



## When virulence originates from non-agricultural hosts: New insights into plant breeding

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Titre	When virulence originates from non-agricultural hosts: New insights into plant breeding
Type de publication	Article de revue
Auteur	Leroy, Thibault [1], Le Cam, Bruno [2], Lemaire, Christophe [3]
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Mots-clés	Approximate Bayesian Computation (ABC) [4], Emergence [5], Gene-for-gene interaction [6], genome scan [7], Resistance genes [8], Virulence [9]
Résumé en anglais	Monogenic plant resistance breakdown is a model for testing evolution in action in pathogens. As a rule, plant pathologists argue that virulence - the allele that allows pathogens to overcome resistance - is due to a new mutation at the avirulence locus within the native/endemic population that infects susceptible crops. In this article, we develop an alternative and neglected scenario where a given virulence pre-exists in a non-agricultural host and might be accidentally released or introduced on the matching resistant cultivar in the field. The main difference between the two scenarios is the divergence time expected between the avirulent and the virulent populations. As a consequence, population genetic approaches such as genome scans and Approximate Bayesian Computation methods allow explicit testing of the two scenarios by timing the divergence. This review then explores the fundamental implications of this alternative scenario for plant breeding, including the invasion of virulence or the evolution of more aggressive hybrids, and proposes concrete solutions to achieve a sustainable resistance.
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### Liens

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