are resistant to whitefly infection for out-scaling among farming communities. Additionaly, effective regulation of exchange and movement of planting material between households and between regions needs to be emphasized.

ACKNOWLEDGMENT

This work was financed by the Bill & Melinda Gates Foundation and The United Kingdom Foreign, Commonwealth & Development Office (FCDO), under grant number OPP1082413 to the Central and West African Virus Epidemiology (WAVE) Programme for root and tuber crops - through a subgrant from Université Félix Houphouët-Boigny (UFHB) to the Institut Facultaire des Sciences Agronomiques de Yangambi.

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