

Identifying the main routes followed by an invasive species has significant management implications and may help to understand its colonization process. The obscure mealybug, *Pseudococcus viburni* (Signoret, 1875), is an important agricultural pest native to South America that infests fruit crops worldwide. The genetic diversity and structure of *P. viburni* samples collected around the globe was investigated here, and the most likely invasion routes were inferred using state-of-the-art population genetics methods. The results obtained include: (1) identification of low intrapopulation genetic diversity (mean number of alleles per locus below 4 and heterozygosity below 50%) and high genetic differentiation among populations (average  $F_{ST} = 0.29$ ); (2) strong evidence of an initial colonization from South America towards Europe and secondary introductions from Europe towards other continents, (3) evidence of population structure within Europe and, (4) support for introductions from North America and Europe to South Africa. These results improve our understanding of the worldwide distribution and invasion pathways of *P. viburni* and suggest further exploring South America as the best source for potential biological control agents.