Research Application Summary

Unraveling the vector transmission biology of the ipomovirus *Sweet potato mild mottle virus* (*Potyviridae*) in sweetpotato (Lam.)

Tugume, A.K.[1], Settumba Mukasa, B.[2] & Omongo, C.A.[3]
[1]Department of Biological Sciences, College of Natural Sciences (CONAS), Makerere University, P. O. Box 7062, Kampala, Uganda
[2]Department of Agricultural Production, College of Agricultural and Environmental Sciences (CAES), Makerere University, P. O. Box 7062, Kampala, Uganda
[3]National Crops Resources Research Institute (NaCRRI), Namulonge, P. O. Box 7084, Kampala, Uganda
Corresponding author: aktugume@botany.mak.ac.ug; aktugume@gmail.com

Abstract

This study undertakes to unravel vector transmission biology of *Sweet potato mild mottle virus* (SPMMV), a type member of the genus *Ipomovirus* in the family *Potyviridae*. This study will be conducted in four selected districts of Uganda for two sweetpotato growing seasons of 2012 and 2013. The districts include Masaka and Mpigi (around Lake Victoria basin in Central region); and Mbale and Soroti (Eastern region). Sweetpotato is the second most important root crop in East Africa, but production there is greatly constrained by viruses including SPMMV, a critical component of the devastating sweet potato virus disease (SPVD) complex. While the vectors disseminating other common viruses of sweetpotato in East Africa are well known, the vector transmitting SPMMV has remained cryptic. Consequently, the epidemiological relationship between incidence of SPMMV and its potential vectors in the fields is unknown. The vector transmitting SPMMV in sweetpotato and the SPMMV-vector epidemiological relations under field conditions will be determined. Farmer awareness of SPVD complex effects of sweetpotato yield will be enhanced through field activities involving farmers.

Key words: East Africa, *Ipomovirus*, *Potyviridae*, sweetpotato, sweet potato virus disease, vector-host plant preferences, virus transmission

Résumé

Cette étude vise à dénouer la biologie de la transmission des vecteurs du virus de tache légère de la patate douce (SPMMV), un membre type du genre *Ipomovirus* dans la famille *Potyviridae*. Cette étude sera menée dans quatre districts sélectionnés de l'Ouganda pour deux saisons de croissance de la patate douce de 2012 et 2013. Les districts comprennent Masaka et Mpigi (aux environs du bassin du lac Victoria dans

la région centrale) ainsi que Mbale et Soroti (dans la région de l'Est). La patate douce est la deuxième plus importante culture des racines comestibles en Afrique Orientale, mais la production est fortement contrainte par des virus, y compris SPMMV, un constituant essentiel du complexe des maladies dévastatrices causées par le virus de la patate douce (SPVD). Alors que les vecteurs de diffusion d'autres virus communs de la patate douce en Afrique de l'Est sont bien connus, le vecteur de transmission de SPMMV est resté énigmatique. Par conséquent, la relation épidémiologique entre l'incidence de SPMMV et ses vecteurs potentiels sur terrain est inconnue. Le vecteur de transmission de SPMMV dans la patate douce et les relations épidémiologiques SPMMV-vecteur sur le terrain seront déterminés. La sensibilisation des agriculteurs sur les effets complexes de SPVD sur le rendement de la patate douce sera augmentée.

Mots clés: Afrique de l'Est, *Ipomovirus, Potyviridae*, patate douce, maladie du virus de la patate douce, préférences des plantes vecteur-hôte, transmission du virus

Background

With a global annual production of 106.5 million tons, of which more than 95% is in developing countries, sweetpotato ranks as the world's third most important root crop (FAOSTAT, 2010). In Africa, sweetpotato is especially important in East Africa, where unfortunately, production is greatly hampered by viruses of several taxonomic groups which incite the devastating sweetpotato virus disease (SPVD) (Clark *et al.,* 2012). The three most important viruses implicated in sweetpotato yield loss in East Africa include *Sweet potato feathery mottle virus* (SPFMV, genus *Potyvirus*; family *Potyviridae*), *Sweet potato chlorotic stunt virus* (SPCSV, genus *Crinivirus*; family *Closteroviridae*), and *Sweet potato mild mottle virus* (SPMMV, genus *Ipomovirus*; family *Potyviridae*). Knowledge of the agents transmitting viruses and how the transmission occurs is important in implementing virus disease control measures.

Literature Summary

SPMMV is geographically restricted to East Africa (Tairo *et al*., 2005; Tugume *et al*., 2010) where its decimating impact on sweetpotato is enhanced when in dual infection with SPCSV or triple infection with SPCSV and SPFMV (Mukasa *et al*., 2006), and where there is perpetual super-abundance of vectors transmitting these viruses. A vector transmitting a given plant virus may prefer to colonise a host depending on host genotype,

disease status or physiological state which influences the epidemiology of the associated virus disease.

Like other known ipomoviruses, SPMMV was originally reported to be transmitted by whitefly *Bemisia tabaci* (Hollings *et al.*, 1976). However, subsequent studies over three decades have failed to validate its whitefly transmissibility. In East Africa, the odds of co-occurrence of SPMMV and the aphid-transmitted SPFMV are high, despite differences in the vector species.

Despite being the type member of genus *Ipomovirus*, SPMMV is the only known HCPro-encoding ipomovirus (Mbanzibwa *et al.*, 2009) similar to a putative ipomovirus, *Eggplant mild leaf mottle virus* (Dombrovsky *et al.*, 2012). Subsequently, phylogenetic and evolutionary analyses show a high divergence of SPMMV from other ipomoviruses, but close resemblance of its genomic structures with those of potyviruses (Mbanzibwa *et al.*, 2009). The possession of potyvirus aphid transmissibility motifs in the HCPro of SPMMV and frequent SPFMV+SPMMV seemingly point towards possibility of a potyvirus-assisted aphid transmission of the ipomovirus SPMMV (Tugume *et al.*, 2010).

Study Description

This study will be conducted at two fronts; epidemiological and virological. The epidemiological front will involve surveys to collect and identify adult whiteflies, aphids and other potential insect vectors and to determine their incidence and abundance. The study will be done in Masaka and Mpigi districts in the Lake Victoria basin in central Uganda; a region of high virus infection pressure. It will also be done in the low virus infection pressure districts of Mbale and Soroti in eastern Uganda (Mukasa *et al.*, 2003; Aritua *et al.*, 2007) (Fig. 1).

In the sweetpotato fields, the relative abundance of insects as potential vectors of SPMMV, insects' preferences of diseased versus healthy-looking plants, insect preferences according to host cultivar will be documented. From each farmer's field, plant samples with virus symptoms and healthy-looking ones will be sampled, established in an insect-proof screenhouse and used for virus indexing. Colonies of insects will be raised on appropriate caged host plants (other than sweetpotato) to facilitate assessments of their host preferences. Assessements will be done for preference of cultivars, diseased or healthy plants. Effect of single, double and triple infections with SPFMV and SPVD complex will also be assessed.

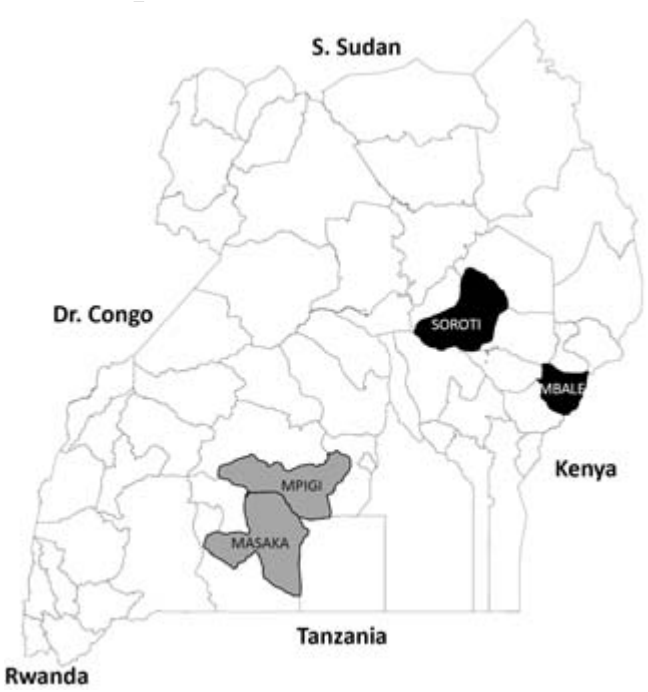

Figure 1. Map of Uganda showing four districts that will be surveyed under this study; two are in the central region (Masaka and Mpigi; grey shades) and the other two in eastern region (Mbale and Soroti; black shades).

The virology front will involve experimental acquisition of SPMMV by test insect vectors and subsequent inoculation of SPMMV onto test healthy sweetpotato plants of cv Tanzania in insect-proof cages at Makerere University Agricultural Research Institute, Kabanyolo (MUARIK). Procedures for virus acquisition access and inoculation access (onto 4-wk old virus-free sweetpotato plants of cv. Tanzania) will be done according to Gamarra *et al.* (2010). SPMMV will be acquired by the test vectors from source plants infected with different virus combinations including single SPMMV, duo SPMMV+SPFMV or triple SPMMV+SPFMV+SPCSV infections that will be artificially constructed in the screenhouse or obtained from the field. Procedures (including replications to enable subsequent statistic analysis of data) for virus acquisition and inoculation access will be according to Gray (2008). Also, sequential feeding of aphids on plants infected singly with SPFMV, then on single SPMMV and vice-versa, before inoculation access onto healthy plants will demonstrate if SPFMV indeed assists in transmission of SPMMV. The virus combinations as used for whiteflies and aphids will be used for other candidate insect vectors. Observations and recording of virus-like disease symptoms on inoculated plants, and subsequent immuno- and RNA-dot blot

assays for the viruses in test plants will be carried out 4-5 weeks after inoculation access.

Research Application

Field data relating incidences of insects and viruses will help in identifying the vector of SPMMV. Host preferences of the vector will explain the role of other viruses in the spread of SPVD and thus facilitate the designing of appropriate management options. If SPFMV helps in aphid transmission of SPMMV, it becomes obvious that the control of SPFMV doubly controls also SPMMV and hence is critical in the management of SPVD complex.

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References

Aritua, V., Bua, B., Barg, E., Vetten, H.J., Adipala, E. and Gibson R.W. 2007. Incidence of five viruses infecting sweetpotatoes in Uganda; the first evidence of Sweet potato caulimo-like virus in Africa. *Plant Pathology* 56:324–331.

Clark, C.A., Davis, J.A., Abad, J.A., Cuéllar, W., Fuentes, S., Kreuze, J., Gibson, R., Mukasa, S.B., Tugume, A.K., Tairo, F. and Valkonen, J.P.T. 2012. Sweetpotato viruses: 15 Years of progress on understanding and managing complex diseases. *Plant Disease* 96:168-185.

Dombrovsky, A., Sapkota, R., Lachman, O. and Antignus, Y. 2012. Eggplant mild leaf mottle virus (EMLMV), a new putative member of the genus Ipomovirus that harbors an HC-Pro gene. *Virus Genes* 44:329–37.

FAOSTAT, 2010. FAO http://faostat.fao.org/site/567/default.aspx#ancor. Accessed 22-May-2012.

Gamarra, H.A., Fuentes, S., Morales, F.J., Glover, R., Malumphy, C. and Barker, I. 2010. Bemisia afer sensu lato, a vector of Sweet potato chlorotic stunt virus. *Plant Disease* 94:510–514.

Gray, S.M. 2008. Aphid transmission of plant viruses. *Current Protocols in Microbiology, Supplement* 10:16B.1.1-16B.1.10.

Hollings, M., Stone, O.M. and Bock, K.R. 1976. Purification and properties of Sweet potato mild mottle, a whitefly born virus from sweetpotato (*Ipomoea batatas*) in East Africa. *Annals of Applied Biology* 82:511–528.

Loebenstein, G., Thottapilly, G., Fuentes, S. and Cohen, J. 2009. Virus and phytoplama diseases. pp. 105–134. In: The

Sweetpotato. Loebenstein, G. and Thottapilly, G. (Eds). Springer Science+Business Media.

Mbanzibwa, D.R., Tian, Y., Mukasa, S.B. and Valkonen, J.P.T. 2009. Cassava brown streak virus encodes a putative Maf/HAM1 pyrophosphatase implicated in reduction of mutations and a P1 proteinase that suppresses RNA silencing but contains no HC-Pro. *Journal of Virology* 83:6934–6940.

Mukasa, S.B., Rubaihayo, P.R. and Valkonen, J.P.T. 2003. Incidence of viruses and virus-like diseases of sweetpotato in Uganda. *Plant Disease* 87:329–335.

Mukasa, S.B., Rubaihayo, P.R. and Valkonen, J.P.T. 2006. Interactions between a crinivirus, an ipomovirus and a potyvirus in co-infected sweetpotato plants. *Plant Pathology* 55:458–467.

Tairo, F., Mukasa, S.B., Jones, R.A.C., Kullaya, A., Rubaihayo, P.R. and Valkonen, J.P.T. 2005. Unraveling the genetic diversity of the three main viruses involved in sweetpotato virus disease (SPVD), and its practical implications. *Molecular Plant Pathology* 6:199–211.

Tugume, A.K., Mukasa, S.B., Kalkinen, N. and Valkonen, J.P.T. 2010. Recombination and selection pressure in the ipomovirus *Sweet potato mild mottle virus* (Potyviridae) in wild species and cultivated sweetpotato in the centre of evolution in East Africa. *J. Gen. Virol* 91:1092–1108.