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Studies on host range of okra enation leaf curl virus

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Abstract

Abelmoschus esculentus L. is commonly known as lady's fingers, bhindi, okra or gumbo is a flowering plant belongs to family Malvaceae. To study host range of OELCuV Healthy seedlings of different plant species, representative of the families Fabaceae, Malvaceae, Solanaceae, Cucurbitaceae, Caricaceae etc. were raised in a Screenhouse of Department of Plant Pathology, College of Agriculture, VNMKV, Parbhani and inoculated with viruliferous 10 whiteflies/plant after a 24 hrs AAP on infected okra leaves. After a 24 hrs IAP, the inoculated plants were sprayed with imidacloprid to keep the plants vector free and observed for symptom development that among the ten hosts, only two hosts Okra (*Abelmoschus esculentus*) were recorded as host of Okra Enation Leaf Curl Virus (OELCuV).

Keywords: Okra, OELCuV, whiteflies, *B. tabaci*, host

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) is an economically important vegetable crop belonging to the family Malvaceae and originated from Ethiopia and widely spread all over tropical, sub-tropical and warmer parts of temperate regions of the world (Singh *et al.*, 2014)^[13]. The word *Abelmoschus* perhaps originated from the Arabian word "abul-l-mosk" meaning "source of musk," referring to the musky smell of the seeds (Charrler, 1984)^[5]. It is also known as *Hibiscus esculentus* (L.) is a member of the mallow (Malvaceae) family and can be found as an annual or as a perennial in India and Africa. It is considered to be an often-cross pollinated crop since honey bee (*Apis mellifera*) and bumble bee (*Bombus auricomus*) can affect cross-pollination (Lamont, 1999)^[9]. Okra can be grown on wide range of soils, but well drained fertile soils with adequate organic matter result to high yield (Akinyele and Taye, 2007)^[1].

Okra crop is attacked by a number of fungi, bacteria, phytoplasma, viruses, nematodes and insect pests (Ali *et al.*, 2000)^[2]. Commonly occurring diseases of okra are powdery mildew (*Erysiphe cichoracearum*), damping off (*Pythium vexans*), pod rot (*Alternaria* spp.), anthracnose (*Colletotrichum* spp.), leaf spot (*Pseudocercospora abelmoschi*), yellow vein mosaic (*Yellow vein mosaic virus*), okra leaf curl (*Okra leaf Curl virus*), okra mosaic, (*Okra mosaic virus*) and okra enation leaf curl disease (Kumar *et al.*, 2016)^[8]. Production of okra is threatened quite a long time due to high incidence of yellow vein mosaic virus (YVMV) disease which infects crop at all growth stages (Verma, 1952)^[16] and causes production losses ranged from 50 to 90 % (Sastry and Singh, 1974)^[12]. Enation leaf curl disease is transmitted by insect vector, whitefly (*Bemisia tabaci*). Whiteflies cause damage to plants in two ways firstly by sucking the sap and transmitting viral disease secondly honeydew secreting onto leaves where black mold can grow (Gangwar and Gangwar, 2018)^[7].

Recently, associations of betasatellites and alphasatellites causing enation leaf curling disease in okra have been reported from India (Yadav *et al.*, 2018)^[17]. The virus is member of the genus Begomovirus of the family Geminiviridae (Venkataravanappa *et al.*, 2014)^[14]. Viruses belonging to family Geminiviridae have a single-stranded (ss) circular DNA genome with characteristic twinned quasi-icosahedral particles that are transmitted by the whitefly, *Bemisia tabaci* and infect dicotyledonous plants (Lazarowitz, 1992)^[10]. The family Geminiviridae is divided into nine genera such as *Becurtovirus*, *Begomovirus*, *Capulavirus*, *Curovirus*, *Eragrovirus*, *Grablovirus*, *Mastrevirus*, *Topocovirus* and *Turncurtovirus* (Zerbini *et al.*, 2017)^[18] based on genome organization, insect vector and host range. Begomoviruses can have bipartite DNA (having two molecules, DNA-A and DNA-B) or monopartite DNA (having a single DNA molecule, resembling DNA-A (Fondong, 2013)^[6]. The majority of the monopartite begomoviruses are found to be associated with a class of ssDNA satellites known as betasatellites Genus; Betasatellite and Family; Tolecusatellitidae (Lozano *et al.*, 2016)^[11];

previously known as DNA b (Bridson and Stanley, 2006) [4]. Begomoviruses are small ssDNA viruses vectored in a circulative persistent manner by the whitefly, *Bemisia tabaci* (genus *Homoptera*, family *Aleyrodidae*). The host range of the virus was shown to be very narrow, limited to two species in the family Malvaceae, okra (*Abelmoschus esculentus*), hollyhock (*Althea rosea*) and seven in the family Solanaceae (Venkatravanappa *et al.*, 2014) [14].

Material and Methods

Ten seedlings of each plant species upto the first leaf stage

were grown in to polythene bags containing a mixture of soil and farm yard manure (2:1). Individual healthy seedlings were inoculated with 10 viruliferous whiteflies. After 24 hrs AAP on infected okra leaves. After 24 hrs IAP, the inoculated plants were sprayed with imidacloprid to keep the plants vector free. The inoculated plants were kept in an insect-free screen house and monitored weekly for the disease incidence and appearance of symptoms of infection. Observations were recorded on transmission rate, days to first appearance of symptoms and type of symptoms developed.

Table 1: Treatment details

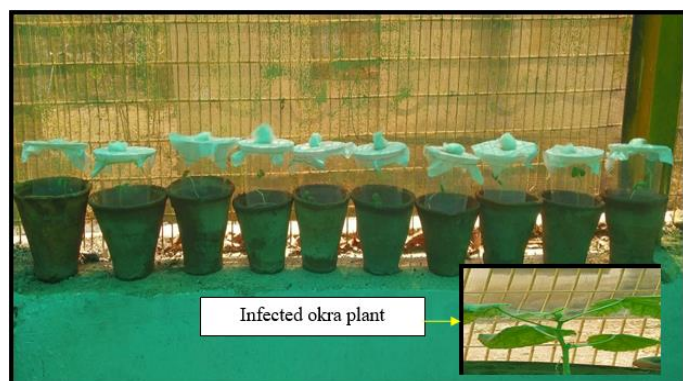
Tr. no.	Common name	Botanical name	Family	No. of plants inoculated
T ₁	Okra	<i>Abelmoschus esculentus</i> (L.) Moench	Malvaceae	10
T ₂	Cotton	<i>Gossypium hirsutum</i> L.	Malvaceae	10
T ₃	Hollyhock	<i>Alcea rosea</i> L.	Malvaceae	10
T ₄	Chilli	<i>Capsicum annuum</i> L.	Solanaceae	10
T ₅	Tomato	<i>Lycopersicon esculentum</i> Mill.	Solanaceae	10
T ₆	Brinjal	<i>Solanum melongena</i> L.	Solanaceae	10
T ₇	Cucumber	<i>Cucumis sativus</i> L.	Cucurbitaceae	10
T ₈	Papaya	<i>Carica papaya</i> L.	Caricaceae	10
T ₉	Sunflower	<i>Helianthus annuus</i> L.	Asteraceae	10
T ₁₀	Groundnut	<i>Arachis hypogea</i> L.	Fabaceae	10

Results and Discussion

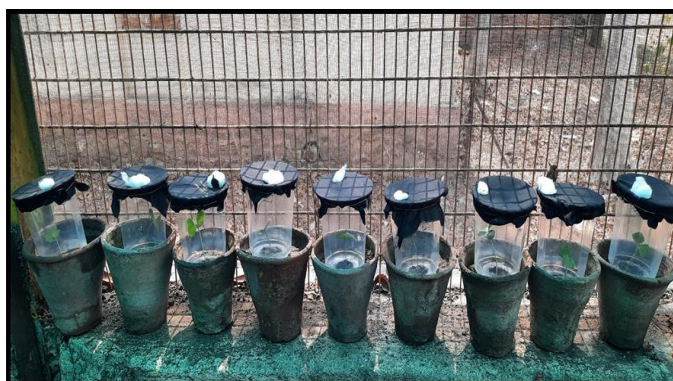
Host range of OELCuV (Pot culture)

Results of the experiment conducted on host range of ELCuV

of okra by viruliferous whitefly transmission with 10 different hosts belonging to different families were presented in Table 1, Plate 1 to 5.



1. Host: *Abelomachus esculentus* L. (Okra)



2. Host: *Gossypium hirsutum* L. (Cotton)

Plate 1: Determination of OELCuV host range by whitefly (*B. tabaci*) transmission 1. Host: *Abelomachus esculentus* L. (Okra) 2. Host: *Gossypium hirsutum* L. (Cotton)



3. Host: *Alcea rosea* L. (Hollyhock)



4. Host: *Capsicum annuum* L. (Chilli)

Plate 2: Determination of OELCuV host range by whitefly (*B. tabaci*) transmission 3. Host: *Alcea rosea* L. (Hollyhock) 4. Host: *Capsicum annuum* L. (Chilli)



5. Host: *Lycopersicon esculentum* Mill. (Tomato)



6. Host: Host: *Solanum melongena* L. (Brinjal)

Plate 3: Determination of OELCuV host range by whitefly (*B. tabaci*) transmission, 5. Host: *Lycopersicon esculentum* Mill. (Tomato) 6. Host: *Solanum melongena* L. (Brinjal)



7. Host: *Cucumis sativus* L. (Cucumber)



8. Host: *Carica papaya* L. (Papaya)

Plate 4: Determination of OELCuV host range by whitefly (*B. tabaci*) transmission, 7. Host: *Cucumis sativus* L. (Cucumber) 8. Host: *Carica papaya* L. (Papaya)



9. Host: *Helianthus annuus* L. (Sunflower)



10. Host: *Arachis hypogea* L. (Groundnut)

Plate 5: Determination of OELCuV host range by whitefly (*B. tabaci*) transmission, 9. Host: *Helianthus annuus* L. (Sunflower) 10. Host: *Arachis hypogea* L. (Groundnut)

The observations of the experiment was revealed that among the ten hosts, only two hosts exhibited OELCuV symptoms i.e., small pin head enations, upward leaf curling. Okra (*Abelmoschus esculentus*) showed 90 per cent transmission of OELCuD within 10-15 days latent period. Whereas, 40 per cent OELCuD transmission within 12-35 days was recorded in Hollyhock (*Althea rosea*), belonging to the same family Malvaceae. Other species viz., Cotton, Chilli, Tomato, Brinjal, Cucumber, Papaya, Sunflower and Groundnut did not showed any symptoms of OELCuD.

The present findings are in conformity with that of Venkataravanappa *et al.*, (2015) [15] who reported that under

controlled conditions the host range of the virus was shown to be very narrow, limited to two species in the family Malvaceae, okra (*Abelmoschus esculentus*) and hollyhock (*Althea rosea*), and seven in the family Solanaceae. Whereas, on the contrary, Bananej *et al.*, (2016) [3] noticed that papaya plant with severe leaf curling and vein swelling. Phylogenetic analysis with available OELCuV sequences support the identification of the papaya-infecting begomovirus from Iran was isolate of OELCuV and papaya recorded as host of OELCuV.

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