established (Patoka et al. 2016b). The target area was defined as the territory of Hungary containing 14 climatic stations from the database of the WorldClim project (Hijmans et al. 2005). Where the climate match between the source area and the climatic station in the target area reached a score of ≥ 7.0, this was interpreted as there is no environmental barrier to survival (Kalous et al. 2015).

Risk assessment

To evaluate the invasive potential of decapod crustaceans pet-traded in Hungary, we used the Freshwater Invertebrate Invasiveness Scoring Kit produced by the UK Centre for Environment, Fisheries & Aquaculture Science (FI-ISK, v.1.19, Tricarico et al. 2010). Based on the FI-ISK score, each evaluated species was subsequently classified as (i) low-risk (score <1), (ii) medium-risk (score ≥1 but <16), or (iii) high-risk (score ≥16) from a Hungarian perspective.

Field sampling

Selected localities were sampled for potential occurrence of pet-traded decapods from January 2015 to March 2017. It covered a range of both thermal localities (warm-water ponds and their outflows, sometimes connected with thermal spas; n = 11) and those possessing regular temperature conditions (n = 17) in the Danube river, its side arms and tributaries. Since then, several new populations of exotic aquatic species and potential habitats were identified (Takács et al. 2017, Weiperth et al. 2015, 2016). We sampled 1 km long section of each selected waterbody using five baited traps set every two weeks from spring to autumn. Thermal localities were additionally monitored during the winter. The traps were exposed and checked for two consecutive days. The morphological identification of captured crayfish followed Holthuis (1949) and Souty-Grosset et al. (2006).

Genetic analysis

Due to confusion in the taxonomy of some *Cherax* species (see Austin 1996, Bláha et al. 2016), we included DNA analysis in our study. The importance of DNA identification has been previously highlighted for several non-native crayfish species (Filipová et al. 2011).

The morphological identification of each captured specimen was confirmed by a polymerase chain reaction (PCR) of a selected gene (mitochondrial cytochrome oxidase subunit I – COI), utilizing universal primer pair LCO1490 (5′-GGTCAACAAATCATAAAGATATTGG-3′) and HCO2198 (5′-TAAACTTCAGGGTGACCAAAAAATCA-3′) (Folmer et al. 1994). The