

**MV (Massive)** *Pelophylax bergeri*

<b>Date assessed</b>	2021-10-18
<b>Year published</b>	2021
<b>Eicat category</b>	MV (Massive)
<b>Justification for EICAT assessment</b>	Impact through hybridisation between <i>P. bergeri</i> and <i>P. lessonae</i> is massive, hybrids have completely replaced the native <i>P. lessonae</i> (Dubey et al. 2014, Dufresnes et al. 2007, Dufresnes and Dubey 2020). The deep introgression has collapsed the genetic structure of the native <i>Pelophylax</i> populations (Dubey et al. 2014).
<b>Confidence rating</b>	High
<b>Mechanism(s) of maximum impact</b>	Hybridisation
<b>Countries of most severe impact</b>	Switzerland; France
<b>Description of impact</b>	Hybridisation - genetic introgression between <i>Pelophylax bergeri</i> and the native species <i>P. lessonae</i> and <i>P. esculentus</i> has led to the replacement of most pure native populations.
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<b>Reviewers</b>	EICAT authority
<b>Recommended citation</b>	F. André de Villiers. (2026). <i>Pelophylax bergeri</i> . <a href="#">IUCN Environmental Impact Classification for Alien Taxa (EICAT)</a> .

