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Biological performance of different *Chilo partellus* populations on diverse maize genotypes

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ABSTRACT

Genetic variation within plants and herbivores influence the biological attributes and insect-plant interactions. We studied biological performance of different agro-ecological *Chilo partellus* (Swinhoe) populations on diverse maize genotypes during 2016–17 at ICAR-Indian Agricultural Research Institute, New Delhi. There was significant variation in larval period, larval survival, pupal period, pupal weight, and adult emergence of *C. partellus* populations on the test maize genotypes. Larval period of Hisar, and pupal periods of Hisar and Parbhani populations were significantly longer than other *C. partellus* populations across test maize genotypes. Pupal weight across maize genotypes was significantly higher in Delhi as compared to other populations. Larval survival and adult emergence were significantly higher in Delhi and Hisar, while lower in Raichur and Parbhani populations than other *C. partellus* populations across maize genotypes. Longer developmental periods, lower survival and adult emergence of *C. partellus* across populations on CPM 2 and CPM 8 indicate stable resistance in these maize genotypes against this pest. Higher survival in Hisar and Delhi populations across maize genotypes indicate their higher aggressiveness than other *C. partellus* populations. The differential resistance reaction, development and survival of different stem borer populations on diverse maize genotypes indicate the existence of different biotypes/ecotypes of *C. partellus* in India.

Keywords: Agro-ecological region, Biotypes, *Chilo partellus*, Maize, Population, Spotted stem borer

Spotted stem borer, *Chilo partellus* (Swinhoe) is one of the most widely distributed pests of coarse cereals, causing 18–25% yield loss in maize under different agro-climatic conditions in Asia and Africa (Dhaliwal *et al.* 2015, Dhillon *et al.* 2017). Maize (*Zea mays* L.) is considered as one of the most important cereal crops after rice and wheat (Yonow *et al.* 2017). Several strategies namely insect resistant varieties, cultural manipulation, biological control and synthetic pesticides have been in use to manage *C. partellus*, but none of them is effective particularly when the larvae enter inside the stalks (Sharma *et al.* 2007). The occurrence, onset of infestation, and relative abundance of *C. partellus* under natural conditions is sporadic and highly influenced by environment (Dhillon *et al.* 2017). Moreover, *C. partellus* undergoes facultative diapause under unfavorable climatic conditions, wherein resumption of normal developmental activity during favorable conditions could result in variation in damage potential across crops and agro-ecological regions (Dhillon *et al.* 2017, 2019a). Mating among varying aged male and female adults of *C. partellus* influences the reproductive physiology and population buildup (Dhillon *et al.* 2019b). The cross-mating among adults of diapause and nondiapause *C. partellus* within and across geographical regions could result in genetic polymorphism (Dhillon *et al.* 2020).

Due to long-term genetic differentiation or direct physiological response to environmental conditions, existence of ecotypes in different insect species is widely prevalent. The existence of genetic variation within plants and herbivore communities in nature ultimately influence the biological attributes of the insect resulting in evolutionary change in the insect population and ecological speciation, and ultimately insect-plant interaction (Zytynska and Preziosi 2011, 2013). Thus, we studied biological performance of different agro-ecological *C. partellus* populations on diverse maize genotypes, to reveal whether different biotypes/ecotypes exist in spotted stem borer under Indian conditions. Findings of present studies will be useful for designing intensive genetic research on insects and explore alternative ways to manage insect pests of economic importance.

MATERIALS AND METHODS

The *C. partellus* populations and plant material: *Chilo partellus* larvae were collected from sorghum and maize farmer's fields in various agro-ecological regions of India, viz. Delhi, Hisar, Jhansi, Surat, Parbhani, Hyderabad, Raichur and Coimbatore. These *C. partellus* populations were brought to ICAR-Indian Agricultural Research Institute

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(ICAR-IARI), New Delhi, India, and reared on green maize stalks under laboratory conditions till pupation. The next generation of field collected *C. partellus* populations along with round-year laboratory-maintained *C. partellus* culture were used for further studies. Six maize types, viz. CPM 2, CPM 8, CPM 18, CPM 19, CML 345 (resistant check), and Basi Local (susceptible check) were sown in 2 row plots of 2-m length, and the rows were 75 cm apart. There were three replications in a randomized complete block design. The crop was maintained using all the recommended agronomic practices for maize cultivation, except insecticide spray. These field raised maize genotypes were used in the studies.

Biological performance of different C. partellus populations on maize genotypes: The biological performance of aforesaid *C. partellus* populations was carried out on above mentioned maize genotypes under laboratory conditions at 27 ± 1ºC, 65 ± 5% RH, and 12L: 12D during 2016–17 at Division of Entomology, ICAR-IARI, New Delhi, India. We used the seedlings of the test maize genotypes starting at 15 days after germination from the field. A total of 50 neonate larvae of each test *C. partellus* population were released in plastic jars fitted with wire-mesh on their lids (250 ml) with stem cuttings (≈2–2.5') of respective test maize genotypes separately. The experiment was laid out in nine replications for each treatment in a completely randomized design. The food was changed whenever required. The larval mortality was recorded at every food change and the dead larvae were recorded and discarded from the experimental jars. Observations were recorded on larval period, larval survival, pupal period, pupal weight, and adult emergence. Data on various biological parameters of different *C. partellus* populations on test maize genotypes were used for computing various indices as per the method given by Dhillon *et al.* (2005), thus used for computing resistance indices. Various growth and development indices for different *C. partellus* populations were computed over laboratory population across maize genotypes. However, the indices for different maize genotypes were computed over susceptible check, Basi Local across *C. partellus* populations. The resistance indices for different *C. partellus* populations and maize genotypes were computed as: Resistance index = Larval period index + Pupal period index + Weight index + Larval survival index + Adult emergence index.

The data on biological parameters of *C. partellus* populations, reared on different maize genotypes, and the population × genotype interactions for these parameters were subjected to analysis of variance. The significance of differences were tested by *F*-tests, and the treatment means were compared by post-hoc Tukey's HSD test carried out using statistical software SPSS®.

RESULTS AND DISCUSSION

Development of different C. partellus populations on maize genotypes: The larval period of different agro-ecological populations of *C. partellus* reared on diverse maize genotypes varied from 18.4 to 25.3 days (Table 1). Across genotypes, the larval period of *C. partellus* populations was significantly longer ($F = 63.99$; d.f. = 8, 40; $P<0.001$) in Hisar as compared to other populations, being significantly shorter in Raichur and Surat populations (Table 1). The larval period across *C. partellus* populations was significantly longer ($F = 19.49$; d.f. = 5,40; $P<0.001$) on CPM 19 and CPM 18 as compared to those reared on other test genotypes (Table 1). The genotype × population interactions also showed significant differences in larval period of *C. partellus* ($F = 39.14$; d.f. = 40,320; $P<0.001$). Across populations and genotypes, the larval period was significantly longer in Hisar and Jhansi populations when reared on Basi Local and CPM 2, respectively, while shorter in Delhi and Surat populations when reared on CPM 2 (Table 1). The longer developmental period of *C. partellus* across populations on CPM 2 and CPM 18 indicate the detrimental effect of these genotypes on all the test populations. Generally, the prolongation in larval duration is linked to suboptimal nutrient content of the host plant (Pascacio-Villafan *et al.* 2016). The variation in biological attributes of a given ecological *C. partellus* population

Table 1 Larval and pupal periods of different *Chilo partellus* populations reared on various maize genotypes

Genotypes	Developmental period of *Chilo partellus* populations on different maize genotypes (days)								
	Coimbatore	Delhi	Hisar	Hyderabad	Jhansi	Parbhani	Raichur	Surat	Laboratory
CPM 2	22.9 (7.2)	18.4 (6.8)	24.8 (7.2)	23.1 (7.4)	25.0 (7.5)	21.8 (8.2)	20.2 (7.6)	18.7 (6.2)	23.5 (7.5)
CPM 8	22.2 (6.4)	23.4 (7.9)	22.7 (7.5)	23.4 (7.6)	22.7 (6.9)	22.2 (7.7)	19.7 (6.3)	20.4 (6.8)	22.9 (7.5)
CPM 18	23.3 (7.4)	22.8 (6.5)	23.8 (7.5)	23.8 (7.1)	21.3 (7.0)	22.5 (7.2)	21.6 (7.5)	22.8 (7.6)	22.9 (7.0)
CPM 19	23.2 (6.7)	23.5 (7.4)	21.9 (7.6)	22.5 (7.5)	22.6 (6.8)	23.7 (7.1)	22.3 (6.8)	23.2 (6.6)	23.0 (7.4)
CML 345	20.8 (6.4)	23.5 (7.4)	23.7 (7.2)	20.8 (6.4)	23.2 (6.8)	23.1 (7.5)	23.7 (7.7)	22.1 (7.2)	22.4 (7.8)
Basi Local	23.6 (8.1)	23.6 (7.2)	25.3 (7.6)	23.3 (7.1)	21.3 (7.6)	22.0 (6.8)	20.6 (7.1)	21.1 (7.5)	21.2 (7.3)
For comparing	Genotypes			Populations			Genotypes × Populations		
P-value	<0.001 (<0.001)			<0.001 (<0.001)			<0.001 (<0.001)		
Tukey's HSD	0.20 (0.13)			0.25 (0.16)			0.61 (0.39)		

The values outside and inside the parenthesis are larval period and pupal period, respectively.

on different maize genotypes indicate variability in the nutritional quality of the test genotypes. Earlier studies have also reported that the genetic variation among crop genotypes lead to differential herbivory by insect pests from different agro-ecological situations (Rowntree *et al.* 2011, Shikano and Cory 2015, Giron *et al.* 2018, Williams and Howells 2018).

Pupal period of *C. partellus* populations ranged from 6.2 to 8.2 days when reared on different maize genotypes (Table 1). The pupal period of *C. partellus* across maize genotypes was significantly longer (F = 9.13; d.f. = 8,40; P<0.001) in Hisar and Parbhani populations as compared to other populations, while on par with laboratory population (Table 1). Pupal period across *C. partellus* populations was significantly longer (F = 4.62; d.f. = 5,40; P<0.001) on Basi Local and CPM 2 as compared with other maize genotypes (Table 1). Genotype × population interaction was also significant for pupal period of *C. partellus* (F =11.36; d.f. = 40,320; P<0.001). A comparison across *C. partellus* populations and maize genotypes revealed significantly prolonged pupal period in Parbhani and Coimbatore populations on CPM 2 and Basi Local, respectively. However, it was significantly shorter in Surat population on CPM 2, Coimbatore and Raichur populations on CPM 8, and Coimbatore and Hyderabad populations on CML 345 as compared to other populations and maize genotypes (Table 1). Genetic variation within plants and herbivore communities could influence their biological attributes and genotype–insect preference and/or performance (Zytynska and Preziosi 2011, 2013). The variation in various biological attributes of different agro-ecological *C. partellus* populations on a given maize genotype could be due to genetic differentiation in insect populations or their physiological response and nutritional quality of the host genotype.

The pupal weight across maize genotypes was significantly higher (F = 16.16; d.f. = 8,40; P<0.001) in Delhi population, being significantly lower in Parbhani as compared to other populations (Fig 1). Across populations, the *C. partellus* pupae were significantly heavier (F = 15.26; d.f. = 5,40; P<0.001) on Basi Local and CML 345 as compared to those reared on other test maize genotypes (Fig 2). The genotype × population interaction was also significant for pupal weight of different *C. partellus* populations on the test maize genotypes (F =17.33; d.f. = 40,320; P<0.001). The lighter pupal weight of Parbhani as compared to other populations, indicate poor feeding response of this population on the test maize genotypes (Fig 1).

Survival of different C. partellus populations on maize genotypes: The larval survival in different *C. partellus* populations fed on various maize genotypes varied from 47.3 to 66.6% (Table 2). The larval survival across test maize genotypes was significantly higher (F = 18.82; d.f. = 8,40; P<0.001) in Delhi as compared to other *C. partellus* populations (Table 2). However, it was significantly lower in Parbhani and Raichur as compared to other populations. Across population, the larval survival was significantly

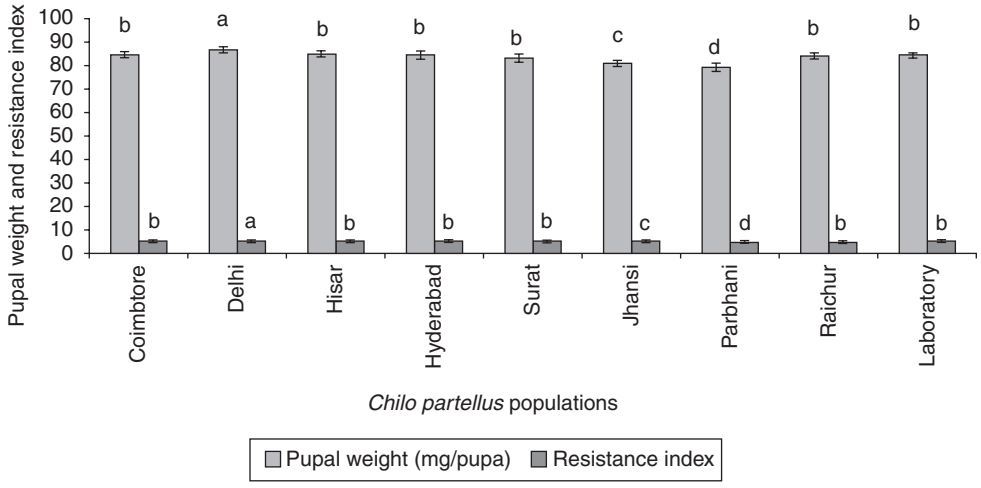

Fig 1 Pupal weight and resistance index of different agro-ecological populations of *Chilo partellus* populations across diverse maize genotypes. The bars following different letters across *C. partellus* populations for a particular parameter are significant at P = 0.05.

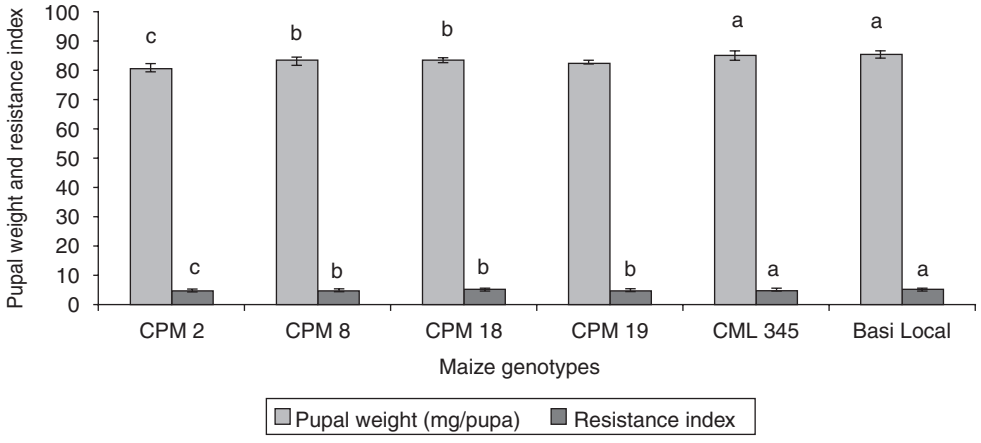

Fig 2 Pupal weight and resistance index of *Chilo partellus* on diverse maize genotypes across different agro-ecological populations. The bars following different letters across maize genotypes for a particular parameter are significant at P = 0.05.

Table 2 Larval survival and adult emergence of different *Chilo partellus* populations reared on various maize genotypes

Genotypes	Survival (%) of *Chilo partellus* populations on different maize genotypes								
	Coimbatore	Delhi	Hisar	Hyderabad	Jhansi	Parbhani	Raichur	Surat	Laboratory
CPM 2	54.9 (43.7)	51.7 (46.0)	50.7 (46.6)	51.0 (44.8)	55.6 (46.1)	50.1 (45.4)	49.7 (38.8)	59.4 (46.1)	49.2 (40.6)
CPM 8	50.9 (43.0)	61.0 (50.2)	52.1 (45.4)	55.7 (45.6)	52.3 (42.2)	52.9 (40.1)	47.7 (37.6)	49.7 (41.2)	53.3 (43.2)
CPM 18	60.9 (51.7)	65.3 (51.8)	53.9 (49.1)	60.1 (48.4)	57.1 (45.8)	57.6 (48.9)	55.3 (45.2)	53.9 (41.6)	61.2 (50.6)
CPM 19	57.0 (48.7)	51.3 (40.9)	66.1 (55.4)	55.2 (47.2)	51.0 (45.0)	48.9 (45.4)	53.1 (44.0)	55.2 (48.9)	47.3 (37.0)
CML 345	53.8 (38.1)	56.1 (45.7)	50.0 (32.3)	57.9 (51.1)	50.2 (46.8)	50.2 (39.4)	55.8 (50.3)	46.3 (40.8)	57.3 (48.7)
Basi Local	55.1 (50.6)	66.6 (61.7)	64.6 (61.4)	51.2 (49.2)	61.0 (55.8)	52.9 (50.3)	55.7 (48.8)	55.7 (51.6)	53.6 (51.1)
For comparing	Genotypes				Populations		Genotypes × Populations		
P-value	<0.001 (<0.001)				<0.001 (<0.001)		<0.001 (<0.001)		
Tukey's HSD	1.04 (0.96)				1.28 (1.17)		3.13 (2.87)		

The values outside and inside the parenthesis are larval survival and adult emergence, respectively.

lower (F = 45.77; d.f. = 5, 40; P<0.001) on CPM 2 and CPM 8 as compared with other maize genotypes (Table 2). Genotype × population interactions were also significant (F = 14.70; d.f. = 40,320; P<0.001) for survival of *C. partellus* larval populations on different test maize genotypes. Across populations and genotypes the larval survival in Delhi, Hisar, Hyderabad, Parbhani and Raichur populations on CPM 2; Coimbatore, Hisar, Jhansi, Parbhani, Surat and Raichur populations CPM 8; Delhi, Jhansi and Parbhani on CPM 19; and Coimbatore, Hisar, Jhansi, Parbhani and Surat on CML 345 was significantly lower as compared to other populations and maize genotypes (Table 2). The variation in survival of insect populations on test maize genotypes is an indicator of antibiosis mechanism of resistance in the host plants.

The adult emergence in different *C. partellus* population fed on various maize genotypes varied from 32.3 to 61.7% (Table 2). Across genotypes the adult emergence was significantly higher (F=18.13; d.f. = 8,40; P<0.001) in Delhi and Hisar populations, while lower in Raichur and Parbhani populations as compared to other *C. partellus* populations (Table 2). Across *C. partellus* populations the adult emergence was significantly (F = 125.80; d.f. = 5,40; P<0.001) lower on CPM 2, CPM 8 and CML 345 as compared to that on other maize genotypes (Table 2). The genotype × population interaction was also significant for emergence of *C. partellus* adults in different populations fed on test maize genotypes (F = 19.91; d.f. = 40,320; P<0.001). Across populations and genotypes, the adult emergence in Raichur on CPM 2; Parbhani and Raichur on CPM 8; Delhi on CPM 19; and Coimbatore, Hisar, Parbhani and Surat populations on CML 345 was significantly lower as compared to other populations and maize genotypes (Table 2). These differences in different populations may be due to long-term genetic differentiation or as a direct physiological response to host genotypes (Ikten *et al.* 2011). Such variations in larval survival and growth have also been reported in six geographic strains of *Chilo suppressalis* on different rice genotypes (Ishiguro and Tsuchida 2006).

Resistance indices of various maize genotypes against different *C. partellus populations*: The resistance index of various maize genotypes against different *C. partellus* populations over the laboratory population varied from 4.34 to 5.91 (Fig 1). Across test maize genotypes, *C. partellus* populations from Delhi and Hisar were found most aggressive followed by Coimbatore and Hyderabad as compared to other populations (Fig 1). The resistance index of various maize genotypes over the susceptible check, Basi Local against different *C. partellus* populations varied from 4.13 to 5.44 (Fig 2). Across populations, genotypes CPM 2, CPM 8 and CML 345 showed higher resistance index against *C. partellus* as compared to other test genotypes (Fig 2). It is difficult to judge resistance or susceptibility in the host plant against given insect based on individual biological attribute, as there could be genetic polymorphism within insect species, resulting in spatial and temporal variation in insect-plant interactions (Caroline and Simon 2002, Dhillon *et al.* 2005, 2015, 2017). The intraspecific genetic variation in the host plants contribute to evolutionary change in the insect population, and the host associated differentiation can lead to development of ecological speciation (Matsubayashi *et al.* 2010). Furthermore, geographic distance also contributes to phenological differentiation among populations of same species, as genetic exchange among neighbor populations is more likely than geographically distant populations. Thus, the differential resistance reaction, development and survival of different agro-ecological spotted stem borer populations on the test maize genotypes suggest the existence of different ecotypes/biotypes of *C. partellus* under different agro-ecological conditions in India.

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