



Recombination-prone bacterial strains form a reservoir from which epidemic clones emerge in agroecosystems

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Résumé en anglais	<p>The acquisition of virulence-related genes through horizontal gene transfer can modify the pathogenic profiles of strains and lead to the emergence of new diseases. <i>Xanthomonas arboricola</i> is a bacterial species largely known for the damage it causes to stone and nut fruit trees worldwide. In addition to these host-specific populations called pathovars, many nonpathogenic strains have been identified in this species. Their evolutionary significance in the context of pathogen emergence is unknown. We looked at seven housekeeping genes amplified from 187 pathogenic and nonpathogenic strains isolated from various plants worldwide to analyze population genetics and recombination dynamics. We also examined the dynamics of the gains and losses of genes associated with life history traits (LHTs) during <i>X. arboricola</i> evolution. We discovered that <i>X. arboricola</i> presents an epidemic population structure. Successful pathovars of trees (i.e. <i>pruni</i>, <i>corylina</i> and <i>juglandis</i>) are epidemic clones whose emergence appears to be linked to the acquisition of eight genes coding for Type III effectors. The other strains of this species are part of a recombinant network, within which LHT-associated genes might have been lost. We suggest that nonpathogenic strains, because of their high genetic diversity and propensity for recombination, may promote the emergence of pathogenic strains.</p>
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