

Short Note

Exploring the speciation continuum of slow worms: Location and extent of the *Anguis fragilis/veronensis* hybrid zone in southeastern France

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Supplementary material

Table S1. Information on the sequence markers examined in this study. Only *ND2*, *PRLR* and *HA1* were polymorphic and could be successfully genotyped in our target lineages.

Gene	Product	Primers (5'–3')	Source
<i>ND2</i>	1500bp	H5934: AGR GTG CCA ATG TCT TTG TGR TT	1
		L4437n: AAG CTA TTG GGC CCA TACC	2
<i>PRLR</i>	550bp	PRLR_F1: GAC ARY GAR GAC CAG CAA CTR ATG CC	3
		PRLR_F3 GAC YTT GTG RAC TTC YAC RTA ATC CAT	3
<i>HA1</i>	1000bp	HA1_E3F: GCC TGA AGA AGA ACC ATG AA	4
		HA1_E5R : CCT CCC TGT TTA GCT CTT CC	4
<i>C-mos</i>	none	CMOS_S77: CAT GGA CTG GGA TCA GTT ATG	5
		CMOS_S78: CCT TGG GTG TGA TTT TCT CAC CT	5
<i>RAG1</i>	none	RAG1_R13: TCT GAA TGG AAA TTC AAG CTG TT	6
		RAG1_R18: GAT GC T GCC TCG GTC GGC CAC CTT T	6

¹Macey et al. (1997); ²Gvoždik et al. (2010); ³Townsend et al. (2008); ⁴Adapted from Dalla Valle et al. (2011); ⁵Lawson et al. (2008); ⁶Groth and Barrowclough (1999).

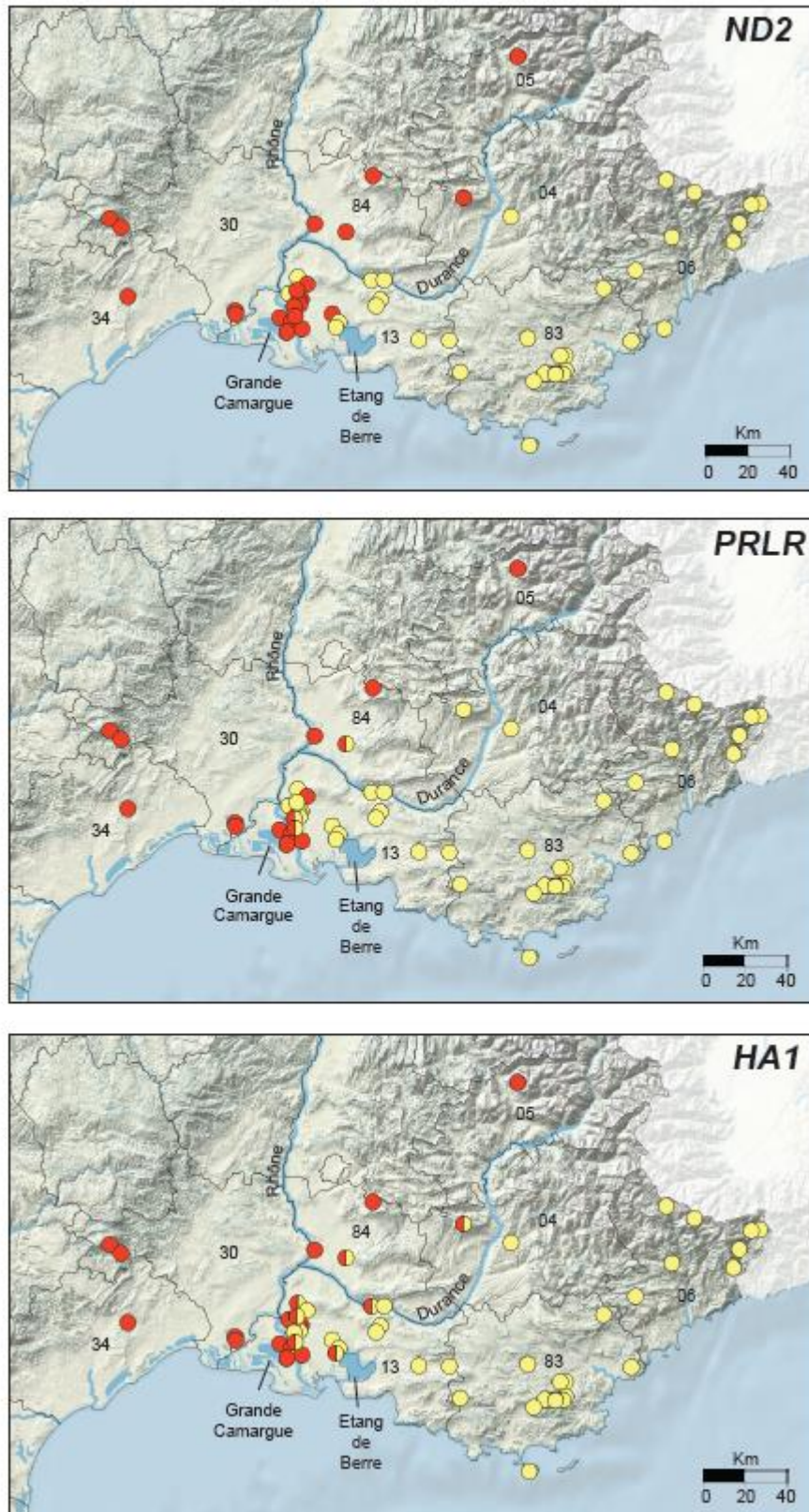


Figure S1. Proportion of species-specific haplotypes in each locality for each marker separately. Red: *Anguis fragilis*; yellow: *Anguis veronensis*.