

The phytopathogen *Xylella fastidiosa* colonizes the lumen of xylem vessels from its hosts and the mouth apparatus of the insect-vector. It is responsible for severe diseases in grapevine, orange and olive trees, among other plants of economic relevance. There is evidence for specificity between *X. fastidiosa* strains and the different plant species they colonize, but the molecular bases of this interaction are unknown. The main objective of this work was elucidate the complete repertoire of expressed and/or differentially expressed genes by different *X. fastidiosa* strains in distinct media and growth times and associate transcriptional responses to virulence mechanisms, pathogenicity and host specificity. Transcriptomes of orange strains (9a5c, J1a12, U24d and Fb7), coffee (3124), hibiscus (Hib4), plum (Pr8x) and grapevine (Temecula1), were sequenced, analyzed and compared from cells at the beginning and end stages of exponential growth phase in rich medium PWG and in minimum medium PIM6, which mimics xylem sap. It was observed that the majority of *X. fastidiosa* genes is expressed, although, depending of the strain and experimental condition, 40-80% of transcripts are less abundant. On the other hand, it was verified a set of more abundant transcripts, some of them shared by all strains, including 6S and RNase P ncRNAs as well as transcripts for microcins, proteases, lipases, stress response proteins and proteins of unknown function. Besides the definition of transcriptional profiles, 5' and 3' untranslated regions of transcripts were described. The structure of 545 and 386 expressed operons, respectively for 9a5c and Temecula1 strains, were also mapped, and for the first time the expressed profile of sRNAs in *X. fastidiosa* was obtained. The differential expression analyzes between transcriptomes of two growth phases in the same medium indicate that the stress generated by nutritional limitation of PIM6 medium required more drastic changes in gene expression than PWG medium. It was also observed that different strains respond in distinct manners to a same condition, indicating that orthologous genes are regulated in different ways. Moreover, comparative transcriptomics revealed relevant differences in gene regulation of strain of distinct plant hosts that can be related to host specificity. Lastly, transcriptomic analyzes pointed to several gene candidates that could be further investigated for their roles in *X. fastidiosa* biology and virulence.