Members of the genus *Hepatozoon* Miller 1908 are the most common intracellular protozoan parasites reported in snakes (Wozniak et al., 1994). Although the morphology of gamonts in reptile blood cells is generally very conserved (Telford, 1984), many species have been described, historically sometimes according to the reptile species infected. The recent development of PCR-based methods for amplifying the 18S rRNA of parasites directly from host blood and tissue samples has shed light on various aspects of the evolutionary history of *Hepatozoon* (Barta et al., 2012), and also on their distribution across vertebrate hosts in which *Hepatozoon* had not previously been reported, such as bats (Pinto et al., 2013) and caecilians (Harris et al., 2014). Furthermore, finding of similar genetic lineages in predators and prey, both in mammal (Allen et al., 2011; Maia et al., 2014) and squamate (Tomé et al., 2013; 2014) systems indicated the potential for trophic transmission. Identification of distinct haplotypes of 18S rRNA has also been used to support the description of new species of *Hepatozoon* from snakes (O’Dwyer et al., 2013; Han et al., 2015). On the other hand, other studies of *Hepatozoon* from snakes have indicated limited geographic patterns or congruency in host association (Haklová et al., 2014). It is clear therefore that data from different geographical regions and snake hosts are needed, both to improve knowledge on the distribution of these parasites, but also to evaluate diversity within the 18S rRNA gene, and in turn highlight its utility as a marker for describing new *Hepatozoon* species. In this study, we aim to detect *Hepatozoon* parasites from African rock pythons, *Python sebae* (Gmelin 1789), from a region of their range where few studies on snake parasites have been conducted, namely southern Mauritania, northern Senegal and western Mali. The diet of these snakes (Luiselli et al., 2001) is different from most snakes so far assessed for *Hepatozoon* prevalence such as *Natrix*, *Coronella* and *Malpolon* (Tomé et al. 2014). Thus, data from West Africa may provide additional information about trophic transmission of *Hepatozoon*. Finally, we then compare identified 18S rRNA haplotypes with published data to assess diversity within and between various snake hosts.

Twelve *P. sebae* were collected by hand during various periods of fieldwork from 2008-2014 (Figure 1). In each case a small tail-tissue sample was taken and stored in 96% ethanol, and animals were then released at the collection site. DNA was extracted using standard high salt methods (Sambrook et al., 1989). Hemogregarine-specific primers HepF300 and HepR900 (Ujvari et al., 2004) were used to target part of the 18S rRNA of potential parasites. PCR conditions consisted of 94°C for 30secs, 60°C for 30 secs and 72°C for 1 minute, with 35 cycles. Positive and negative controls were included, and positive PCR products were purified and sequenced by a commercial facility (Beckman-Coulter, UK). New sequences were deposited in GenBank; accession numbers KR653312 and KR653313.

Two of the twelve specimens gave positive PCR reactions, and in both cases obtained sequences were
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compared against published data from GenBank using the BLAST algorithm. Both sequences were 537 bp long, and were identical to each other. They were also identical to *Hepatozoon* sequences on GenBank, from a Saharan horned viper *Cerastes cerastes* Linnaeus 1758 (EF125058, unpublished), four isolates of *Hepatozoon chinensis* Han et al. 2015 from king ratsnakes, *Elaphe carinata* (Gunther 1864), from China (isolates 1, 5, 6 and 8, Han et al., 2015), from the sand racer *Psammophis schokari* (Forskal 1775) (KC696569, Tomé et al., 2013), and from the mangrove snake, *Boiga denrophila* (Boie 1827) from Thailand (KF524356, unpublished). A sequence from *Hepatozoon domergui* Landau et al. 1970, isolated from *Madagascarophis colubrinus* Schlegel 1837, from Madagascar, differed by a single nucleotide, as did other isolates of *H. chinensis* from king ratsnakes *E. carinata*.

Various phylogenetic assessments of *Hepatozoon* species from snakes have indicated that those from Africa and Madagascar and the Mediterranean region form a lineage, along with *Hepatozoon* recovered from small mammal hosts (Maia et al., 2014). The new sequences obtained in this study from *P. sebae* are identical to samples from *C. cerastes*, and *P. schokari*, and are therefore another member of this lineage, along with the newly described *H. chinensis* from king ratsnakes from China (Han et al., 2015). *Python sebae* can prey on larger mammals such as dogs and goats (Luiselli et al., 2001), but in general prey on small mammals, so the recovery of the *Hepatozoon* as members of this lineage is not unexpected. However, the finding of an identical haplotype in very different groups of snakes, and from as far apart as China, Thailand and West Africa does raise questions about the use of this marker in supporting new species diagnoses. A larger segment of the 18S rRNA gene can be obtained by using multiple primers, but the section amplified by the Hep primers is generally more variable, and estimates of phylogeny based on the longer region tend to be very similar or identical to those estimated from the shorter fragment (Maia et al., 2012). Furthermore, Haklová et al. (2014), using sequences from another region of the

Figure 1. Geographic location of the samples of *P. sebae* screened for *Hepatozoon* infection in this study.
18S rRNA gene, also reported identical haplotypes of *Hepatozoon* recovered from different snake species from geographically diverse regions and Sumrandee et al. (2015) report this for snakes from Thailand as well, with identical *Hepatozoon* in different snake hosts, however with some genetic differences between the *Hepatozoon* recovered from two different tick species infecting them. It may be that the 18S rRNA marker used in these studies is too conservative to distinguish between different *Hepatozoon* species and thus 18S rRNA gene sequences may not be useful in distinguishing between potentially different species of *Hepatozoon* parasitizing snakes, and that faster-evolving markers will be needed to support species descriptions.

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