

## Worldwide invasion routes of the pinewood can we infer from population genetics ana

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**Abstract** Identifying the invasion routes and determining the origin of new outbreaks of invasive species are of crucial importance if we are to understand the invasion process, improve or establish regulatory measures and, potentially, limit the damage. We focused here on the invasion of Europe by the pinewood nematode (PWN), *Bursaphelenchus xylophilus* (Steiner & Buhner, 1934; Nickle 1970; Nematoda: Aphelenchoididae), a major pest of forest ecosystems, native to North America and already invasive in Asia since the beginning of the twentieth century. We evaluated the genetic diversity and structure of worldwide field PWN samples by classical and Bayesian population genetics methods to

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: source of the European invasive pop-  
the number of introduction events in  
found (1) a very strong spatial genetic  
ative PWN populations, (2) a very low  
morphism in each of the invaded areas  
asted results concerning the origin of  
asive populations. Our findings provide  
(1) a large effect of genetic drift on the  
cle of the PWN, due to intense demo-  
necks during tree infections, not com-  
y effective dispersal of its vector; (2) a  
ction event for each of the invaded areas  
Europe and a small effective size for the  
pulations and (3) a mainland Portuguese  
N populations from Madeira. However,  
cated methods of invasion route infer-

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ader sampling are required to conclude the origin of the European outbreak.