

Title of the presentation**Times new roman, Sentence case, 10 pt, Bold**

Authors (presenting/registered author name should be underlined)

Times new roman, Capitalize Each Word, 10 pt

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Full mailing address. Add e-mail address of the presenting (registered) author:

Times new roman, Capitalize Each Word, 10 pt, Italic

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The text of the abstract should be written here as a single paragraph (Times New Roman, 10 pt) and should not exceed 250 words without any acknowledgement and references if any.

Sample Abstract**Molecular characterization of *Citrus tristeza virus* isolates from India based on CPG/Hinf I restriction fragment length polymorphism (RFLP) group analysis**

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From six different districts of Punjab, India, 85 isolates of Citrus tristeza virus (CTV) were collected and characterized based on coat protein gene (CPG) analysis. All isolates were collected from field trees showing various CTV symptoms such as decline in most citrus varieties, inverse pitting on some sour orange rootstocks below bud union, mild-to-moderate stem-pitting on the trunk of some sweet orange. The CTV CP gene of all isolates was amplified by reverse transcriptase polymerase chain reaction (RT-PCR) using CP gene-specific primers yielding 672 bp. The maximum disease incidence was found in sweet orange followed by mandarin and grapefruit. These isolates were then subjected to CPG/Hinf I restriction fragment length polymorphism (RFLP) analysis. Mixed infection of CTV isolates was found very common in the field trees in India. The most dominant CPG/Hinf I RFLP groups III, I and VI are the basic causal epidemic in India. Moreover, based on symptoms in the field trees, CPG/Hinf I RFLP groups III, I and VI are considered to be the obvious causes of decline and stem-pitting in India.