



Realização:



Apoio:

**XVII CIC
X ENPOS**Conhecimento sem fronteiras
XVII Congresso de Iniciação Científica
X Encontro de Pós-Graduação
11, 12, 13 e 14 de novembro de 2008

Differences between the *Xanthomonas arboricola* pv. *pruni* genome and the model strains Xcc B100 and Xcv 85-10 using DNA microarray technology

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Resumo:

The phytopathogenic bacteria *Xanthomonas arboricola* pv. *pruni* is the causal agent of Prunus Bacterial Spot disease (PBS) that infects cultivated Prunus species and their hybrids. In southern Brazil this pathovar is an important pathogen in peach and plum crops, causing considerable economic losses annually. On the other hand, most of the *Xanthomonas* species including *X. arboricola* pv. *pruni* produces by an aerobic fermentation process the xanthan gum, an important biopolymer used in the food, oil and cosmetic industry. To the Comparative genomic Hybridisation five strains isolated from peach and plum trees at the Centro de Pesquisas Agropecuárias de Clima Temperado (EMBRAPA, Pelotas, RS, Brazil) were used. For this study were choice strains with different capacity for xanthan production (data not shown) in MPEII medium. The genomic DNA was hybridized with the model strains *X. campestris* pv. *campestris* B100 and *X. campestris* pv. *vesicatoria* 85-10 using the microarray technology. Data analysis was done by applying the ImaGene 6.0 software (Biodiscovery Inc., Los Angeles, CA) for acquisition of the mean signal for each spot of the microarray and the EMMA 2.2 software (Bielefeld University, Germany) for normalization and t-statistics. A gene was considered to have a statistically significant difference if the P value was ≤ 0.01 , the M value (\log_2 -ratio) was ≥ 2 or ≤ -2 and the A value (mean intensity) was ≥ 7 . The results shown a high genetic similarity among the five strains used. Several gene clusters present in the *X. campestris* pv. *campestris* B100 and *X. campestris* pv. *vesicatoria* 85-10 genome were found to be missing in the *X. arboricola* pv. *pruni* genome. Of these, were identified VirB genes (VirB1, virB2, virB5, virB8, virB9, virB11), icm genes (icmB, icmC, icmJ, icmT) and pil genes (pilC, pilE, pilL, pilO, pilQ, pilR, pilX, pilY, pilV). VirB and icm genes belong to the type IV secretion system, which is used to transport toxic molecules to host cells and also to DNA or protein-DNA complexes transport. The genes pilX, pilY and pilV are Tfp pilus assembly proteins and the other pil genes are involved with secretion systems and membrane proteins. These pilus assembly proteins are important for virulence and DNA transfer in a variety of prokaryotes. In conclusion, the absent of the VirB, icm and pil gene groups in the *X. arboricola* pv. *pruni* genome are probably partially responsible of the low pathogenicity of this pathovar.