

BREEDING FOR WHITEFLY RESISTANCE IN VEGETABLE CROPS

Mr. Pratik Raval

Assistant Professor, School of Agriculture, Rai University, Ahmedabad, Gujarat, India.

Dr. Soham Trivedi

Associate Professor, School of Lifesciences, Rai University, Ahmedabad, Gujarat, India.

ABSTARCT

Vegetables occupy an important place in diversification of agriculture and have played a vital role in food and nutritional security of ever-growing population of our large vegetarian society. Improving the insect resistance of crops is an important study in vegetable science. Whiteflies are complex cryptic species distributed across Africa, Southern Europe, the Middle East, the Indian Subcontinent, Asia, Australia, the Pacific and the Americas. Traits like, fecundity, oviposition, number of eggs/plant and number of nymphs/plant, nymphal viability %, no. of pupae, development time, survival rate, number of adults/plant, trichomes density are important for identifying genotypes resistance/tolerant against whitefly. Genotypic differences exist for fecundity, oviposition, number of eggs/plant and number of nymphs/plant, nymphal viability %, number of pupae, development time, survival rate, number of adults/plant, trichomes density thus facilitates selection of desirable genotypes. Mechanisms like non-preference and antibiosis imparts resistance against whitefly. Molecular markers are available to identify QTLs imparting resistance against whitefly.

KEY WORDS: *Whitefly, Resistance, vegetable*



INTRODUCTION

Vegetables occupy an important place in diversification of agriculture and have played a vital role in food and nutritional security of ever-growing population of our large vegetarian society. The average yield of vegetables is low in India (17.6 Mt/ha) (Anonymous, 2013) as compared to Japan and some developed countries because nearly 100 per cent area occupies in these countries is under hybrid varieties.

Generally, there are more than 1500 species of whitefly found in the world but among these only four species cause considerable yield loss in vegetables *i.e*.(1) Banded wing whitefly (*Trialeurodes abutilonea*) (2) Greenhouse whitefly (*T. vaporariorum*) (3) Silver leaf whitefly (*B. tabaci* biotype B) and (4) Sweet potato whitefly (*B. tabaci* biotype A). In this regard, there is urgent need to develop whitefly resistance varieties in vegetable especially in Tomato, Brinjal, Chilli and Okra.

REVIEW OF RESEARCH WORK

Tomato (B.N.: S. lycopersicon L., Family: Solanaceae)

Maliepaard *et al.* (1995) studied the whitefly life history components Preadult Survival (PS), Adult Survival (AS) and Oviposition Rate (OR) as measures of plant resistance and they revealed lower Oviposition Rate and Preadult Survival in F_2 generation than cultivated variety Moneymaker.

Fancelli and Vendramim (2002) conducted research on development of *Bemisia tabaci* biotype B on tomato genotypes. Whitefly oviposition was influenced by tomato genotype. "LA716" showed the lowest number of eggs per leaflet (2.4). The number on the other genotypes ranged from 2.4 to 75.7 eggs per leaflet. Egg viability was affected by genotype, the lowest value, was recorded on "LA1609" (74.7%). The genotypes also differed in relation to the number of nymphs and nymphal viability. The lowest number of nymphs (1.0) was recorded on "LA716". Thus, "LA716" is resistance against whitefly through antixenotic effect.

While working on the Root Knot Nematode resistance gene "Mi-1.2" of tomato, Nombela *et al.* (2003) revealed that "Mi-1.2" is responsible for the resistance in tomato for both B- and Q- biotypes. "Mi-1.2" is unique among characterized resistance gene in its activity against three very different organisms (RKN, Aphids and Whiteflies). Their study also indicated that "Mi-1.2" is a valuable resource in insect resistance breeding programs.

Lucatti *et al.* (2010) conducted study with free choice test with natural infestation condition to classify the tomato genotypes from resistance to susceptible. The most resistance group included "FCN 3-5". The intermediate group included "FCN 93-6-2" and "Uco Plata" and the susceptible group included "FCN 13-1-6-1" and "LC 138". The number of immatures in the plant middle part on the different tomato was classified into two groups. The resistance group, containing the "FCN 3-5", with zero immatures per 4 cm² of leaf.

Cucurbits (B.N.: Cucumis spp., Family: Cucurbitaceae)

Kishaba and Castle (1992) studied mean trichome density on three Cucurbits species. Mean abaxial trichome density highest on *Cucurbita ecuadorensis*. On adaxial surface, highest density on *L. siceraria*. Leaf trichome density varied among and within *L. siceraria* accessions. On the abaxial surface, the highest density was on plant number 4 of PI 432342. Leaf trichome counts of leaves from seven plants of PI 432342 ranged from 35.7 to 52.0 mm² and covered the full range found among the other *Lagenaria sp*. The highest adaxial trichome density was on PI 419090.



In the field, abaxial whitefly counts on the two *Cucurbita lundelliana* inbreds were the highest, with the adult counts of 753 and 560 compared with a low of 21 on *L. siceraria* PI 432342. Whitefly counts were the lowest on *L. siceraria* PI 419215, PI 419090, PI 432341 and PI 432342. On the adaxial surface, the lowest counts were on PI 419090, 0.2 flies. Thus, higher the trichome number is least prefered by whitefly.

Baldin *et al.* (2012) concluded that "The Hales Best" was outstanding with the least number of adults per plant in the assessments at 24 and 48 hours after infestation, showing that it was the least attractive to *B. tabaci* biotype B.

In no choice test "Amarelo Ouro", "Hales Best", "AF-646" and "Vereda" were the least oviposited by whitefly, unlike "Nilo" and "Jangada". The Trichome quantification showed that the "Hales Best" cultivar had highest number of Trichome density compared to the other cultivars. It is suggested that as the number of trichome increased, whitefly oviposition rate decreased.

The significant prolongation observed in "Hales Best" and "Jangada", in the 3rd and 4th instars, respectively, suggested that there was non-preference for feeding and/or antibiosis.

Cassava (B.N.: *M. esculenta*L., Family: Euphorbiaceae)

Carabali *et al.* (2009) studied the parameters of life history of *A. socialis*on TST-26 and TST-18 alongwith susceptible (CMC-40) and resistant (MEcu-72) cultivar. They revealed important levels of resistance to the whitefly on TST-26 and -18 accessions was due to the marked differences found for longevity and reproduction, which influenced and were consistent with the differences found in the net reproduction rate (R_0) instrinsic growth rate (r_m) and population doubling time (DT).

Soybean (B.N.: *Glycine max* L., Family: Fabaceae)

Zhang *et al.* (2013) constructed genetic linkage map, using Simple Sequence Repeat (SSR) markers to identify QTLs associated with whitefly resistance, on F_2 population (Huapidou x Qihuang 26) of JRB1 consisting of 170 plants. They revealed that Eight QTLs, directly associated with whitefly resistance, were identified in the F_2 population of JRB1. Six QTLs were detected in Jinan, in which the maximal accounts for 37.3% on chromosome 17 between sat_326 and sat_172, whereas, the minimal accounts for 9.2% on chromosome 5 between satt236 and sat_271. Two QTLs were detected in Guanxian, accounting for 36.9% and 16% on chromosome 1 and 2, respectively. These identified QTLs would be beneficial for MAS of whitefly resistance soybean variety.

CONCLUSION

Improving the insect resistance of crops is an important study in vegetable science. Whiteflies are complex cryptic species distributed across Africa, Southern Europe, the Middle East, the Indian Subcontinent, Asia, Australia, the Pacific and the Americas. Traits like, fecundity, oviposition, number of eggs/plant and number of nymphs/plant, nymphal viability %, number of pupae, development time, survival rate, number of adults/plant, trichomes density are important for identifying genotypes resistance/tolerant against whitefly. Genotypic differences exist for fecundity, oviposition, number of eggs/plant and number of nymphs/plant, nymphal viability %, number of pupae, development time, survival rate, number of nymphs/plant, nymphal viability %, number of pupae, development time, survival rate, number of adults/plant, trichomes density thus facilitates selection of desirable genotypes. Mechanisms like non-preference and antibiosis imparts resistance against whitefly. Molecular markers are available to identify QTLs imparting resistance against whitefly.



REFERENCES

- Anonymous (2013), "Socioeconomic statistical information about India", National Horticulture Board, Available at: *www.indiastat.com*.
- Baldin E. L., Silva J. P. and Panniti L. E. (2012), "The Hales Best" *Horticultura Brasileira*, 30, 4, 600-606.
- Carabali A., Bellotti A. C., Leama J. and Fregene M. (2009), "Resistance to the whitefly, *Aleurotrachelus socialis*, in wild populations of cassava, *Manihot tristis*", *Journal of Insect Science*, 10, 70, 78-82.
- Fancelli M. and Vendramim J. D. (2002), "Development of *Bemisia tabaci* (Gennadius, 1889) biotype B on *Lycopersicon* spp. Genotypes", *Scientia Agricola*, 59, 4, 665-669.
- Kishaba, A. N., Castle S., McCreight J.D. and P.R. Desjardins (1992), "Resistance of White-flowered Gourd to Sweetpotato Whitefly", *HortSci*ence, 27, 11, 1217-1221.
- Lucatti A.F., Alvarez A.E., Machado C.R., Gilardon E. (2010), "Resistance of tomato genotypes to the greenhouse whitefly *Trialeurodes vaporariorum* (West)", Hemiptera: Aleyrodidae, *Neotropical Entomology*, 39, 5, 792–798.
- Maliepaard C., Bas N. and Heusden S. V. (1995), "Mapping of QTLs for glandular trichome densities and *Trialeurodes vaporariorum* (greenhouse whitefly) resistance in an F₂ from *Lycopersicon esculentum* × *Lycopersicon hirsutum f. Glabratum*", *Heridity*, 75, 425-433.
- Nombela G., Williamson V. M. and Muniz M. (2003), "The Root-Knot Nematode Resistance Gene Mi-1.2 of Tomato Is Responsible for Resistance against the Whitefly *Bemisia tabaci*", *The American Phytopathological Society*, 16, 7, 645-649.
- Zhang J., Zhang L., Li W., Dai H., Ci. D and Xu R. (2013), "Genetic linkage map, using Simple Sequence Repeat (SSR) markers to identify QTLs associated with whitefly resistance, on F₂ population", *Australian Journal of Crop Science*, 7, 8, 1212-1218.