

Short Paper

Temporal abundance and distribution of rice yellow mottle virus vectors in farmers' fields in Morogoro, Tanzania

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Abstract: Rice yellow mottle virus (RYMV), endemic to Africa, is spread within and between rice fields by several species of Chrysomelid beetles and grasshoppers. In Tanzania and particularly in Morogoro, the virus is increasingly becoming a serious problem to rice production. The part of the field and developmental stage of rice at which RYMV vectors are predominantly abundant were not known since the need for the study. The assessment of population abundance of RYMV insect vectors were conducted in the three divisions of Mngeta, Ifakara and Mang'ula of Kilombero district, in Morogoro Tanzania using sweep net in 4 m² quadrats. Results revealed the highest abundance of two RYMV vectors, *Oxya hyla* Serville, 1831 and *Chaetocnema* sp, on the border parts of the rice fields rather than in the middle parts. The study established that the density of RYMV vectors was dependent on crop growth stages where the number of vectors increased with increase in crop age and it is concluded that the two insects are the main vectors of RYMV in the study area.

Keywords: Rice yellow mottle virus, Vectors, *Oxya hyla*, *Chaetocnema* sp

Introduction

Rice yellow mottle virus (RYMV) is a highly infectious virus consisting of a single-stranded-positive RNA genome that specifically infects rice and is mechanically transmitted in the field by insect vectors, vertebrates, wind mediated means and irrigation water (Sarraf, 2005; Nwilele *et al.*, 2008). It was first observed in 1966 in Kenya (Baker, 1970) and later reported from almost in all Sub-Saharan countries of Africa (Abo and Sy, 1998). The first incidence of the virus in Tanzania was reported in 1993 in Mkindo village at Morogoro Region (Kanyeka *et al.*, 1996). From

there, the disease was then reported to have spread in almost all rice growing regions of the country. Rice yellow mottle virus disease (RYMVD) is a variable and very serious disease in Tanzania. Fagia, Kimyanga, Kimbwengu, Kinasa, Mbekese are common known local name (Hurbert *et al.*, 2015). Almost all irrigated and rain-fed lowland rice producing agro-ecologies of Africa are known to have incidences of the disease (Hull and Fargate, 2005). The virus is readily transmitted either through mechanical injuries when the infected leaves come in contact with uninfected leaves or through insect vectors. The severity and incidence of RYMVD can be influenced by population abundance of RYMV vectors. Banwo *et al.* (2001) revealed the wide distribution and abundance of *Chaetocnema* sp in Ivory Coast suggests that the insects as important vectors could be responsible for new infections of RYMV

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in these areas. Information on the disease outbreak areas and their causal vectors is already known (Banwo *et al.*, 2001; Ali, 2001). However, the field part and stages of crop growth where RYMV vectors tend to be abundant had not been well documented prior to this study. Several insect species with chewing mouthparts, particularly Chrysomelid beetles and grasshoppers can bring the inoculum from weeds and wild host into the rice crop (Kanyeka *et al.*, 2007). Different host plant growth stages may influence the vectors of RYMV population density. Sere *et al.* (2008) stated that the identity of RYMV host species, population of their vectors and presence of susceptible hosts are the key determinants of the disease prevalence in the host community.

Materials and Methods

The experiment was conducted from 2010 to 2011 in Kilombero, Morogoro Tanzania which is located at Longitude: 8°15'0"S, Latitude: 36°25'0"E in three main sites which were 100 km apart from each other. These locations included Mngeta located at 8°1'47"S and 36°24'56"E at an altitude of 830 m a.s.l.; Ifakara: 10°50'12.2"N, 14°56'37.2"E at 308 m a.s.l., and Mang'ula: 7°46'16.91"S; 36°31'51.83"E at 6029 m a.s.l. In each site five experimental fields of one acre (70 × 70 m), each of which at least a distance of 1 acre apart, were selected for trial adopting a split-plot design. The Kalimata, SARO5 and India were common rice varieties selected from the three divisions of Mngeta, Ifakara and Mang'ula respectively and where data were collected. From each site a total number of five fields, on which the same rice variety was growing, were randomly selected for trial. Each field was divided into three equal main parts: one middle part and two border parts where data were collected. Farmers' fields were considered as main plot and field parts as subplots.

Insect sampling

Sampling was conducted during cropping season from February to June 2011. A four

square meter quadrat (4m²) was used as sampling unit for collecting RYMV insect vectors from each of the three field parts. Three quadrats were set in each field part, one at the middle and two at the edges. The total number of insects sampled in each field part was the average of the three quadrats. Sampling was done during the morning hours (from 8:00-10:00 A. M), when most of vector species are assumed to land on the crop. The targeted insects during each sampling were based on already known RYMV vectors in Africa. In each field, sampling was done five times i.e. pre-planting stage (before tillage), one month after sowing (at seedling stage), two months after sowing (at vegetative stage), at reproduction stage and at the ripening stage. Rice yellow mottle virus vectors population were sampled using sweep net as described by Banwo *et al.* (2001) in the 4 m² quadrat. Five random sweeps were made per sampling unit (a quadrat of 4m²).

The numbers of different insect species collected were recorded in a specially designed record sheet. Representative specimens of each vector species collected during the sampling including orthopterans and coleopterans were sent to Kilombero Agricultural Training and Research Institute (KATRIN) Entomology Laboratory for identification and/or confirmation of their identity. Insects were placed in a plastic bottle labelled with their name, date and location collected and name of collector and then refrigerated at 4 °C. Sorting was carried out in the laboratory under stereoscopic binocular microscope, and then transferred into 80% alcohol pending identification. Only RYMV insect vectors were considered in the records on recording sheet. Non RYMV vectors were discarded and not considered in the counts.

Data analysis

Data were analysed using the GenStat 13th Edition statistical software. Analysis of variance (ANOVA) was used to determine whether there was significant difference among the insect population density at different plant

growth stages. Mean separation test was done at 0.05 confidence interval using least significant difference (LSD).

Results

RYMV Insect Vectors Present in the Study Area

After carefully sorting based on already known RYMV vectors two insect species *Oxya hyla* and *Chaetocnema* sp were found to exist in the study area. Rice yellow mottle virus insect vector species, *Chaetocnema* sp and *O. hyla* were found to be widespread and abundant in all the sampled

rice fields. In each field, population density of these insects was higher at the borders (field margin) than at the middle parts of the fields throughout the crop growth stages (Fig. 1). The population of *Chaetocnema* sp was higher than that of *O. hyla* in all crop growth stages (Table 1). Analysis of variance and mean separation tests (Table 2) indicates significant variations between RYMV insect vector counts in parts of the fields sampled. A slight variation was recorded in *O. hyla* whereby the number of insects at border 2 did not differ significantly with that of the middle part of the field.

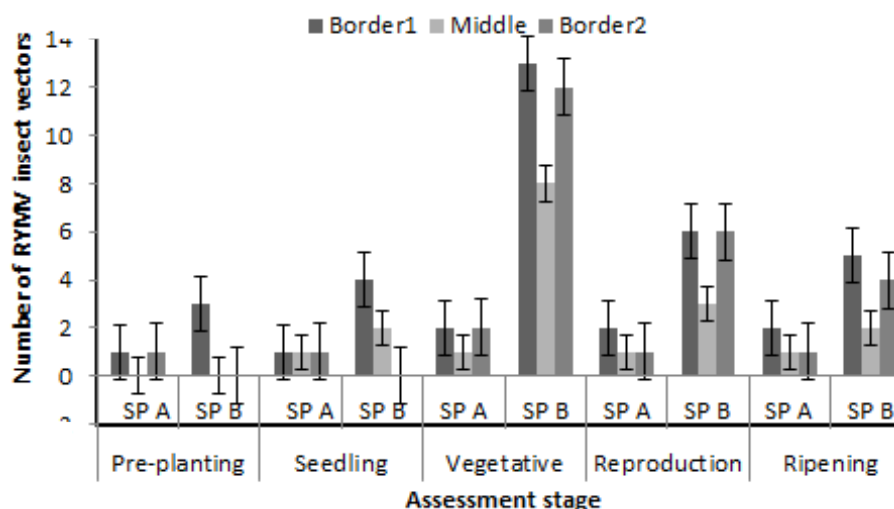


Figure 1 Mean RYMV insect vectors abundance in three rice field parts at five different crop assessment stages in 4m² quadrat in Mgeta, Ifakara and Mang'ula. SP A, indicates *Oxya hyla* and SP B, indicates *Chaetocnema* spp. Error bars were established based on the computed standard error for each of the parameters.

Table 1 Temporal abundance of RYMV vectors with respect to crop growth stages in three study sites of Mgeta, Ifakara and Mang'ula.

Growth stage	<i>Oxya hyla</i> (Insects / 4 m ²) (Mean ± SE) ¹	<i>Chaetocnema</i> spp (Insects / 4 m ²) (Mean ± SE) ¹
Pre-planting	0.58 ± 0.12a (19.93%)	2.33 ± 0.35a (80.07%)
Seedling	1.16 ± 0.13b (23.38%)	3.80 ± 0.34b (76.61%)
Vegetative	1.91 ± 0.19c (14.35%)	11.40 ± 0.65c (85.65%)
Reproduction	1.36 ± 0.18ab (21.28%)	5.03 ± 0.37b (78.72%)
Ripening	1.40 ± 0.16ab (26.37%)	3.91 ± 0.32b (73.63%)
	LSD = 0.52	LSD = 0.93

¹Values followed by different letters in a column were significantly different ($P \leq 0.05$). Proportions in row are presented in parenthesis.

Table 2 Temporal abundance and distribution of RYMV insect vectors in rice field parts in three study sites of Mgeta, Ifakara and Mang'ula.

Field Part sampled	<i>Oxya hyla</i> (Insects /4 m ²) (Mean ± SE) ¹	<i>Chaetocnema</i> spp (Insects/4 m ²) (Mean ± SE) ¹
Border1	1.59 ± 0.14a (20 %)	6.36 ± 0.52a (80%)
Middle	0.93 ± 0.12b (21.88%)	3.32 ± 0.38b (78.12%)
Border2	1.32 ± 0.14b (17.35%) LSD = 0.55	6.29 ± 0.47a (82.65%) LSD = 1.17

¹ Values followed by different letters in a column were significantly different ($P \leq 0.05$). Proportions in row are presented in parenthesis.

Discussion

It has been revealed from this study that the two insect vectors, *O. hyla* and *Chaetocnema* sp, contribute to RYMV transmission in farmers' fields in all three study locations of Mgeta, Ifakara and Mang'ula. These two insects were found to be the only vectors of RYMV with *Chaetocnema* sp being more abundant than *O. hyla*. The temporal abundance of *Chaetocnema* sp found in the study area was much higher with average proportion of 85% compared to that of *O. hyla* with average proportion of 15%. This indicates that beetles were the most abundant insect species than grasshoppers in the study area. As such *Chaetocnema* sp might either be highly competitive or favored by existing environment when compared to *O. hyla*. This observation also concurs with the report of Abo (1998), who associated the fast spread of RYMV in rice fields by *Chaetocnema pulla* in Cote d'Ivoire due to its agile behavior. The temporal abundance and distribution assessment of the vectors indicated that, the population density of both *O. hyla* and *Chaetocnema* sp decreased with the distance from the borders to the inner parts of the field. Both vector species were more abundant at the borders than in the inner parts. This is possibly because field borders were closer to the surrounding bushy vegetation where most of the alternative host plants of the insect species are believed to survive (Nwilene *et al.*, 2009). Thus, RYMV vectors survive more in alternative host plants outside the fields than within the fields. These observations suggest that there could be many alternative host plants particularly of graminaceae family in which

insect vectors survive during off season or after the rice crop has been harvested. Future work should aim at identifying the alternative host plants of *O. hyla* and *Chaetocnema* sp in order to widen the knowledge on alternative options available hence the increased options for the control of the vectors that would ultimately reduce incidences of RYMVD in rice fields. This study also revealed that population density of RYMV vectors is dependent on crop growth stages. The vector numbers were found to increase as crop grows old where the number of *Chaetocnema* sp was higher than that of *O. hyla* at each crop growth stage. The insect population density in all crop growth stages for *Chaetocnema* sp was found on the average 5.29 insects/4 m² and that of *O. hyla* was 1.28 insects/4 m² which translates to a proportion of 80.5% and 19.48% respectively. Vector numbers was lowest at pre-planting (3 insects/4 m²) and attained peaks at vegetative stage (13 insects/4 m²) and sharp decline was observed at reproduction to ripening stages. The causes of such differences may be due to the insect pest preference of leaves which are tender and which are always abundant during initial stage of rice growth and at vegetative stage. The crop is at its limited growth stage at reproduction and ripening stage when limited tender leaves are produced for insect's food and survival and so they tend to migrate to new areas where they can find more palatable food.

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Statement of conflicting interest

There is no conflict of interest of this paper by the authors.

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چکیده: ویروس پیسک زرد برنج (RYMV) بومی آفریقا است و توسط آفات متعددی نظیر ملخ‌ها و سوسک‌های Chrysomelid در مزارع برنج شیوع یافته است. در تانزانیا و به‌خصوص در مزارع کشاورزی موروگورو این ویروس به یک مشکل جدی تولید برنج روبه گسترش است. در حال حاضر مشخص نیست که ناقلین این ویروس غالباً در کدام قسمت‌های مزرعه و در کدام مرحله رشدی گیاه فراوانی بیش‌تری دارند. لذا موضوع فوق در این پژوهش بررسی شده است. ارزیابی فراوانی جمعیت ناقلین ویروس RYMV در سه منطقه از حوزه کیلومبورو شامل منگتا، ایفاکارا و منگولا که جزئی از شهر موروگورو کشور تانزانیا است انجام گرفت. نمونه‌برداری‌ها توسط تور حشره‌گیری در کادرهای ۴ متر مربعی انجام شد. نتایج نشان داد که ملخ *Oxya hyla* Serville, 1831 و سوسکی از جنس *Chaetocnema* به‌عنوان ناقلین ویروس بیش‌ترین فراوانی را در مزارع برنج دارند. به‌طوری‌که فراوانی این حشرات در حاشیه مزارع بیش از داخل مزرعه می‌باشد. این مطالعه نشان می‌دهد که تراکم جمعیت ناقلین با افزایش سن گیاه افزایش می‌یابد و به‌عنوان جمعیت غالب ناقلین ویروس RYMV شناخته می‌شوند.

واژگان کلیدی: ویروس پیسک زرد برنج، ناقل، *Oxya hyla*, *Chaetocnema* sp