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Host plant genotypes determine bottom-up effect of *Cucumis melo* var. *callosus* against melon fruit fly

S.M. Haldhar*, D.K. Samadia, R. Bhargava, D. Singh

ICAR-Central Institute for Arid Horticulture, Sri Ganganagar Highway, Beechwal Industrial Area, Bikaner 334006, India

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ABSTRACT

The melon fruit fly, *Bactrocera cucurbitae* (Coquillett) (Tephritidae: Diptera) is an important pest of cucurbits and is found to be effecting kachri (*Cucumis melo* var. *callosus*), leading to significant losses in yield potential in the hot arid agro-climate of India. The objectives of this study were to identify and categorize sources of resistance in kachri genotypes to *B. cucurbitae* from the arid region of India. Two genotypes were found to be highly resistant; 4 further genotypes were found to be resistant; 10 genotypes were moderately resistant; 6 genotypes were susceptible and two genotypes were found to be the highly susceptible to melon fruit fly infestation. The phenols ($r = -0.90$), tannin ($r = -0.89$), total alkaloids ($r = -0.80$) and flavonoid ($r = -0.96$) contents had significant negative correlations with percent fruit infestation. The percent fruit infestation did not correlate with fruit length ($r = 0.17$), fruit diameter ($r = 0.31$) and had significant negative correlation with length of ovary pubescence ($r = -0.95$), rind hardness ($r = -0.94$) and rind thickness ($r = -0.91$). Flavinoid and tannin contents explained (91.2 and 92.1%, respectively) of the total variation in fruit fly infestation and in larval density per fruit. Maximum variation in fruit infestation and larval density was explained by the length of ovary pubescence (89.5 and 84.8%, respectively) followed by rind hardness (4.3 and 3.3%, respectively). Based on the Kaiser Normalization method, two principal components (PCs) were extracted explaining the cumulative variation of 88.2% in melon fruit fly infestation. PC1 explained 71.6% of the variation while PC2 explained 16.6% of the variation. Kachri genotypic variability can improve plant fitness via bottom–up effects on fruit fly infestation. Growers can adopt potential genotypes of kachri as identified for resistance (two genotypes) with minimal financial investment for obtaining higher yields. Hence, a benefit of diversity for yield potential is recognized and thus genotypes diversity is used to become an important answer for sustainable management.

1. Introduction

A goal of many integrated pest management (IPM) researchers and practitioners has been to develop sustainable management programmes that are more resilient and less reliant on synthetic pesticides (Sharma and Ortiz, 2002; Lin, 2011; Tooker and Frank, 2012; Bustos-Segura et al., 2017). It has been widely recognised that biological diversity plays and a vital role in structuring community ecosystem processes (Tilman et al., 2006; Snyder et al., 2006; Haddad et al., 2011; Tooker and Frank, 2012). The genotypic variation may influence the distribution and damage levels of herbivores on focal plants through processes referred to as associational resistance or susceptibility (Barbosa et al., 2009). The bottom-up effects in the crop plant is an economical and environment-friendly method of insect management. The attractive and beneficial feature of botton up effect is that it is farmer friendly and does not need much financial investment for pest control. The identification and development of crop specific genotypes with resistance to pests is determined by the nutrients and concentrations of secondary metabolites. Host plants play an important role in determining insect populations in respect to concentrations and proportions of nutrients and differ among species (Schoonhoven et al., 2005). Plants having antibiosis characters such as flavinoid, alkaloid, phenols, tannins etc. may cause reduced insect survival, prolonged development time, decreased

* Corresponding author. Agricultural Entomology, ICAR-Central Institute for Arid Horticulture, Sri Gananagar Highway, Beechwal Industrial Area P.O, Bikaner 334006, India.
E-mail address: haldhar80@gmail.com (S.M. Haldhar).

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size and reduced fitness of new generation adults (Sarfraz et al., 2007; Gogi et al., 2010; Haldhar et al., 2013). Hence such mechanisms of plant resistance have been effectively and widely used for managing insect pests in fields and horticultural crops (Dhillon et al., 2005; Gogi et al., 2010; Moslem et al., 2011; War et al., 2012; Haldhar et al., 2015a, 2015b).

Cucumis species is an important genus of cucurbitaceous vegetable crops and is widely grown for their fresh fruits at various stages. Kachri, a non-desertic form of *Cucumis melo* var. *callosus* is an under-exploited drought-hardy cucurbit vegetable of the Indian Thar Desert. Kachri is the Hindi name of the species, which is also known as mango melon in English, and as karkati in Sanskrit belongs to the family Cucurbitaceae which is a widely found in rainy season crop in arid and semi-arid regions of India. The rural people collect the fruits of kachri from rain-fed/traditional mixed crops and received income as a bonus (Samadia and Pareek, 2000). In arid regions, it is widely cultivated as mixed crop or a sole crop in a resource constrained environment. Mature fruits are usually cooked with various vegetable preparations, chutneys, pickles and are also used for garnishing vegetables or salad. Mature fruits are also dehydrated for off-season use.

The melon fruit fly, *Bactrocera cucurbitae* (Coquillett) (Diptera: Tephritidae) is a serious insect pest of cucurbits in India and outbreaks cause substantial crop losses to growers. Cultivation of genotypes resistant to fruit fly is a major component of integrated pest management programs and therefore kachri was first taken for the present studies. Development of kachri genotypes resistant to fruit fly had not yet been initiated owing to inadequate information on the sources of plant traits and understanding of the bottom up effects of crop variability. The present investigation was undertaken to identify various biophysical (phenotypic structures) and biochemical (allelochemical compounds) traits of kachri genotypes associated with resistance to melon fruit fly in terms of fruit infestation and larval density under field conditions.

2. Materials and methods

2.1. Preliminary screening of kachri genotypes (summer season, 2015)

Sixty-eight genotypes of kachri were sown at the experimental farm of ICAR-Central Institute for Arid Horticulture, Bikaner (28°06′03.8″N 73°21′12.5″E). The crop was sown in the summer season, 2015 with three replicates (blocks) for each genotype with a randomized block design. The area of each bed was 5 m × 2 m containing 10 plants and the plant to plant distance was maintained at 50 cm with drip irrigation system. All the recommended vegetable practices (e.g. weeding, fertilization, hoeing, etc.) were performed equally in each experimental bed (Haldhar et al., 2013). Two pickings were done during the entire growing season of kachri. Ten fruits were randomly selected from each picking from each experimental bed (replication) of each genotype and were brought to the laboratory for microscopic examination for fruit fly infestation. The infested fruits were sorted and percent fruit infestation was calculated. All the genotypes were found to be similar in the occurrence of flowering and fruiting (ranged within 10 days) which means that they reached the stage of susceptibility to melon fruit fly at around the same time. The genotype were categorised by following the rating system given by Haldhar et al. (2013) for fruit infestation as: immune (no damage), highly resistant (1–10%), resistant (11–20%), moderately resistant (21–50%), susceptible (51–75%) and highly susceptible (76–100%).

2.2. Final screening of the selected kachri genotypes (rainy 2015 and summer 2016)

Twenty-four selected genotypes of kachri were sown from preliminary screening on the basis of fruit fly infestation at the experimental farm of ICAR-Central Institute for Arid Horticulture (CIAH), Bikaner in July, 2015 and February, 2016 following a randomized block design, with three blocks for each genotype with each block representing a replication. The picking and examination of fruits was performed as described for preliminary screening (Plate-1).

2.3. Biochemical fruit traits of the re-evaluated kachri genotypes

Two fresh fruits of each genotype from each replication were selected, cut into small pieces and dried. For the estimation of biochemicals, the procedures used for each biochemical were flavonoid, phenols, alkaloid and tannins content and the analyses were also determined on the basis of these procedures (Haldhar et al., 2015b).

2.4. Morphological fruit mechanism of the re-evaluated kachri genotypes

Ten marketable fresh fruits of each of the twenty-four kachri genotypes were used to record data on the morphological traits (length of pubescence, rind hardness, rind thickness, fruit length and fruit diameter). The length of ovary pubescence, pericarp thickness, flesh thickness, fruit diameter and fruit length were measured at five different positions of each fruit using Digital Vernier Caliper (MITU-TOYO, 300 mm, 0.01 mm reading capacity). The rind hardness of fruit at the immature and mature stages was assessed using fruit pressure tester (Model FT 327, 0–14 kg/cm^2).

2.5. Statistical analysis

Transformations (angular and square root transformed values) were used to achieve normality in the data before analysis, but untransformed means were also present in all the tables. The data on percentage fruit infestation and larval density per fruit, biochemical fruit traits and principal component analysis were analyzed by one-way ANOVA using SPSS 16 software (O'Connor, 2000). The means of significant parameters among tested genotypes were compared using Tukey's honestly significant difference (HSD) tests for paired comparisons at a probability level of 5%. Correlations between fruit fly parameters (percent fruit infestation and larval density per fruit) with biophysical and biochemical fruit traits were determined using correlation analysis of the 95 and 99% significance level.

3. Results

3.1. Preliminary screening of kachri genotypes

The 68 kachri genotypes were taken for preliminary screening against *B. cucurbitae* and significant differences were found in percentage fruit infestation and larval density per fruit. The larval density per fruit had a significant positive correlation with percentage fruit infestation ($r = 0.965$; $p < 0.01$). The genotypes IC-350933and IC-373479 were found to be highly resistant; IC-350953, IC-351005, IC-351088, IC-258131 and DKS 2011/01 were found to be resistant whereas IC-351258, DKS 2011/02 and DKS 2011/03 were highly susceptible to melon fruit fly (Table 1). The larval densities ranged from 4.87 to 15.50 larvae per fruit and were found to be significantly lower in resistant genotypes than in the