VARIABILITY AMONGST ‘*CANDIDATUS* LIBERIBACTER AFRICANUS’ POPULATIONS OF CITRUS IN SOUTH AFRICA

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In South Africa, Citrus Greening disease is associated with the phloem-limited, α-proteobacterium ‘*Candidatus* Liberibacter africanus’ (Laf) which is spread by the Triozid, *Trioza erytreae* Del Guercio. Typical symptoms on commercial citrus crops infected with Laf include; leaf mottling along veins, the formation of lopsided, bitter-tasting fruit which remains green and early fruit drop.

Two other ‘*Candidatus* Liberibacter’ species are known which cause symptoms resembling Citrus Greening disease on citrus i.e. ‘*Candidatus* Liberibacter asiaticus’ (Las) which is associated with Citrus Huanglongbing and ‘*Candidatus* Liberibacter americanus’ (Lam). Las has been identified from a number of citrus producing countries worldwide, whereas Lam has to date only been described from South America.

Sweet orange tree in Mpumalanga displaying typical Citrus Greening symptoms.

Laf is the only ‘*Candidatus* Liberibacter’ species known to occur on commercial citrus crops in South Africa, however, different populations of Laf may be present in the country based on observations in 1991 that Laf populations from Rustenburg (Central Transvaal) were more readily transmitted through grafting than Laf populations from Mpumalanga (Eastern Transvaal).

Additionally, different citrus cultivars respond in varying degrees of severity to Laf infection with sweet orange, tangelo and mandarins being severe, grapefruit, sour orange and lemon being classified as moderate and lime, trifoliate orange and pomelo being considered tolerate.

It is unknown what factors influence the host response of different cultivars. In this study, our aim was to determine whether variable populations of Laf exist in different citrus cultivars or geographical areas.

Fifty simple sequence repeat (SSR) regions were identified across the whole genome of Laf, and primers were designed which flagged these regions. The primer pairs were screened for polymorphisms by amplifying the target SSR regions of 20 Laf isolates obtained from five different provinces where citrus is grown as well as 11 citrus species and cultivars. Of these 50 genome regions, only five differentiated between various Laf populations. Preliminary data suggests that Laf populations in South Africa are formed by citrus species and cultivar selection rather than geographical isolation, and this may suggest that the varying degree of virulence of Laf on different citrus species and cultivars may be due to this. Information regarding the variability of Laf could potentially be exploited to control Citrus Greening disease in South Africa in a future mild strain cross protecting strategy.