

Bionomics and Importance of Two Species of *Chaetocnema* in Rice Yellow Mottle Virus Transmission in Lowland Rice in Tanzania

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Regular samplings were done of two important vectors in farmers' fields during the 1999/2000 and 2000/01 rice seasons at crop stages susceptible to rice yellow mottle virus (RYMV) on a traditional rice variety ('Supa') under rainfed lowland conditions to provide information on the bionomics and importance of these vectors in the disease transmission. The population of *Chaetocnema* sp. (nr. *varicornis* Jacoby) (Coleoptera: Chrysomelidae) was significantly higher in hotspot than non-hotspot areas. However, there was no significant difference in the *C. pulla* Chapuis population between these two areas. In general, the *Chaetocnema* sp. population was higher than that of *C. pulla*, and both vectors reached the peak of their population at 63 days after planting. Early planting in the hotspot areas is suggested as a disease management strategy. Both vectors are naturally infective and *Chaetocnema* sp. proved more efficient than *C. pulla* in the transmission of RYMV.

KEY WORDS: Bionomics; *Chaetocnema* sp.; *Chaetocnema pulla*; epidemiology; hotspot; vectors; non-hotspot; rice yellow mottle virus; lowland rice.

INTRODUCTION

Rice yellow mottle sobemovirus (RYMV) is not found outside Africa. It was first reported in Kenya in 1966 (4), with subsequent reports from Sierra Leone (22), Cote d'Ivoire (9), Nigeria (16), Tanzania, Zanzibar (26), Burkina Faso, Mali (17), Niger (23) and Guinea (11). Abo (1) reported that the incidence of the disease is gradually increasing in other countries of Africa.

In Tanzania, RYMV is widely believed to be the most important disease on rice. Luzi-Kihupi *et al.* (19) reported a yield loss of 92% on the 'Supa' variety. Rice yellow mottle is prevalent in major rice-growing regions like Mbeya, Morogoro and Mwanza (3) and is spreading rapidly between and within regions. Very recently, the Japan International Cooperation Agency (JICA) observed the disease on their irrigation plots in the Kilimanjaro region, and it has now been observed in the Kilosa district within Morogoro region (19). Severe outbreaks have been reported mainly from irrigated and rainfed production systems on lowland cultivars introduced from Asia, whereas local cultivars

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have been relatively less severely affected (28). In Tanzania, rice production from lowland and upland systems is 80% and 20%, respectively (18). RYMV, which is transmitted mechanically, belongs to the sobemovirus group (4). Bakker (5) reported the following as vectors: chrysomelid beetles (Coleoptera: Chrysomelidae): *Oulema dunbrodiensis* Jac. nr *Apophylla*, *Monolepta flaveola* Gerst., *M. haematura* Fairm., *Sesselia pusilla* Gerst., *Chaetocnema abyssinica* Jac., *C. pulla* Chapuis, *Dactylispa bayoni* Gest., *Dicladispa paucispina* (Weise), *D. viridicyanea* (Kraatz) and *Trichispa sericea* Guerin-Meneville; and the long-horned grasshopper (Orthoptera:Tettigonidae) *Conocephalus merumontanus* Sjöstedt. In Tanzania, Banwo *et al.* (6) reported RYMV vectors to include a novel and yet to be described *Chaetocnema* sp. (nr *varicornis*, Jacoby), *C. pulla* Chapuis and *Dactylispa* sp. (not *Dactylispa bayoni* Gest.). However, they reported *Dactylispa* sp. as a potentially important vector even though it is not found in all the places where RYMV exists. Although RYMV had been noted in Tanzania much earlier, it attracted attention for research only lately, with the first detailed study on the epidemiology of the disease published in 1999 by Ali (3). The West Africa Rice Development Association (WARDA) is of the opinion that, as in other RYMV-prevalent countries, the epidemiology of the disease is still poorly understood and a main mode of transmission capable of explaining the dynamic nature of RYMV is yet to be fully elucidated (Y. Sere, *pers. commun.*).

The present study was initiated to investigate the vector bionomics in two RYMV situations, hotspot and non-hotspot. This information is to be used for an understanding of the dynamics of RYMV on rice and the importance of vectors in the transmission of the disease in Tanzania. Effective control measures depend on a thorough understanding of the virus epidemiology and vector bionomics and ecology.

MATERIALS AND METHODS

The experiment was conducted at Ifakara in the Morogoro region of Tanzania during the 1999/2000 and 2000/01 rice seasons. Four fields (replicates) were used for the two treatments (RYMV normally infected/hotspot and no recorded history of RYMV infection/non-hotspot). The hotspot areas were chosen within places believed to be RYMV-infected areas/fields, which have a high rate of spread occurring consistently over the years. The non-hotspot areas/fields were chosen within those believed to have no recorded history of RYMV. The two types of fields (hotspot and non-hotspot) were within an ~1 km radius of one another. The traditional lowland rice variety 'Supa' (susceptible to the disease), requiring 135 to 150 days of growth and widely cultivated by farmers, was used. The crop was sown by broadcasting in January of 2000 and 2001 under rainfed lowland conditions. Quadrats measuring 15 m × 15 m were used in each selected field.

The population of insect vectors (*Chaetocnema* sp. and *C. pulla*) was determined by taking 20 sweeps (with a net) per quadrat on a bi-weekly basis as from 21 to 91 days after planting (DAP). It is believed that after this stage, there is less chance of RYMV infection to the crop (author, unpublished). Insect vector populations of these two treatments were compared over time by means of a paired 't'-test. To test the efficiency of both vectors, transmission tests were carried out in a screenhouse (mean temperature = 23 °C) using var. Supa. The vectors *Chaetocnema* sp. and *C. pulla* were collected from rice fields (in which var. Supa was grown) by the use of aspirators and sweep-nets. During transportation from the field, the insects were kept in closed bottles with a perforated cover. An electronically operated aspirator and camel hair brush were used to collect and transfer insects from plant

to plant and from cage to plant. The insects were kept in wooden cages, measuring 70 cm × 80 cm × 70 cm, before being used for the transmission tests.

Acquisition feeding by adult insects was conducted for 3 days on caged rice plants (6), which had been transplanted to pots 2 days previously; one insect was placed on one infected plant. For the transmission tests (inoculation feeding), seedlings at the 2- to 3-leaf stage were used, because rice plants are most susceptible to RYMV at this stage (5). Tubes measuring 2.5 cm and covered with a netting, retained the viruliferous insects on plants for the transmission test. Ten potted plants were used for each treatment. The treatments consisted of different numbers of the adult beetle vectors (*viz.* 0, 1, 2, 3 and 4). The treatments (vector numbers) were replicated five times using a randomized complete block design. The plants with no insect (0) served as control. The plants exposed to the insects were kept in the screenhouse for 3 weeks for symptom observations. To verify the presence or absence of RYMV, plants were evaluated by enzyme-linked immunosorbent assay (ELISA). The transmission percentage for the treatments (vector numbers) was calculated on the basis of the presence or absence of RYMV in each of the ten plants of each replicate.

An infectivity test was carried out to determine whether or not the vectors are naturally infective. Var. Supa seedlings grown in small cage-like containers were taken to the field. The *Chaetocnema* sp. and *C. pulla* collected live from fresh growth of Supa ratoon rice which was infected with RYMV, were immediately placed on the rice seedlings. One insect was placed on each rice plant; there were ten test plants and ten controls (with no insect) for each of the three experimental runs/replicates. The plants, with the insects, were taken to the screenhouse and kept for 3 days of inoculation access feeding. After this, the insects were removed and, as in the above-described experiment, the plants including the control were tested for the presence of RYMV.

RESULTS

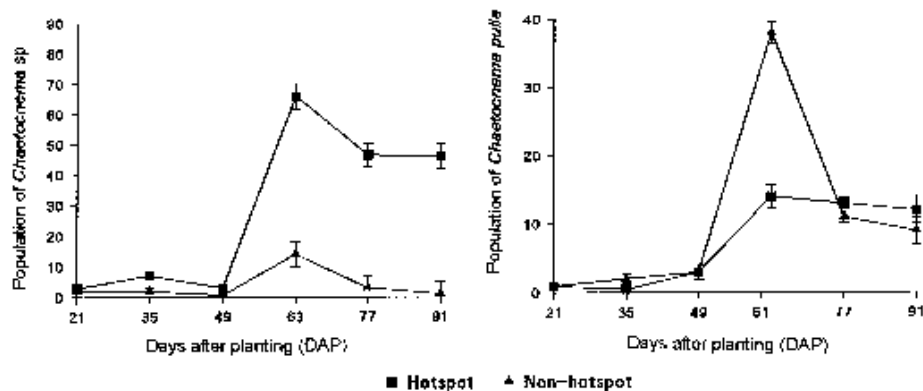


Fig. 1. Vector populations (*Chaetocnema* sp., left; *Chaetocnema pulla*, right) in hotspot and non-hotspot areas of rice yellow mottle sobemovirus, at various days after planting, 1999/2000 season. Bars indicate S.E.

The trend of the population of vectors (*Chaetocnema* sp. and *C. pulla*) with DAP in two RYMV areas is shown in Figures 1 and 3. Figure 1 (left) shows statistically significant differences ($P < 0.05$) between *Chaetocnema* sp. population in hotspot and non-hotspot areas/fields at 35 and 49 DAP, with a higher vector population in hotspot areas. Also, highly significant differences ($P < 0.001$) were recorded at 63, 77 and 91 DAP, whereas *C. pulla* showed a highly significant difference ($P < 0.001$) in vector population only at 63 DAP (Fig. 1, right), with the population higher in non-hotspot areas. No significant differences ($P > 0.05$) in vector population were observed at other DAP between the two RYMV areas. The findings (Fig. 1) can be summarized as in Figure 2, in which the DAP are grouped as a single entity within the treatments (hotspot and non-hotspot areas). Figure 3 (left) shows a statistically significant difference ($P < 0.05$) between the *Chaetocnema* sp. population in hotspot and non-hotspot areas/fields at 35 and 77 DAP, with a higher vector population in hotspot areas. Statistically significant differences ($P < 0.01$) were obtained also at 63 and 91 DAP, whereas *C. pulla* shows a highly statistically significant difference ($P < 0.05$) in vector population only at 63 DAP, with the vector population higher in non-hotspot areas (Fig. 3, right). No significant differences ($P > 0.05$) in vector population were observed at other DAP between the two RYMV areas. The findings presented in Figure 3 can also be summarized as in Figure 4, in which the DAP are grouped as a single entity within the treatments (hotspot and non-hotspot areas). Table 1 shows a significant difference ($P < 0.001$) between *Chaetocnema* sp. and *C. pulla* in the efficiency of transmission, with *Chaetocnema* sp. capable of infecting more plants than *C. pulla*. The results on infectivity of the two vectors under field conditions are presented in Table 2; there was no statistically significant difference ($P > 0.05$) in virus transmission between the vectors when naturally infective.

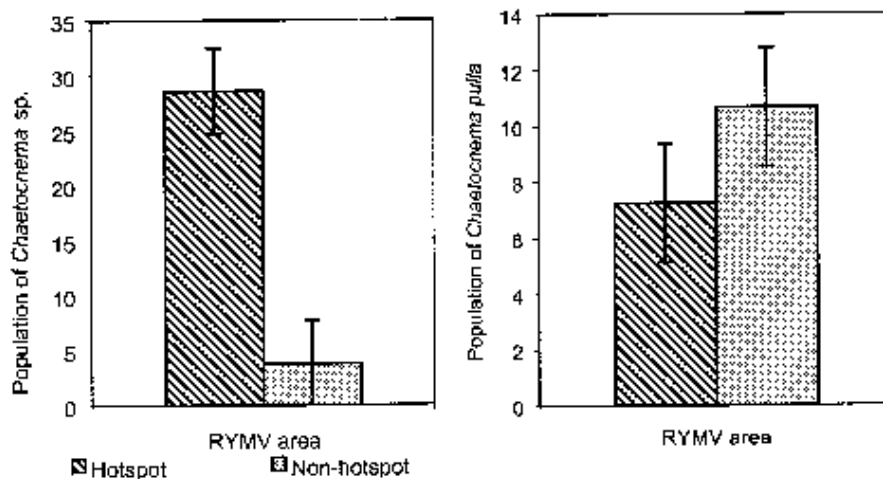


Fig. 2. Populations of *Chaetocnema* sp. (left) and *Chaetocnema pulla* (right) in hotspot and non-hotspot areas of rice yellow mottle sobemovirus, 1999/2000 season. Bars indicate S.E.

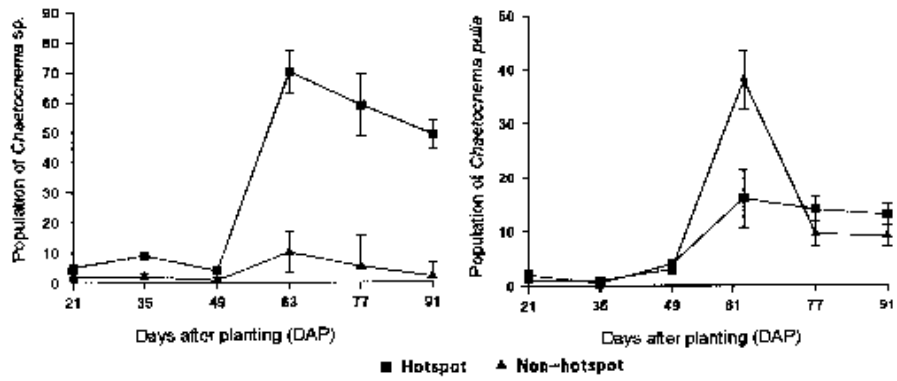


Fig. 3. Vector populations (*Chaetocnema* sp., left; *Chaetocnema pulla*, right) in hotspot and non-hotspot areas of rice yellow mottle sobemovirus, at various days after planting, 2000/2001 season. Bars indicate S.E.

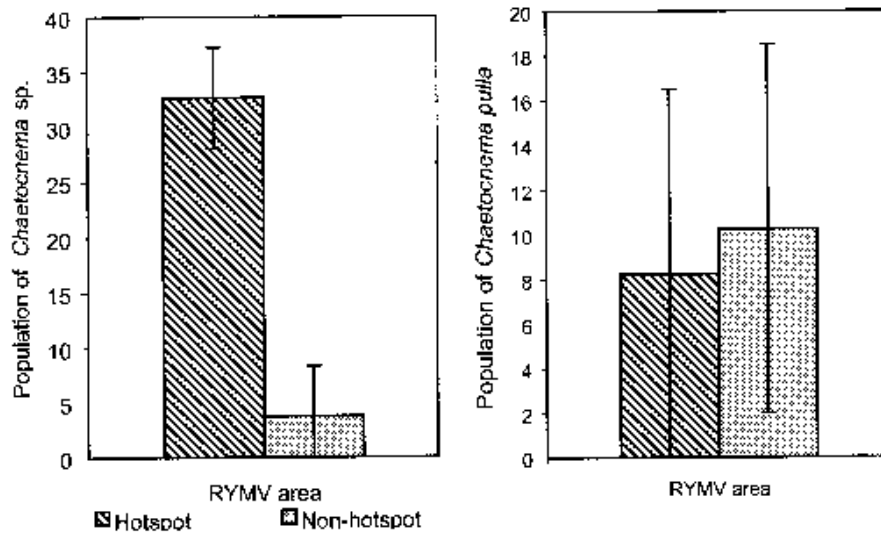


Fig. 4. Populations of *Chaetocnema* sp. (left) and *Chaetocnema pulla* (right) in hotspot and non-hotspot areas of rice yellow mottle sobemovirus, 2000/2001 season. Bars indicate S.E.

TABLE 1. Efficiency of *Chaetocnema* sp. and *C. pulla* in the transmission of rice yellow mottle virus ($R^2 = 0.919$; C.V. = 22.17%)

Number of insects	Mean % of plants infected		P
	<i>Chaetocnema</i> sp.	<i>Chaetocnema pulla</i>	
0 (Control)	0	0	-
1	45	28	<0.05
2	58	40	<0.05
3	68	54	<0.05
4	80	56	<0.01
LSD (P= 0.05)	13.56	12.22	

TABLE 2. Transmission of rice yellow mottle virus by naturally infected *Chaetocnema* sp. and *C. pulla*

Exp. No.	Number of infected plants (out of ten)		
	Control	<i>Chaetocnema</i> sp.	<i>C. pulla</i>
1	0	6	3
2	0	4	1
3	0	5	2
Mean infection	0 (0%)	5 (50%)	2 (20%)
S.D.	0	± 1	± 1
S.E.	0	± 0.58	± 0.58
LSD (0.05)		7.37	

DISCUSSION

In order to understand the importance of vectors in RYMV transmission, it is necessary to know the relationship between vector population and RYMV infection. The results of the regular sampling of the RYMV vectors in two RYMV areas (hotspot and non-hotspot) (Fig. 1) showed clearly that there were more *Chaetocnema* sp. in hotspot than in non-hotspot areas, a difference which increased with DAP. WARDA (29) reported that severe RYMV infections in rice variety Bouaké 189 at Sakassou, Cote d'Ivoire, were associated with high *Trichispa sericea* populations. However, Heinrichs *et al.* (14) in Mbe (also in Cote d'Ivoire) found no correlation between vector abundance and RYMV incidence. It is known that virus-infected plants differ from healthy plants as hosts of insects and this influences virus spread. Ajayi (2) reported that virus vectors (especially aphids) were more common on infected hosts, in part because more alighted on diseased plants than healthy ones and in part because those on diseased plants multiplied more quickly. It remains to be known if this might help to explain why this *Chaetocnema* sp. was observed in larger numbers in hotspot than in non-hotspot areas, since transmission of beetle-vectored viruses is not clearly understood (12).

The *Chaetocnema* sp. populations in the two areas reached their peaks at 63 DAP. Ecological factors, especially meteorological conditions (*e.g.* temperature and humidity), are widely believed to influence insect population. It seems possible that beneficial environmental factors were present at this time which favored the population buildup. For *C. pulla*, an obvious difference in population was observed only at 63 DAP and, surprisingly, the vector population was higher in non-hotspot than in hotspot areas. This might indicate that there is no strong and positive relationship between *C. pulla* population

and RYMV infection in the areas studied.

Although transmission results in the greenhouse indicated a positive relationship between *C. pulla* population and RYMV infection (Table 1), it should be noted that the vectors were confined to the plant for 3 days each (for virus acquisition and for feeding), reducing the chance of vector movement away from the plant. However, this would not be the case under field conditions. Also, Bakker (5) reported *C. pulla* to be 'restless'; it falls off easily, does not stay for long periods on the same plant and moves over short distances; he collected large numbers of *C. pulla* on plants under humid conditions. The *C. pulla* population at 63 DAP in our study was obviously higher in the non-hotspot than in the hotspot. It is possible that at 63 DAP, conditions encouraging a humid condition were experienced in the non-hotspot areas. In an attempt to rear *C. pulla*, F.M. Kimmins (*pers. comm.*) noticed that *C. pulla* feeds and survives on rice, but does not reproduce on it.

As observed in the present study, *C. pulla* populations were lower than those of *Chaetocnema* sp. at all DAP studied (Fig. 1). The lowest populations of 3 and 5 individuals at 21 DAP and the highest of 38 and 66 individuals at 63 DAP, were obtained for *C. pulla* and *Chaetocnema* sp., respectively. In general, increasing numbers of *Chaetocnema* sp. and *C. pulla* (Table 1) gave rise to a statistically significant increase ($P < 0.001$) in the number of plants infected. The results (Table 1) showed *Chaetocnema* sp. to be more efficient than *C. pulla* ($P < 0.001$) in the transmission of RYMV at all vector numbers. The results on infectivity of the two vectors under natural conditions (Table 2) confirm that both can be naturally infective, and although the number of *Chaetocnema* sp. (5/10) observed to be transmitting the virus was in general higher than for *C. pulla* (2/10), there was no significant difference ($P > 0.05$). The results therefore suggest that the importance of *Chaetocnema* sp. in hotspot areas might be due to their higher numbers and to their effectiveness in transmitting the virus. Gamez and Moreno (13) and Heyland (15) reported that a correlation exists among beetle population, damage, and virus spread.

The presence of a host-plant effect such as antibiosis on *C. pulla* cannot be excluded. Behle and Michels (7) reported that this type of host-plant effect on insects occurs in some wheat and rye cultivars. Information on the biology and life cycle of these vectors is essential but is, unfortunately, not available. Bakker (5) reported that it is possible that certain stages in the development of these insects take place in the soil.

Fomba (10), Taylor (27) and Reckhaus and Andriamasintseho (25) reported that yield losses due to RYMV are generally lower when infection occurs at advanced stages of the crop. As noted above, the Supa variety, which is widely grown by the farmers, has a growth duration of 135–150 days. The high *Chaetocnema* sp. population in this study therefore occurred at stages which are still susceptible (particularly at 63 DAP and possibly at 77 DAP). Thus, making the sowing date 2–3 three weeks earlier, or, in practice, planting at the 'earliest safe-sowing date' in the hotspot areas, would be necessary in order to avoid infection. With this practice, plants should have passed their vulnerable growth stages at the time the *Chaetocnema* sp. population is expected to be high. Manipulations of sowing dates have been reported in the management of RYMV in other countries. Coulibaly (8) suggested early planting before the outbreak of *Trichispa sericea* in Mali. Reckhaus and Andriamasintseho (24) suggested delaying planting until the decline of the *Di cladispa gestroi* population in Madagascar. Alternatively, chemicals have been used to reduce the vector population in Mali (8) and Madagascar (24). However, alongside other disadvantages of their use, these chemicals are beyond the reach of the poor resource

farmers in Tanzania. Plumb (21) is of the opinion that the use of chemicals against virus vectors seems unlikely to prevent primary infection and their effect on the secondary spread could be swamped by a continuous influx of infective vectors. This may explain why little success has been achieved in countries where chemicals have been applied for this purpose. The farmers in Ifakara (where this study was conducted) employ the 'slash and burn' system during land preparation. It therefore seems highly unlikely that infection from stubble (from a preceding crop) and transmitted by soil or water can occur, since these materials are gathered together and burnt (and not plowed back into the soil) (3). Matthews (20) reported that although mechanical transmission is possible, it appears not to be of any significance in the field and hence very doubtful if it can explain the dynamic nature of this disease.

The virus is not seed transmissible and can be found in wild hosts, from where it is transmitted by vectors onto growing crops (1,5). Survival of virus in vectors between crops and transovarial transmission do not occur (5). *Dactylispa* sp., reported as a potentially important vector in Tanzania (6), was not encountered in this study. In Tanzania, farmers have a high preference for the Supa variety mainly because of the characteristic grain quality and aroma. Interviews with farmers indicated that until a resistant/tolerant variety to RYMV possessing such qualities can be found, the recommendation and adoption of another lowland variety seem impossible.

It is thus concluded that vector transmission is important in the epidemiology of RYMV in Tanzania, since differences in the population of the novel and yet to be described *Chaetocnema* sp. could explain the disease infection in two RYMV areas (hotspot and non-hotspot). Nevertheless, the actual mechanism governing the phenomenon of more *Chaetocnema* sp. in hotspot than in non-hotspot areas needs to be studied further in future research. In hotspot areas, planting at the earliest safe sowing date is recommended as a vector-avoidance measure. Integrated Pest Management measures are advocated for the management of RYMV, while the search continues for varieties which are resistant/tolerant to the disease and also accepted by the farmers.

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