SHORT NOTE **The Herpetological Bulletin 146, 2018: 32-33**

The origin of common wall lizards (*Podarcis muralis*) in Wales

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Common wall lizards (*Podarcis muralis*) are not native to Britain, but the species has been repeatedly introduced (Michaelides et al., 2013). A genetic study of 23 populations, which represents the large majority of extant populations, revealed at least nine primary introductions from France and Italy (Michaelides et al., 2015). The remaining populations are more likely to be translocations of animals from already establish non-native populations or repeated introductions from the same captive stock. All except for one of the known wall lizard populations in Britain are found in England. The sole Welsh population exists on a private estate on Gower peninsula, and is of unknown origin.

The Welsh population was not included in the original study of wall lizard origins in Britain due to access restriction. Recently, lizards have been encountered outside of the estate. We took opportunity of this to sequence a region of the cytochrome b (cyt-b) gene in the mitochondrial genome of two adult individuals. A male and a female (Fig. 1) were captured and the outer tip (ca 1 cm) of the tails was removed by gently squeezing with a pair of tweezers. DNA was extracted and approximately a 700 base pair (bp) region of the cyt-b gene was amplified using the same protocol as in our previous work (Michaelides et al., 2015; Michaelides et al., 2013). The two sequences were corrected by eye, aligned and trimmed to a uniform length of 655 bp in GENEIOUS R8.1.9 (Kearse et al., 2012). We constructed a parsimonious phylogenetic network using a median-joining algorithm in NETWORK V.4.6.1.1 (Bandelt et al., 1999) and with an extensive coverage of mitochondrial haplotypes (see Michaelides et al., 2015), we could assign the genetic affinity of the population to other non-native and native populations. New sequences used in this study were submitted to GenBank under the accession numbers MK124973-MK124976.

The two individuals from Wales shared the same haplotype (WALES1). The haplotype network revealed that the Welsh haplotype belongs to the Romagna clade in the native range and is identical to the ROM1 haplotype (Fig. 1). Although the Romagna clade occurs in at least

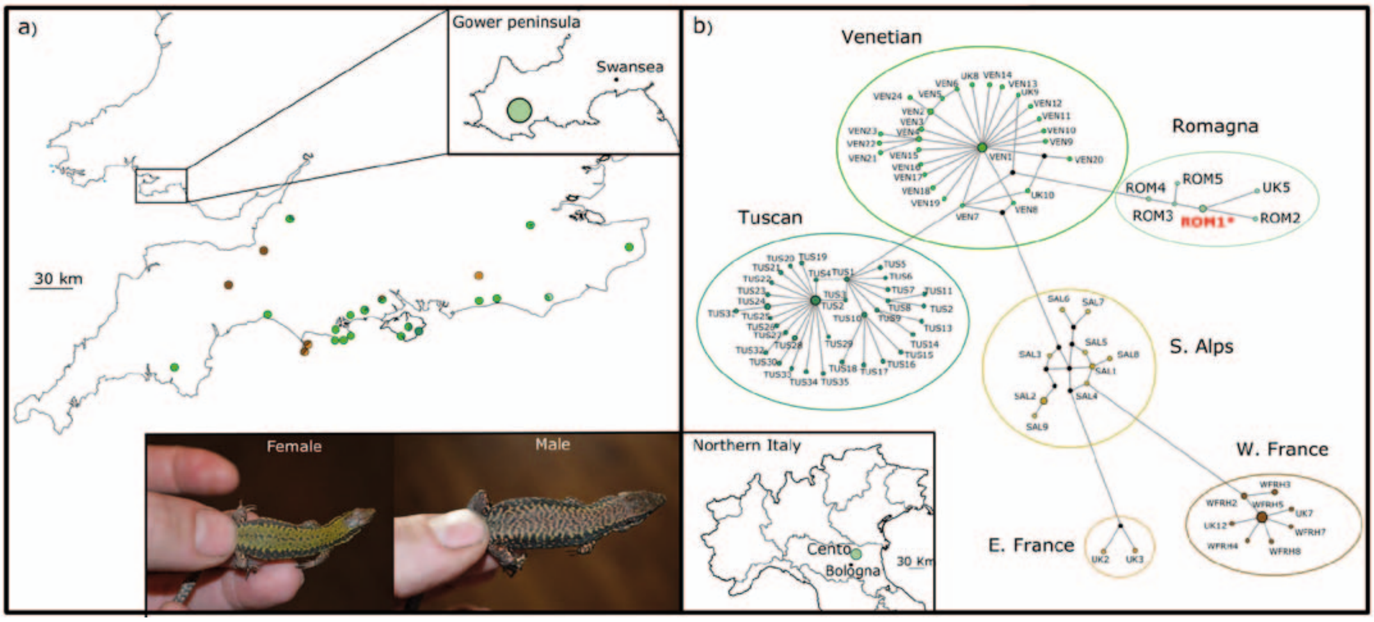

Figure 1. (A) Distribution of non-native populations of *P. muralis* in southern England and the sole Welsh population on Gower peninsula with coloration corresponding to mtDNA lineage origin (see Michaelides et al. 2013 for details). Photographs of the two adults (male and female) used in this study. **(B)** Median-joining network of mitochondrial haplotypes forming six haplogroups of native-range lineages (adapted from Michaelides et al., 2015, with three additional haplotypes; ROM3-ROM5, GenBank accession numbers MK124973, MK124974, MK124976). The haplotype found in Wales belongs to the Romagna lineage and is identical to ROM1 (marked in red) that is found in animals from Cento, northern Italy.

two populations in England, the Welsh haplotype has not been encountered in non-native populations in England (Michaelides et al., 2013; Fig. 1a). This suggests that the Gower population represents a primary introduction. The likely geographic origin is near Cento, Italy, close to the Bologna - Modena - Ferrara region, not very distant from many of the other Italian source populations (Michaelides et al., 2013; Michaelides et al., 2015). The persistence of lizards from substantially warmer climate on the Gower peninsula is further evidence of the highly adaptable nature of common wall lizards (While et al., 2015).

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Accepted: 7 November 2018