



Contrasting recombination patterns and demographic histories of the plant pathogen *Ralstonia solanacearum* inferred from MLSA

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Titre	Contrasting recombination patterns and demographic histories of the plant pathogen <i>Ralstonia solanacearum</i> inferred from MLSA
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Auteur	Wicker, Emmanuel [1], Lefeuvre, Pierre [2], de Cambiaire, Jean-Charles [3], Lemaire, Christophe [4], Poussier, Stéphane [5], Prior, Philippe [6]
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Mots-clés	bacterial wilt [7], coalescent [8], homologous recombination [9], phylogeography [10], population expansion [11]
Résumé en anglais	<p>We used multilocus sequence analysis (MLSA) on a worldwide collection of the plant pathogenic <i>Ralstonia solanacearum</i> (Betaproteobacteria) to retrace its complex evolutionary history. Using genetic imprints left during <i>R. solanacearum</i> evolution, we were able to delineate distinct evolutionary complex displaying contrasting dynamics. Among the phylotypes already described (I, IIA, IIB, III, IV), eight groups of strains with distinct evolutionary patterns, named clades, were identified. From our recombination analysis, we identified 21 recombination events that occurred within and across these lineages. Although appearing the most divergent and ancestral phylotype, phylotype IV was inferred as a gene donor for the majority of the recombination events that we detected. Whereas this phylotype apparently fuelled the species diversity, ongoing diversification was mainly detected within phylotype I, IIA and III. These three groups presented a recent expanding population structure, a high level of homologous recombination and evidences of long-distance migrations. Factors such as adaptation to a specific host or intense trading of infected crops may have promoted this diversification. Whether <i>R. solanacearum</i> lineages will eventually evolve in distinct species remains an open question. The intensification of cropping and increase of geographical dispersion may favour situations of phylotype sympatry and promote higher exchange of key factors for host adaptation from their common genetic pool.</p>
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