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Bacterial blight of fruit trees caused by *Pseudomonas syringae* causes significant economic losses worldwide. With the expansion of bacterial canker of kiwi caused by *P. syringae* pv. *actinidiae* (Psa) and bacterial canker of apricot caused by *P. syringae* pv. *syringae* (Pss), identification of reservoirs of pathogenic strains is required. One potential reservoir is ground covers in orchards. A solution could be the development of ecological engineering practices, particularly ground cover management in order to reduce their impact as a source of inoculum for bacterial diseases of fruit trees caused by *P. syringae* and increase their role as a reserve for microorganisms that are antagonistic to pathogens of fruit trees. However, with the recent discovery of the complexity of the phylogeny of *P. syringae* and the existence of phylogroups containing more aggressive strains than others (Psa in phylogroup 1, Pss in phylogroup 2), one of the first goals is the development of a specific molecular detection method, by PCR, allowing rapid and accurate identification of the different phylogroups of *P. syringae*. This would be much more efficient than the only method currently available - sequencing of specific conserved genes used in phylogenetic identification. The simple implementation of this new method of genotyping makes it possible to screen samples of very large size with little effort. This method can be deployed to develop methods of control of bacterial blight, and can be used as a generic mean of detecting and monitoring orchards and crops. Indeed, the use of a technique targeting a single pathovar may be insufficient, as it is not uncommon for plants to be simultaneously attacked by several different strains of *P. syringae*. The method of detection and identification of phylogroups will be presented and a concrete example for specific samples (ground cover, buds, twigs) from orchards of apricot and kiwi will be described.