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## The change of *Phytophthora infestans* Populations in South Korea using Traditional Markers and Genome Analyses

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### [Abstract]

Late blight, caused by the hemibiotrophic oomycete pathogen *Phytophthora infestans*, has been the most important disease limiting potato production worldwide. *P. infestans* undergo major population shifts in agricultural systems via the successive emergence and migration of asexual lineages. The phenotypic and genotypic bases of these selective sweeps are largely unknown but management strategies need to adapt to reflect the changing pathogen population. Here, we used molecular markers to divide the 86 South Korea isolates into six clonal lineages: KR\_1\_A1, KR\_2\_A2, SIB-1, US-11, SIB-1 like, and KR-2 like. We documented the emergence of a new lineage, termed SIB-1 like, and KR-2 like, and their rapid replacement of other lineages to exceed 35% of the pathogen population across South Korea. Genome analyses of the Korean *P. infestans* populations revealed extensive genetic polymorphism, particularly in effector genes. Importantly, SIB-1 like isolates carry an intact *Avr8* effector gene that triggers resistance in potato carrying the corresponding R immune receptor gene *R8* cloned from *Solanum demissum*. These findings point toward a strategy for deploying genetic resistance to mitigate the impact of the SIB-1 like lineage and illustrate how pathogen population monitoring, combined with genome analysis, informs the management of devastating disease epidemics. Further study is being done on pathogenicity of the SIB-1 like isolates on cultivated potatoes and changes in expression patterns of disease effector genes within the SIB-1 like isolates

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