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The ecology of primate retroviruses – An assessment of 12 years of retroviral studies in the Taï national park area, Côte d'Ivoire

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ABSTRACT

The existence and genetic make-up of most primate retroviruses was revealed by studies of bushmeat and fecal samples from unhabituated primate communities. For these, detailed data on intra- and within-species contact rates are generally missing, which makes identification of factors influencing transmission a challenging task. Here we present an assessment of 12 years of research on primate retroviruses in the Taï National Park area, Côte d'Ivoire. We discuss insights gained into the prevalence, within- and cross-species transmission of primate retroviruses (including towards local human populations) and the importance of virus–host interactions in determining cross-species transmission risk. Finally we discuss how retroviruses ecology and evolution may change in a shifting environment and identify avenues for future research.

Contents

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Introduction

The close evolutionary relationship and similar physiology of non-human primates (hereafter NHP) and humans make NHP a likely source for the zoonotic transmission of viruses (reviewed in: Calvignac-Spencer et al., 2012b; Gessain et al., 2013; Gillespie et al., 2008; Wolfe et al., 1998). NHP retroviruses are arguably the best illustration of this prediction (e.g., simian origins of human immunodeficiency viruses HIV-1 and 2; reviewed in: Sharp and Hahn, 2011) and among the best-characterized NHP viruses. However, despite decades of research, behavioral and ecological factors affecting within- and between-species transmission of retroviruses in NHP remain poorly understood. A full understanding of the ecology of primate retroviruses requires knowledge of the virus itself, the host–virus interface, and the host's ecology. This necessitates multidisciplinary research efforts that are only possible where primatology research projects have been run on a long-term basis in collaboration with veterinarians and molecular biologists.

Taï National Park in the Côte d'Ivoire hosts one of the world's best-studied wild primate populations (Fig. 1). Studies on the chimpanzees and monkeys of Taï National Park were initiated in 1979 and 1989 respectively (Boesch and Achermann, 2000; McGraw et al., 2007). Taï National Park harbors 11 different NHP species, many of which regularly interact (McGraw et al., 2007). For example, many spend much of their time in polyspecific associations (e.g. red colobus – *Piliocolobus badius badius*, sooty mangabeys – *Cercocebus atys*, and Diana monkeys – *Cercopithecus diana*; McGraw and Bshary, 2002; Noë and Bshary, 1997). Hunter–prey relationships also exist in this community as chimpanzees (*Pan troglodytes verus*) regularly hunt other NHP (Fig. 2; Boesch and Boesch, 1989). Local human populations in the area also interact with the primate community, mostly through hunting of NHP (Fig. 2; Refisch and Koné, 2005). This complex set of interactions offers ample opportunities for microorganism transmission: through biting, grooming, mating and hunting-related activities such as butchering of carcasses and meat consumption.

In 2002, a perennial veterinary program began its association with the primatology research program. The latter has provided data and access to three groups of well-habituated chimpanzees (Boesch and Achermann, 2000) and well-habituated monkey species (McGraw et al., 2007). This has helped make the primate community in Taï National Park one of the rare instances where thorough data are generated regarding primate ecology and the microorganisms that infect these same individuals (Calvignac-Spencer et al., 2012b). This is particularly true for retroviruses, whose diversity and transmission patterns have been scrutinized since the very beginning of the veterinary studies of this community (although with some bias). These insights are augmented by human health projects that have spawned in the area around Taï National Park (Ayouba et al., 2013; Calvignac-Spencer et al., 2012a) allowing the study of zoonotic retroviral transmission stemming from this primate community. Here we review 12 years of research on primate retroviruses in the Taï National Park area and highlight how the long-term primatology research program (Boesch and Achermann, 2000; McGraw et al., 2007) allowed virological results to be embedded in a relevant ecological context. We focus on results relevant to the ecology of the three retroviruses that have been extensively studied in Taï National Park; namely the simian immunodeficiency viruses (SIV) and their human counterparts (HIV), the simian T-cell leukemia viruses type 1 (STLV-1) and their human counterparts (HTLV-1), and the simian foamy viruses (SFV). We summarize insights gained into their prevalence, virus–host interactions, within- and between-species transmission, within and between NHP species and into the surrounding human population. Finally, we discuss the likely impact of shifting primate community dynamics in the framework of ongoing "natural" and anthropogenic changes.

Prevalence and diversity of retroviruses in Taï National Park NHP

To date in the NHP of Taï National Park, SIV has been detected in sooty mangabeys (SIVsmm), western red colobus (SIVwrc) and olive colobus (SIVolc). The prevalence of SIVsmm in sooty mangabeys is high (apparent prevalence=59% (95% CI=0.35–0.88); Santiago et al., 2005). Similarly, the prevalence of SIVwrc in the red colobus population is reported to be one of the highest observed in wild NHP (apparent prevelance=82% (95% CI=0.66–0.98); Leendertz et al., 2010), whereas SIVolc has so far only been reported in a single olive colobus monkey (Courgnaud et al., 2003). Strict host specificity was observed for the SIV strains found in these NHP (Courgnaud et al., 2003; Leendertz et al., 2010; Liégeois et al., 2009). A collection of fecal samples obtained from

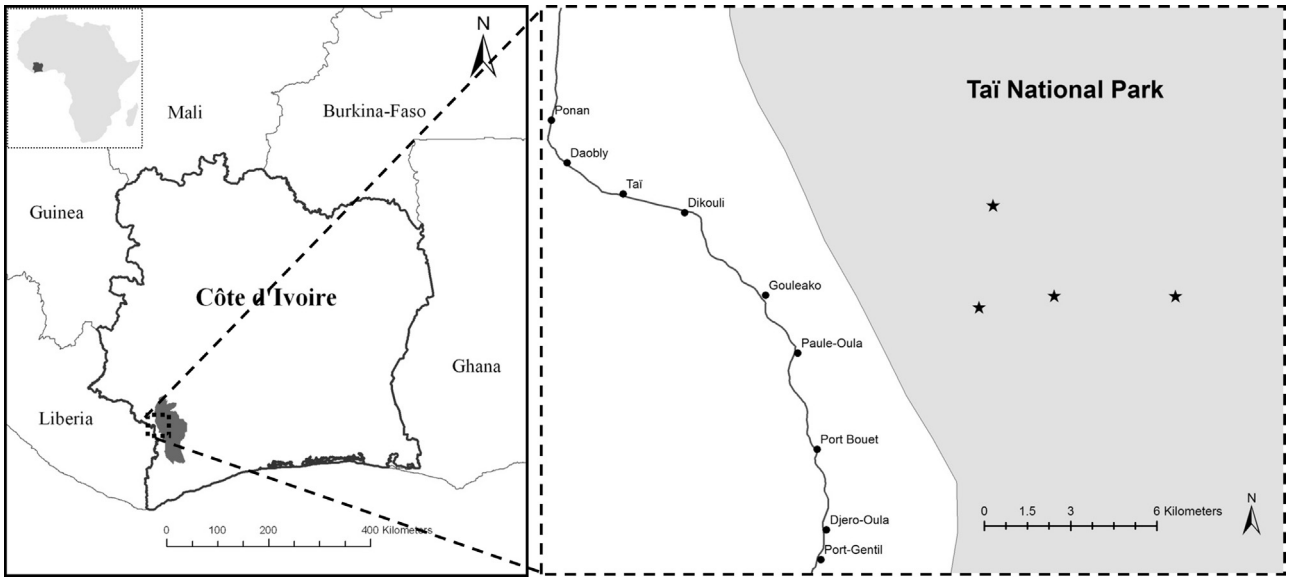

Fig. 1. Location of the main study area. (a) Location of the Taï National Park in Africa and Côte d'Ivoire; (b) close-up of the research area. Stars indicate primatology research camps. This figure was provided by Genevieve Campbell and Hjalmar Kühl and is derived from Campbell et al. (2011).