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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-FILHO¹, C.S. FRANCISCO^{1,2}. ¹Centro de Citricultura / IAC, 13490-000, Cordeirópolis, SP. ²Bolsista 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 subspecies *pauca* of this bacterium using the strain 9a5c as reference. Of 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.
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