

Publication

Molecular confirmation of a *Fasciola gigantica* x *Fasciola hepatica* hybrid in a Chadian bovine**JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 4597195**Author(s)** Evack, Jennifer Giovanoli; Schmidt, Remo S.; Boltryk, Sylwia D.; Voss, Till S.; Batil, Annour A.; Ngandolo, Bongo N.; Greter, Helena; Utzinger, Jürg; Zinsstag, Jakob; Balmer, Oliver**Author(s) at UniBasel** [Giovanoli Evack, Jennifer](#) ; [Schmid, Reto](#) ; [Voss, Till](#) ; [Greter, Helena](#) ; [Utzinger, Jürg](#) ; [Zinsstag, Jakob](#) ; [Balmer, Oliver](#) ;**Year** 2020**Title** Molecular confirmation of a *Fasciola gigantica* x *Fasciola hepatica* hybrid in a Chadian bovine**Journal** Journal of parasitology : official organ of the American Society of Parasitologists**Volume** 106**Number** 2**Pages / Article-Number** 316-322**Keywords** *Fasciola gigantica*; *Fasciola hepatica*; ITS1; ITS2; Cattle; Chad; Fascioliasis; Goats; Hybrid; Sheep

Fascioliasis is a zoonotic infection of humans and, more commonly, ruminants. It is caused by 2 liver fluke species, *Fasciola hepatica* and *Fasciola gigantica*, which differ in size. The traditional morphological methods used to distinguish the 2 species can be unreliable, particularly in the presence of hybrids between the 2 species. The development of advanced molecular methods has allowed for more definitive identification of *Fasciola* species, including their hybrids. Hybrids are of concern, as it is thought that they could acquire advantageous traits such as increased pathogenicity and host range. In 2013, we collected flukes from *Fasciola*-positive cattle, sheep, and goats slaughtered in 4 Chadian abattoirs. DNA from 27 flukes was extracted, amplified, and analyzed to identify species using the ITS1+2 locus. Twenty-six of the 27 flukes were identified as *F. gigantica*, while the remaining fluke showed heterozygosity at all variable sites that distinguish *F. hepatica* and *F. gigantica*. Cloning and sequencing of both alleles confirmed the presence of 1 *F. hepatica* and 1 *F. gigantica* allele. To our knowledge, this is the first unambiguous, molecular demonstration of the presence of such a hybrid in a bovine in sub-Saharan Africa.

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