**Supplementary material**

**Materials and methods**

**Microsatellite PCR**

**F22**: forward primer was labelled with TAMRA; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP, GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 2 min, 35 cycles of 30 sec at 95° C, 30 sec at 47° C, 30 sec at 72° C and a final extension at 72° C for 15 min.

**9H**: forward primer was labelled with 6-FAM; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP, GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 2 min, 35 cycles of 30 sec at 95° C, 30 sec at 52° C, 30 sec at 72° C and a final extension at 72° C for 15 min.

**5F**: forward primer was labelled with 6-FAM; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP, GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 5 min, 35 cycles of 30 sec at 95° C, 30 sec at 50° C, 45 sec at 65° C and a final extension at 60° C for 15 min.

**Bv11**: forward primer was labelled with 6-FAM; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP, GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 5 min, 35 cycles of 30 sec at 95° C, 30 sec at 53° C, 45 sec at 65° C and a final extension at 60° C for 15 min.

**1A**: forward primer was labelled with TAMRA; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP,GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 2 min, 35 cycles of 30 sec at 95° C, 30 sec at 56° C, 30 sec at 72° C and a final extension at 72° C for 15 min.

**8A**: forward primer was labelled with HEX; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP,GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 2 min, 35 cycles of 30 sec at 95° C, 30 sec at 55° C, 30 sec at 72° C and a final extension at 72° C for 15 min.

**10F**: forward primer was labelled with 6-FAM; reaction mix (10 µl) contained 10-20 ng/µl of DNA, 0.25 µM of each primer, 2 mM MgCl2, 0.2 mM of each dNTP,GoTaq Flexi Buffer 1X and 0.5 U of GoTaq DNA Polymerase (Promega); PCR cycling included an initial denaturation at 95° C for 2 min, 35 cycles of 30 sec at 95° C, 30 sec at 58° C, 30 sec at 72° C and a final extension at 72° C for 15 min.

PCR products were assembled in multiplex post-PCR: one including 10F, 1A and Bv11 and another including 9H, 8A and F22; 5F was genotyped alone.

**Spatial thinning of the occurrence database**

To limit the effect of spatial clustering of the occurrences used to calibrate the different algorithms, we applied a spatial thinning in the geographical space to the original 361 occurrence points (Aiello-Lammens et al. 2015). We used the R package spThin which requires the definition of a minimum distance used to randomly remove occurrence records that are closer than the same distance. To empirically determine the thinning distance, we generated 10.000 sets of 361 random points (same number as the available species’ occurrences) covering the calibration area (i.e., the area sampled by the occurrence points); for each of the 10.000 sets we calculated the mean distance between nearest neighbor points, and then we calculated the mean over all 10,000 sets of random points, corresponding to 11.277 meters. Using the same distance, we obtained five alternative datasets with 182 occurrences (each distant at least 11.277 meters from the closest one) used for model calibration and 179 occurrences used for model evaluation.