

Characterization of *Xanthomonas campestris* pathovars by rRNA gene restriction patterns

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Genomic DNA of 192 strains of the *Pseudomonadaceae* family, including 188 strains of the genus *Xanthomonas*, was cleaved by *EcoRI* endonuclease. After hybridization with 2-acetyl-amino-fluorene labelled (AAF) *Escherichia coli* 16+23S rRNA probe, 27 different patterns were obtained. Strains are clearly distinguishable at the genus, species, and pathovar level. Variability of rRNA gene restriction patterns was studied for four pathovars of *Xanthomonas campestris* species. The 16 strains analysed of *X. campestris* pv. *begoniae* gave only one pattern. For *X. campestris* pv. *manihotis* variability of rRNA gene restriction patterns could be related to ecotypes. On the contrary, the variability of patterns observed for *X. campestris* pv. *malvacearum* was neither correlated to pathogenicity nor to the geographical origins of the strains. The highest degree of variability of DNA fingerprints was observed within pathovar *dieffenbachiae*, which is pathogenic to several hosts of the *Araceae* family. In this case, variability could be related to both host plant and pathogenicity.