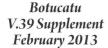


## XXXVI CONGRESSO PAULISTA DE FITOPATOLOGIA

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UNCERTAIN TRANSFERABILITY OF SSR MARKERS AMONG Xylella fastidiosa subspecies / Uso incerto de marcadores SSR entre subspecies de Xylella fastidiosa. H.D. COLETTA-FILHO<sup>1</sup>, C.S. FRANCISCO<sup>1,2</sup>. <sup>1</sup>Centro de Citricultura / IAC, 13490-000, Cordeirópolis, SP. <sup>2</sup>Bolsista FAPESP. E-mail: helvecio@centrodecitricultura.br.

Short Sequence Repeats (SSR) based molecular markers are extremely polymorphic loci are considered to be ideal markers for population genetics studies. Their flanking regions are conserved which, in theory, allows the transferability of SSR loci between closely related species. These markers have been successful used for typing strains of X. fastidiosa at intra population levels, including some already published papers assuming the transferability theory (Yuan et al., Phytopathology 100:601-611, 2010). Here we will show results about the transferability of SSR among X. fastidiosa subspecies. We analyzed SSR-based primers designed on subspecies fastidiosa, multiplex and sandyi of X. fastidiosa used in silico and in vitro -PCR on subspecie pauca of this bacterium using the strain 9a5c as reference. Off 14 SSR tested primers sets seven amplified no repeat genomic regions and one resulted on no template amplification (null allele), by in silico analysis Those seven no-repeat loci, five came from *fastidiosa*, one from *sandyi* and another from *multiplex* subspecies. The *in silico* analysis were reproducible by the in vitro PCR. In conclusion, the transferability of SSR marker among the different subspecies of X. fastidiosa must be used with caution. Supported by Fapesp: 2011/13803-9.





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