Supplemental Information for:

Another chapter in the history of the European invasion by the Western conifer seed bug, *Leptoglossus occidentalis*: the Iberian Peninsula

Farinha A, Branco M, Courtin C, Lesieur V, Gallego D, Sanchez-Garcia F.J., Sousa E., Roques A, Auger-Rozenberg M-A*, and Bras A*

*Contributed equally to this work.

Table S1. Results of the hierarchical Analysis of molecular variance (AMOVA) of *Leptoglossus occidentalis* invasive populations in western Europe computed with mtDNA sequence data from this study and Lesieur et al. (2019).

Source of variation	df	Sum of squares	% of variation	Fixation index
(a) Geographic proximity				
Among groups	1	1.833	8.90	F_{CT} = 0.089 (*p.value*: 0.059)
Among populations within groups	18	8.442	13.39	F_{SC} = 0.147 (*p.value*: 0.006)
Within populations	76	19.714	77.71	F_{ST} = 0.223 (*p.value*: 0.001)
(b) First observation				
Among groups	2	2.061	4.86	F_{CT} = 0.049 (*p.value*: 0.155)
Among populations within groups	17	8.214	14.99	F_{SC} = 0.158 (*p.value*: 0.005)
Within populations	76	19.714	80.15	F_{ST} = 0.198 (*p.value*: 0.001)

Statistical probabilities were derived from 50,175 permutations. (a) two groups: (1) Alessandria, Yvoy-le-Marron, Lavercantière, Serre-Ponçon, Barcelona, Lleida, Soria; (2) Valladolid, Salamanca, Segovia, Murcia, Burgos, Galicia, Coruche, Valencia, Faro, Huelva, Islas Cies, Almeria, Aveiro ; (b) three groups: (1) Alessandria, Lavercantière, Serre-Ponçon, Barcelona; (2) Yvoy-le-Marron, Lleida, Soria, Valladolid, Salamanca, Segovia, Almeria; (3) Murcia, Burgos, Galicia, Coruche, Valencia, Faro, Huelva, Islas Cies, Aveiro.

Figure S1. Correlations between the pairwise F_{ST} values and pairwise geographical distances (in km) for invasive populations (R^2: 0.009) of *Leptoglossus occidentalis*.
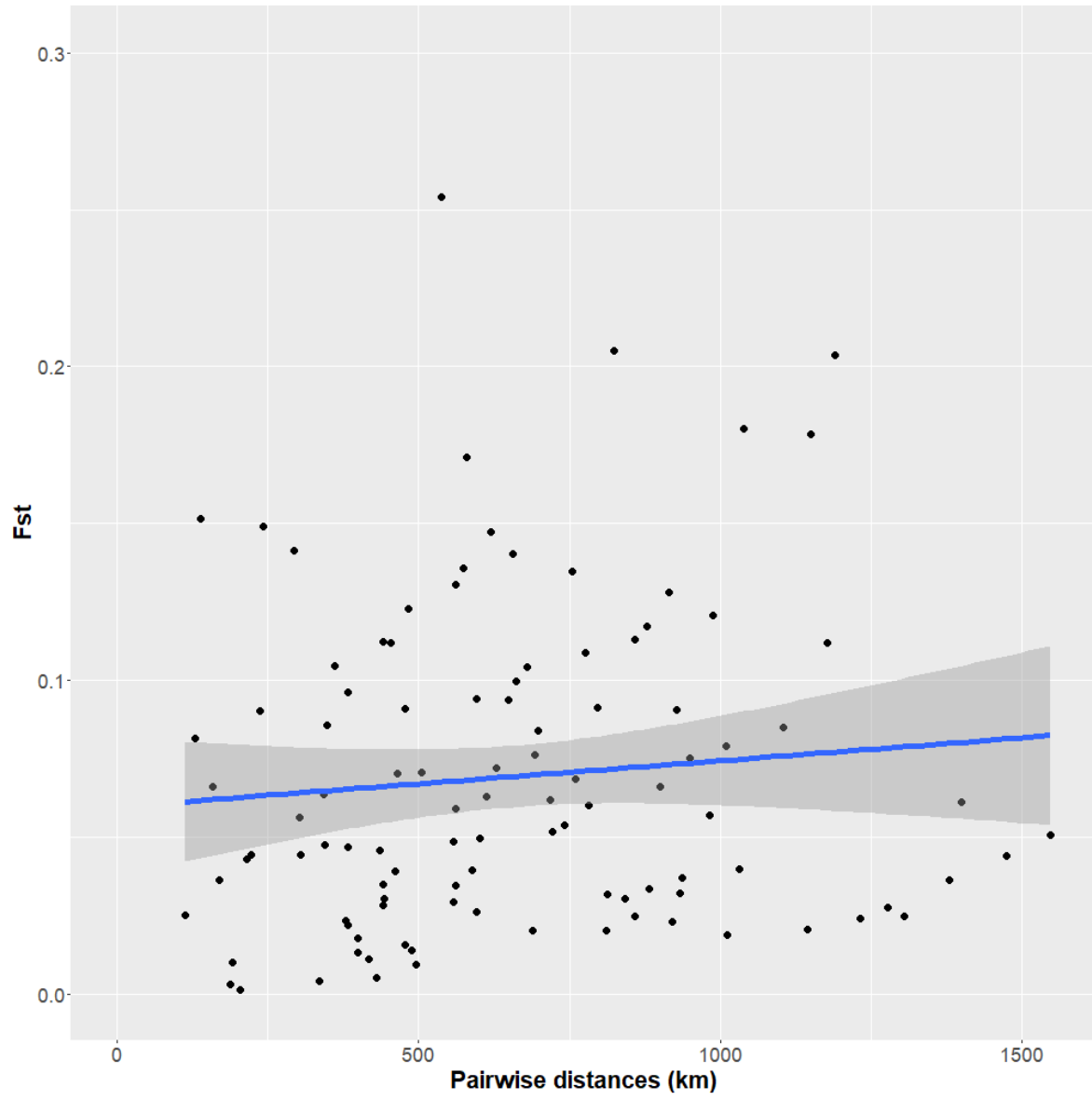
Figure S2. Discriminant Analysis of Principal Components (DACP) for the Iberian Peninsula populations of *Leptoglossus occidentalis*.
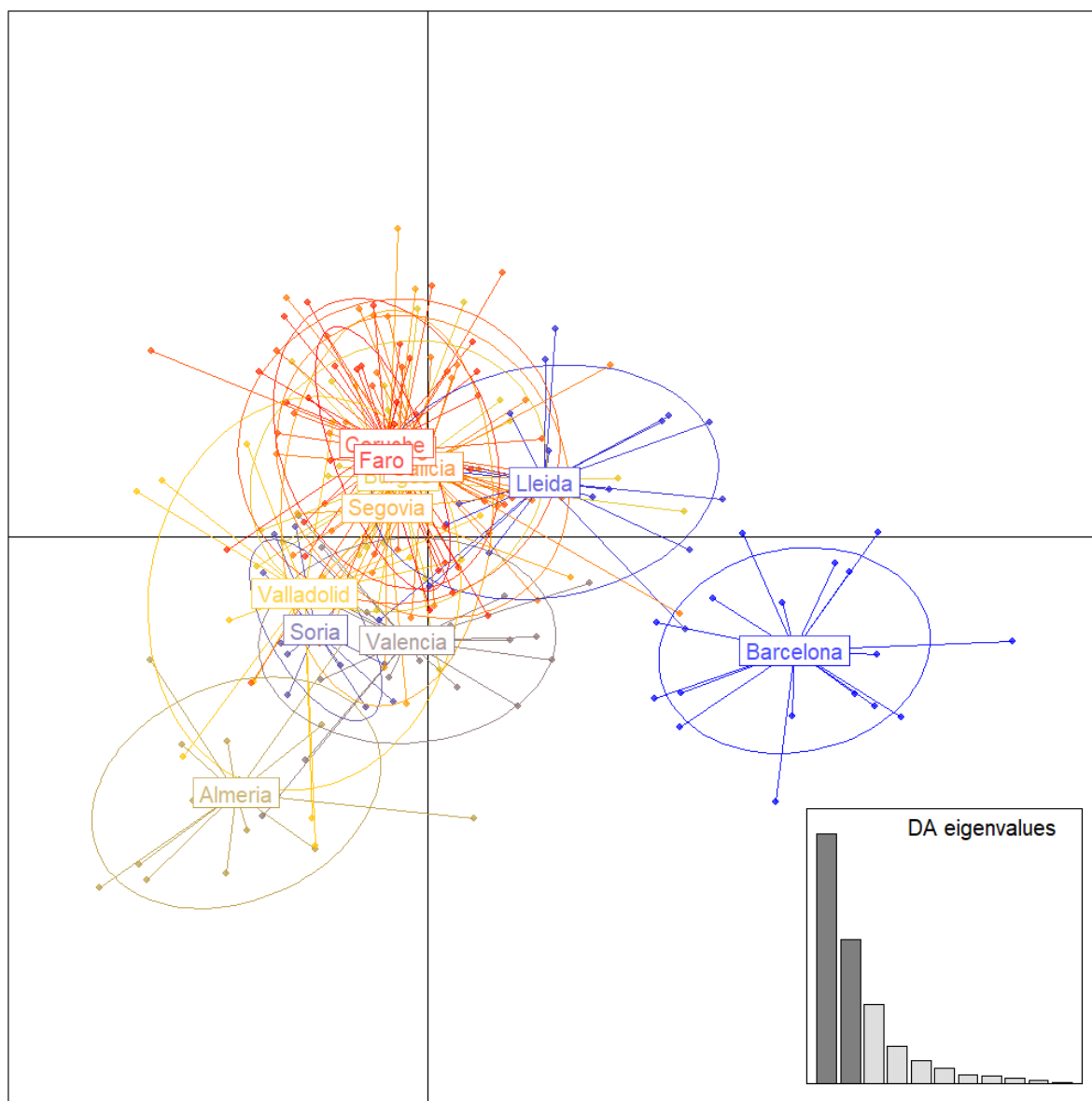
Figure S3. Neighbor-joining tree estimation of Saitou and Nei (1987) for *Leptoglossus occidentalis*.
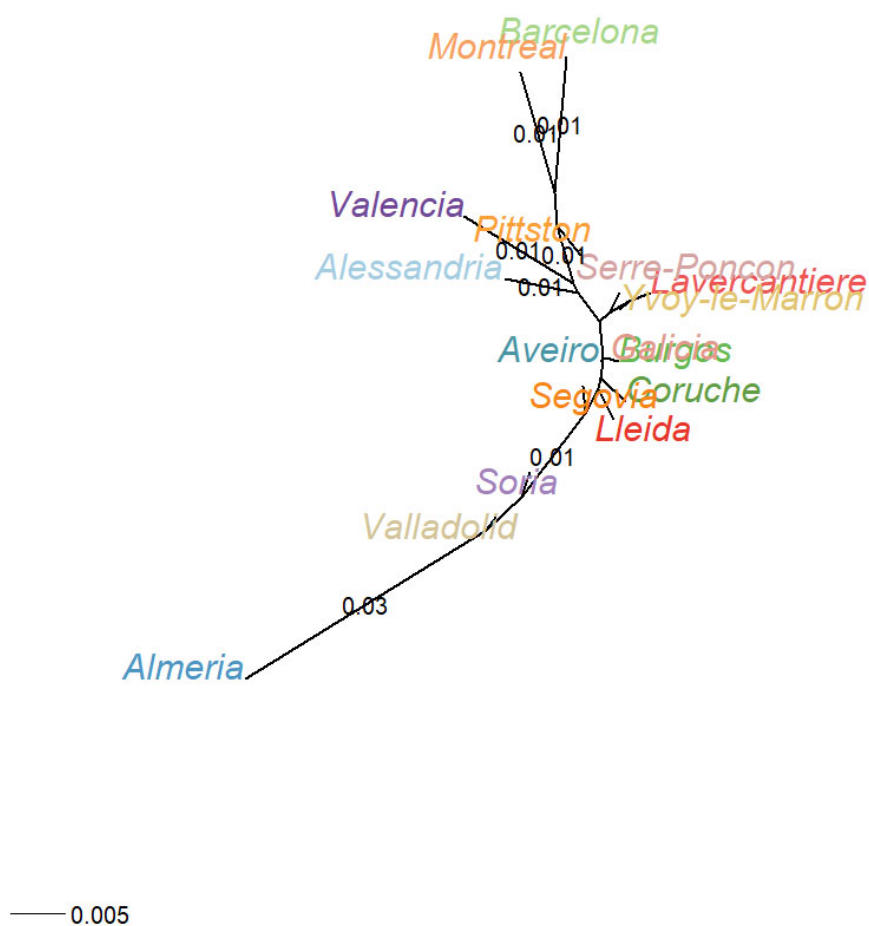
Figure S4. DeltaK plot for the full dataset. DeltaK values were calculated with STRUCTURE Harvester based on the Evanno method.
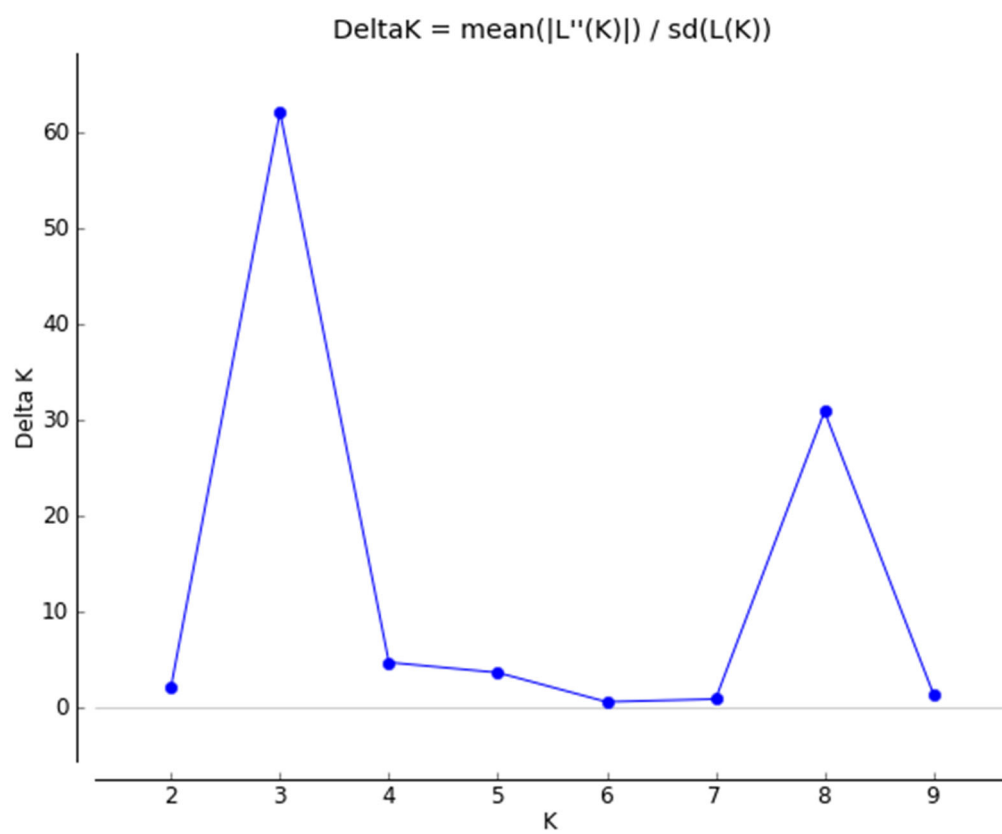

DeltaK = mean(|L''(K)|) / sd(L(K))

Figure S5. Geographical distribution of the genetic clusters identified using STRUCTURE for *Leptoglossus occidentalis* for (A) K=2, best K determined by the Evanno method, and (B) K3. The populations from North East America (E. America), Italy, France, and Barcelona and Valencia in Spain were incorporated to the dataset from Lesieur et al. (2019).