

The chimpanzees of the Taï Forest as models for hominine microorganism ecology and evolution

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Photo 22: A group of two males of one females eating at the same time from a large piece of a red colobus monkey. c/o Liran Samuni

Anecdote

Meeting the chimpanzees of the Taï Forest for the first time, it was striking that researchers have been following many of these individuals for their entire lives. These studies have provided insights into many facets of their lives and for the last 15 years, this has included extensive studies of their health, accompanied by continuous sampling of faeces and necropsies. While the deadly diseases that have devastated these wild populations were a motivator for every author of this chapter in getting involved in work with these communities (see Chapter 23), these chimpanzees, like all humans, are home to entire ecosystems of innumerable microorganisms (i.e. microbial communities) that make up the whole individual. The Taï chimpanzees now provide one of the best insights into the microbial communities of our closest

living relatives. The long-term monitoring of these populations now allows us to go back and look at an individual's microorganisms through time, to examine how these populations are shared and acquired, and provides insights into how our own microorganism communities have changed with the advent of agriculture, cities and international travel. Here, we examine how the chimpanzees of Taï allow us to explore how our viral and bacterial communities may have looked in the past and the potential emergence of these microorganisms into human populations.

Jan Gogarten

22.1 Introduction

Every mammal represents a complex ecosystem, consisting of trillions of microorganisms that exist on and in this host. These microbial communities have been estimated to make up the majority of the cells and most of the unique genes found in a host, although estimates are certainly not exact (Sender et al., 2016). While much of the study of these microbial communities has focused on bacteria and viruses of the host because of their direct impact on the host and technological constraints (and we will focus on viruses and bacteria here), these microbial communities also include bacteriophages (viruses of bacteria), viruses of viruses, fungi, archaea and microbial eukaryotes, which certainly warrant further study and may also play a major role in maintaining host health (Fierer, 2017). Beyond the very clear instances of bacteria or viruses impacting a host's health as pathogens (e.g. see Chapter 23), these microbial communities have also been shown to impact a broad

range of processes including a host's ability to access nutrients (Tremaroli et al., 2012), health via pathogen exclusion and immune system priming (Hooper et al., 2012) and even behaviour and scent (Ezenwa et al., 2014). Interestingly, these host–microbial community ecosystems are short-lived (with an absolute upper bound being a host's lifetime) and little is known about how these microbial communities of individual hosts assemble and are acquired by the next generation, particularly in the ecological and social contexts in which they evolved.

Most present-day humans seem to have depauperate gut microbiomes when compared to great apes and other non-human primates (NHP) (Moeller et al., 2014). Studies of wild NHP, particularly great apes, might thus provide important insights into the ancestral human gut microbiome, which was most certainly heavily modified by changes occurring recently in our history, such as the development of agriculture and the use of antibiotics (Gillings et al., 2015). For example, the shift to carnivory may have significantly changed the composition of the human microbiome (Moeller et al., 2014), while the seaweed-rich diet of Japanese populations has been accompanied by horizontal gene transfer from extrinsic bacteria to their gut microbes that allow these populations to digest recalcitrant polysaccharides in their food (Hehemann et al., 2012; Thomas et al., 2012).

Similarly, homogenization of the global diet, a highly connected world and more sterile built environments seem to be likely culprits for a reduction of microbial community complexity in modern humans (Logan et al., 2015). Critical for such comparisons, though, are insights into the ecological processes that drove the evolution of the human microbial communities during most of our species' lifetime; that is, when humans were exclusively tropical hunter-gatherers living in sympatry with diverse NHP communities. Two approaches allow us to explore this question: first, the study of present-day hunter-gatherer societies, which suggests that most modern human populations may have lost much of their microbial diversity (Schnorr et al., 2014;

Clemente et al., 2015), although even these hunter-gatherer societies have also undergone major societal and environmental changes; and, second, comparative analyses of our closest relatives in their natural environment.

An understanding of the microbial communities of our closest relatives is not possible by studying primates in captivity, where they have significantly altered bacterial gut microbiomes (Amato et al., 2013) that appear to become significantly more similar to that of humans (Clayton et al., 2016). Antibiotic resistance for those antibiotics used heavily in the surrounding human communities and their livestock were found in wild primate gut bacteria (Goldberg et al., 2007). Similarly, several human pathogens have been detected in wild NHP populations, including in the Tai chimpanzees (see Chapter 23; Chi et al., 2007; Kaur et al., 2008; Köndgen et al., 2008; Palacios et al., 2011; Patrono et al., 2018), suggesting humans may have already influenced wild primate microbial communities in ways that obscure ecological and evolutionary signals, highlighting the time sensitivity of this research. Most NHP also live in highly diverse tropical ecosystems, where leaves from an individual tree can be host to more than 400 bacterial taxa (Kembel et al., 2014). Disturbances to these complex ecological habitats can additionally influence gut microbiomes of NHP (Amato et al., 2013; Barelli et al., 2015), highlighting the importance of protected areas like Tai National Park for such studies.

While the microbial communities found on a host do not appear to be strictly inherited from a host's parents, there are indications that some microorganisms have managed to coevolve with their primate hosts over longer evolutionary timescales. For example, a large number of bacterial lineages appear to have codiversified with hominines over the last 6–12 million years, suggesting these bacteria are somehow transmitted between the generations (Moeller et al., 2016a). Similarly, Merkel cell polyomaviruses exhibit strong host-specificity and a number of host and virus divergence events are synchronous, suggesting codivergence is the dominant process at play in the

evolution of these viruses (Madinda et al., 2016). The cospeciation of hosts and their microbial communities can be a sign that there is strong vertical inheritance of a microbe from parents to offspring. On the other hand, anatomy, physiology and life-history traits all covary with host phylogenies, and individuals in the same species tend to have similar genetic and behavioural characteristics. This could allow for codivergence of microbes and hosts by either selectively exposing hosts to certain microbes, or only creating an environment that is hospitable for certain microbes.

For example, milk oligosaccharides in breast milk are thought to foster the growth of certain species of bacteria and every species will produce their own mix of compounds (Ventura et al., 2012), or a host's diet might create compounds that are only exploitable by certain types of bacteria making host switching less likely (Muegge et al., 2011). Similarly, host receptors or resistance factors that are constrained by a host's genetics might allow a host to avoid certain viruses but might be exploitable by others (Ng et al., 2015). Thus, when a host is exposed to multiple types of bacteria or viruses (i.e. virtually every day of their life), filtering takes place, only allowing certain microbes to persist in the host; if closely related hosts filter for and share similar microbes, this could create a pattern similar to codivergence. Another possibility is that individuals may selectively transmit their microbial communities to members of the same species through horizontal transmission of microbes from conspecifics, particularly if animals live in social groups.

It appears that primates are largely born microorganism-free and that they are either seeded with bacteria and viruses in the placenta before birth or are exposed to their first microorganisms during a vaginal birth (Dominguez-Bello et al., 2010; Gritz & Bhandari, 2015). Increasingly, it appears that the importance of this early vertical inheritance of microbes in shaping the adult microbial community is limited and that horizontal transmission of microorganism from family members and the environment subsequently plays a major role in shaping the adult microbial community (Korpela et al., 2018). Primates represent a particularly social order, with 75% of

primate genera forming year-round associations, in contrast with approximately 33% of non-primate mammal genera (van Schaik et al., 1997).

These close social communities might be expected to present opportunities for transmission of the gut microbiome and create the potential for a 'pan-microbiome' shared by a social group. This could be transmitted over long evolutionary timescales allowing for the maintenance of differences observed between host species (Moeller et al., 2016b) and enhancing the community stability of microbial communities within groups and individuals via metacommunity dispersal dynamics (Leibold et al., 2004). This appears to be the case in a number of non-human primate species, including baboons, where individuals in the same social group were observed to have more similar microbiomes and close social partners had more similar bacterial gut microbiomes (Tung et al., 2015). Such processes might be especially important for chimpanzees, where groups appear to have remained as cohesive units for hundreds to at least two thousand years (Langergraber et al., 2014).

While this transmission within social groups might be important, the close evolutionary relationship of primates (including humans) means they are physiologically, immunologically and behaviourally similar, suggesting that cross-primate microbe transmission might be relatively easy. As many primates live in diverse communities, this could lead to homogenization of the microbial communities within a non-human primate community. A prime example of this is that NHP are often sources for the zoonotic transmission of many microorganisms (reviewed in Wolfe et al., 1998; Gillespie et al., 2008; Calvignac-Spencer et al., 2012b; Gessain et al., 2013). Retroviruses are a particularly poignant excellent example of this, with NHP having given rise to the HIV-1 pandemic and the HIV-2 epidemic in West Africa. Unlike modern humans, who largely live isolated from their closest primate relatives, chimpanzees and humans as hunter-gatherers lived in complex ecosystems with many NHP in proximity and interacted with them through the sharing of food and water sources as well as hunting. Understanding

the importance of these interactions and the ecology and evolution of wild great ape microbial communities is an exciting area of future research. Here, we review 15 years of studies on the microbial communities of the chimpanzees of Taï National Park, Côte d'Ivoire, found in one of the world's most extensively studied wild great ape populations.

Studies on the chimpanzees and monkeys of Taï National Park were initiated in 1979 and 1989 respectively and have been ongoing ever since (Boesch & Boesch-Achermann, 2000; McGraw et al., 2007). The NHP community in Taï consists of nine diurnal species; one omnivorous great ape species, the chimpanzee, and eight monkey species, namely three folivorous colobine species (olive colobus – *Procolobus verus*; western red colobus – *Piliocolobus badius*; king colobus – *Colobus polykomos*) and five omnivorous cercopithecin species (sooty mangabey – *Cercocebus atys atys*; Diana monkey – *Cercopithecus diana*; Campbell's mona monkey – *Cercopithecus campbelli*; lesser spot-nosed monkey – *Cercopithecus petaurista*; and greater spot-nosed monkey – *Cercopithecus nictitans*). In Taï, there are three habituated social groups (North, South, East) of chimpanzees with diverse group compositions (see Chapter 3). The chimpanzees at Taï hunt some of the syntopic monkeys, exhibiting a strong preference for red colobus monkeys. In fact, chimpanzees captured 215 red colobus over a 12-year period of observation and during this same time period, only six olive colobus and a single sooty mangabey were observed being captured and eaten (Boesch & Boesch-Achermann, 2000). This research has suggested that over an individual chimpanzee's lifetime, they will be exposed to several hundreds of kilograms of NHP meat, the majority of which will come from red colobus (Leendertz et al., 2011b).

This diverse backdrop and research programme provide a unique opportunity to examine the microbial communities of the chimpanzees, to study the processes driving microorganism transmission within and between social groups of chimpanzees and for understanding the importance of between-species transmission in shaping chimpanzee microbial

communities and the importance of host genetics in constraining transmission of certain microbes. These studies also ultimately inform the role of this NHP community in exposing humans to these microbes. Below, we seek to review the evidence from Taï, though focus on two of the most well-studied communities of microbes found in the chimpanzees of Taï National Park (retroviruses and bacteria) and discuss key insights into the transmission of the microbes within and between groups of chimpanzees, between NHP and ultimately zoonotic transmission of these microbes to humans living around the national park.

22.2 The microbial communities of chimpanzees and other NHP in Taï National Park

In a recent study, we examined the gut bacterial microbiome composition of the nine diurnal, sympatric, wild, NHP species in the park (Gogarten et al., 2018). Briefly, 380 faecal samples were collected, mainly targeting the habituated groups of chimpanzees and a habituated group of sooty mangabeys, but also opportunistically collected from the seven unhabituated monkey species and a neighbouring group of mangabeys. To examine the stability of the chimpanzee bacterial gut microbiome, we collected repeated samples from individuals in the South ($N = 18$ individuals) and North Groups ($N = 11$ individuals), while a single sample was examined from 28 individuals in the East Group to allow for between-group comparisons. All chimpanzee samples were collected between March and July 2014, to reduce the impact of seasonal variation in the bacterial gut microbiome. To examine the bacterial gut microbiome, we looked at the 16S V4 hypervariable as a barcoding region to assign oligotypes present in any sample. We found a staggering 3818 oligotypes in the bacterial gut microbiomes of these NHP, and of these, 3738 could be assigned to a phylum, with most belonging to Firmicutes (2213) and Bacteroidetes (504) and fewer to Proteobacteria (325), Tenericutes (265), Cyanobacteria (98), Actinobacteria (85),

Verrucomicrobia (68) and Spirochaetes (56). In the chimpanzees, after rarefying the data, we found 1719 oligotypes, with most of these being quite rare (Figure 22.1). Highlighting how little is known about this community of bacteria, of the 3818 oligotypes detected in any NHP, only 1481 could be assigned to a previously described genus, suggesting much more work is needed to understand the functional capabilities of this community. The core bacterial gut microbiome, considered as oligotypes found in more than 80% of individuals of a NHP species, varied greatly between NHP species, although all had significant proportions of Firmicutes and Bacteroidetes. For chimpanzees, 89 taxa contributed to the core bacterial gut microbiome of the following phyla: 42 Firmicutes, 26 Bacteroidetes, six Actinobacteria, five Proteobacteria, three Verrucomicrobia, three Euryarchaeota, two Spirochaetes, one Tenericutes, and one Fibrobacteres. The different host species had distinct bacterial gut microbiomes, with the host

species being the strongest predictor of the bacterial gut microbiome that we tested for. An understanding of the underlying factors driving differences in core bacterial gut microbiome requires further study.

To date, the simian immunodeficiency virus (SIV) has been detected in sooty mangabeys, western red colobus and olive colobus, with a high prevalence in sooty mangabeys (Santiago et al., 2005) and red colobus (Leendertz et al., 2010). While other monkey species in the park were tested serologically and by PCR without a positive result, sampling sizes were relatively small, except for black and white colobus ($n = 27$ distinct individuals) and Diana monkeys ($n = 23$ distinct individuals), so SIVs present at low prevalence cannot be ruled out for most other species (Locatelli et al., 2011). Like other *Pan troglodytes verus* populations (Gao et al., 1999; Prince et al., 2002; Santiago et al., 2002), the chimpanzees of the Tai forest do not appear to be infected with SIV ($n = 32$, out of a total of 300 chimpanzees living in the park;

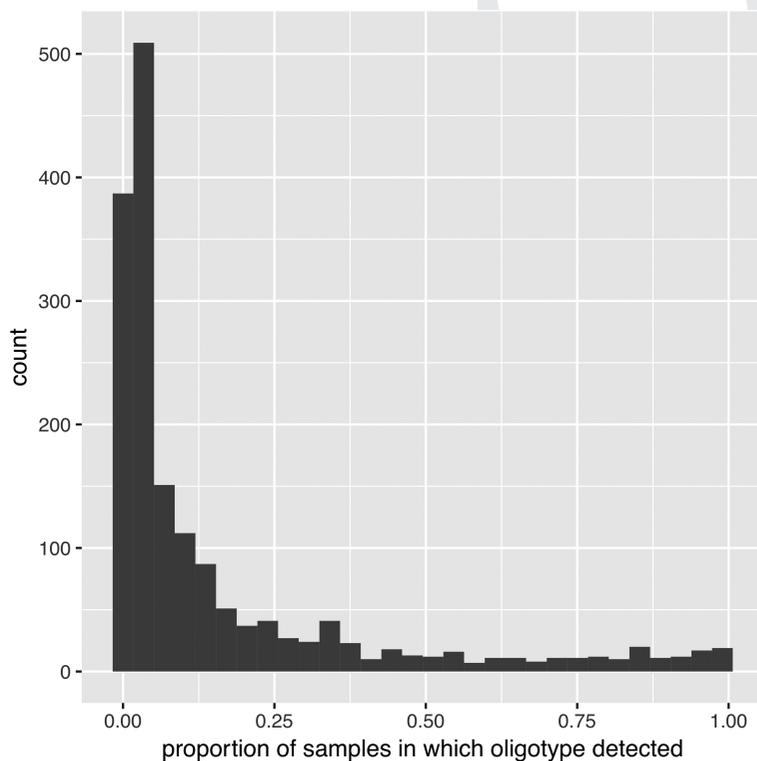


Figure 22.1 Histogram of the proportion of chimpanzee samples in which bacterial oligotypes were detected. The majority of oligotypes were detected in only a small proportion of the samples, while only a few were detected in most samples. (Created with the data available in Gogarten et al., 2018.)

Leendertz et al., 2011b). Simian T-lymphotropic virus type 1 (STLV-1) and simian foamy virus (SFV) were detected in sooty mangabeys, red colobus monkeys and chimpanzees (Leendertz et al., 2003, 2004, 2010; Traina-Dorge et al., 2005; Liu et al., 2008; Morozov et al., 2009; Junglen et al., 2010; Calvignac-Spencer et al., 2012a; Blasse et al., 2013). For sooty mangabeys and red colobus, which have been studied in depth in this ecosystem, there is evidence that they are infected at high prevalence by all three retroviruses, while chimpanzees on the other hand are only infected with STLV-1 and SFV (Gogarten et al., 2014a).

A number of infections seem to be well-established in this chimpanzee population, but are not focused on in more detail here: adenoviruses (Wevers et al., 2011), herpesviruses (Leendertz et al., 2009; Murthy et al., 2013; Anoh et al., 2017), parvovirus 4-like viruses (Adlhoch et al., 2012), polyomaviruses (Leendertz et al., 2011a; Scuda et al., 2013; Madinda et al., 2016; Salem et al., 2016), *Streptococcus oralis* (Denapaite et al., 2016),

Treponema pallidum (Gogarten et al., 2016), malaria parasites (Wu et al., 2018) and *Trypanosoma brucei* (Jirků et al., 2015). In addition, there appear to be occasional spillover events of viruses like Ebola from some other wildlife reservoir that can cause major mortality. However, these viruses induce such high mortality in these low-density host populations that they cannot become established. Similarly, human respiratory pathogens (e.g. human coronavirus OC43, metapneumovirus, human respiratory syncytial virus) occasionally spill over into these populations and cause mortality but quickly burn themselves out.

22.2.1 Within-species transmission

In a recent study of the bacterial gut microbiome of Tai chimpanzees (Gogarten et al., 2018), we found that samples from the same individual were more similar than samples from different individuals (Figures 22.2A,B), suggesting that there is some

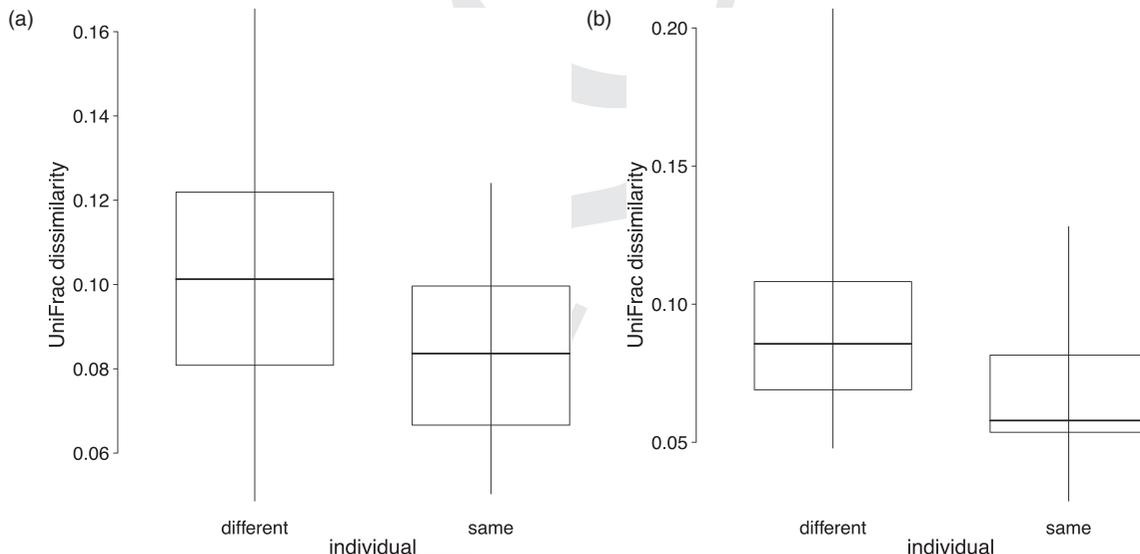


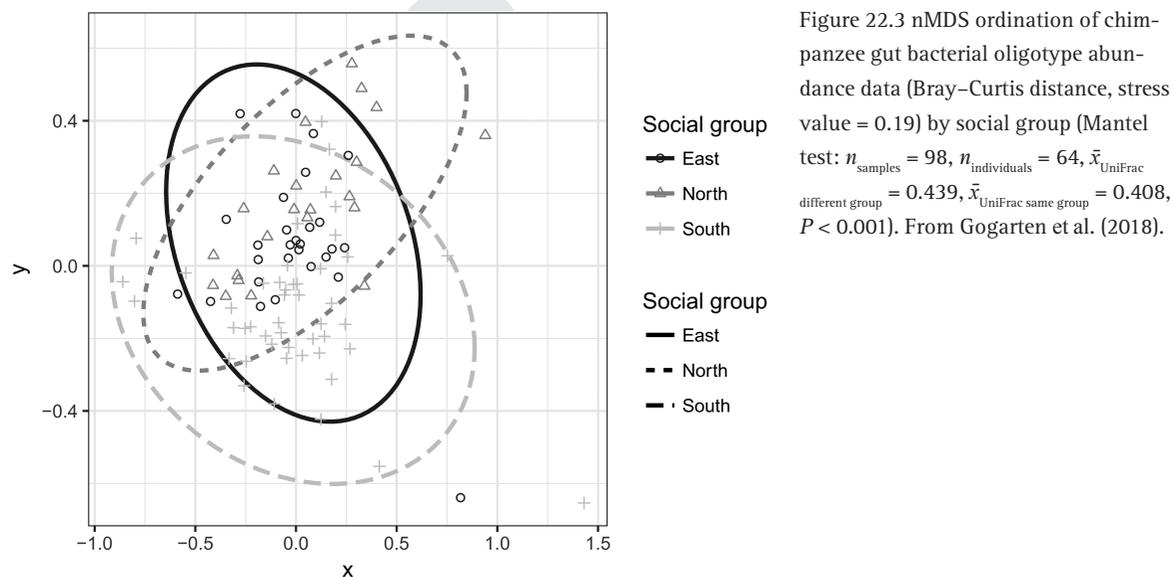
Figure 22.2 Comparison of the UniFrac dissimilarities between the bacterial gut microbiome of samples from chimpanzees in the South Group (A) and North Group (B) when stemming from the same or different individuals. The middle horizontal line represents the median while the rectangle shows the quartiles and the vertical line represents the 2.5% and 97.5% percentiles. UniFrac dissimilarities range from 0, indicating similar communities, to 1 very distinct communities. From Gogarten et al. (2018).

individual consistency to the chimpanzee bacterial microbiome. Healthy humans appear to exhibit a similar pattern of high intra-individual stability in their bacterial gut microbiomes (Faith et al., 2013), although for wild NHP, intra-individual stability in the bacterial gut microbiome appears to vary by species and habitat: yellow baboons (*Papio cynocephalus*) were reported to have extremely high turnover in the course of days (Ren et al., 2015), as was the case for rufous mouse lemurs (*Microcebus rufus*) (Aivelo et al., 2016), where western lowland gorillas (*Gorilla gorilla gorilla*) (Moeller et al., 2015), eastern chimpanzees (*Pan troglodytes schweinfurthii*) (Degnan et al., 2012) and black howler monkeys (*Alouatta pigra*) (Amato et al., 2013) also appear to have more stable gut bacterial microbiome communities.

When we compared samples from the three study groups, we found that samples were more similar within than between groups (Figure 22.3: between-group similarity in nMDS plots). We also looked at whether behaviours prior to the collection of faecal samples were predictors of the microbiome using behavioural data collected either 3 or 6 months prior to the first faecal sample being collected. Briefly, we examined this relationship between social

behaviours and chimpanzee bacterial microbiomes with Mantel tests using the community dissimilarity matrix and social behavioural matrices. We then estimated significance by determining the proportion of permutations that resulted in an absolute Spearman correlation greater than or equal to that of the original data. We only considered samples from adults and subadults as these individuals were targeted by our social behavioural sampling strategy. We measured the association as the 'time AB / (time A + time B - time AB)' and grooming as minutes/observation time. Surprisingly, there was no correlation between grooming or association matrices and dissimilarity in bacterial community composition (Taï Chimpanzee Project long-term data: see Chapter 9).

Sample sizes were quite small for this analysis and future studies are needed to confirm whether social relationships and proximity are truly involved in shaping the chimpanzee bacterial gut microbiome. More social eastern chimpanzees exhibit more diverse microbiomes (Moeller et al., 2016b) and in baboons, close social partners exhibited more similar bacterial gut microbiomes (Tung et al., 2015), suggesting that there may be some



impact of social behaviour on shaping the microbiome in chimpanzees as well and our methods have not yet allowed us to study this phenomenon. To date, no studies at Taï have tested whether mother–offspring pairs have more similar bacterial gut microbiomes, although this was observed in sooty mangabeys (Gogarten et al., 2018). This warrants further study as a mother's microbiome has been shown to have some long-term effect on their infant's gut bacterial microbiome structure in humans (Dominguez-Bello et al. 2010).

The modalities of transmission of retroviruses between Taï chimpanzees have been studied for SFV and STLV-1. STLV-1 appears to only rarely be transmitted from mothers to their offspring (only 2/17 infants and juveniles born from STLV-1-positive mothers tested positive thus far; Leendertz et al., 2004). It is difficult to determine the extent of horizontal transmission in the group, as many infections may be caused by infection from their prey (see below) and the slow evolutionary rate of STLV-1 has made it difficult to use sequence variation to investigate transmission patterns within chimpanzee social groups (Leendertz et al., 2004; Junglen et al., 2010). In contrast, SFV appears to be transmitted both from mother to infant (vertically) and between group mates (Blasse et al., 2013). Interestingly, individual chimpanzees appear to accumulate multiple infections with age, with the first transmission likely occurring between mother and offspring, but subsequent infections from group mates (likely during aggressive interactions), appearing to lead to individuals harbouring multiple infections (Blasse et al., 2013). To date, no studies have linked viral transmission to particular behavioural networks in these chimpanzee populations. This represents an exciting future area of research as viral phylogenies have been linked to contact networks and transmission history in humans, although mainly in rapidly evolving RNA viruses, which we have not detected as established in the chimpanzees of Taï (e.g. Ebola, HIV; Grabowski et al., 2014; WHO Ebola Response Team, 2014).

Recent research suggests that viral communities in a macaque species in another ecosystem are non-randomly assembled across a landscape (Anthony et al., 2015). This analysis was unable to determine the factors driving this pattern, but suggests well-designed studies may be able to identify the factors shaping variance in microorganism communities between NHP across a landscape. An intriguing hypothesis, not looked at in depth in Taï, is that microorganisms may facilitate or prevent infection by other microorganisms. Interestingly, all red colobus individuals in Taï (and Kibale National Park, Uganda) that tested positive for STLV-1 were coinfecting with either SIV or SFV or both (Goldberg et al., 2009; Leendertz et al., 2010), which may suggest such interactions might be occurring, although future research is needed to confirm this hypothesis (Alais et al., 2018).

22.2.2 Between-species transmission

In a recent study, we found that the branching order of host-species networks constructed using the composition of their gut bacterial microbiomes as characters was incongruent with known NHP phylogenetic relationships, with chimpanzees sister to their colobine prey (Gogarten et al., 2018). Interestingly, we also found that the chimpanzee bacterial gut microbiome was strongly phylogenetically overdispersed, in contrast to what was observed in the bacterial microbiomes of all monkeys at Taï, which seems to suggest a broader exposure of chimpanzees to the bacteria present in this ecosystem. This pattern could be the result of hunting and assimilation of the microbiome from their primate prey, although future studies including the generation of full genomes to understand bacterial gut microbiome transmission networks in more detail will be needed to fully understand the processes responsible for these patterns. For retroviruses, strict host specificity was observed for SIV strains found in the Taï monkey community (Courgnaud et al., 2003; Liégeois et al., 2009; Leendertz et al., 2010) and chimpanzees were not infected with SIV despite being exposed to hundreds of kilograms of infected red

colobus meat over their lifetime, suggesting that the strain circulating in red colobus is unable to infect chimpanzees (discussed in detail below). Similarly, SFV also seems to exhibit a pattern at Tai National Park that suggests codivergence between hosts and their viruses, as has been described more broadly across vertebrates (Han & Worobey, 2012; Leendertz et al., 2008; Morozov et al., 2009; Murray & Linial, 2006; Switzer et al., 2005), again suggesting that strains infecting red colobus are not readily able to cross the species boundary. In contrast, STLV-1 strains were not strictly species-specific, with STLV-1 strains infecting sooty mangabeys forming a distinct clade from those infecting red colobus and chimpanzees, which are interspersed and relatively homogenous (Calvignac-Spencer et al., 2012a), suggesting that there is interspecies transmission of this virus between chimpanzees and their red colobus prey. These results suggest that living in a diverse NHP community does expose chimpanzees to a number of microbes and at least results in transient infections of the new chimpanzee hosts. On the other hand, this exposure may sometimes have resulted in chimpanzees evolving resistance to other microbes, making these complex communities exciting areas of future research.

Zoonotic transmission refers to the movement of a microorganism from animals into humans. Once transmitted, only rarely will a microorganism become established in the human population, being spread continuously from human to human. Zoonotic transmission of SFV to humans has been documented in numerous studies, but the extent to which the virus is then able to transmit between humans remains an open question (Switzer et al., 2004, 2008; Wolfe et al., 2004; Betsem et al., 2011; Mouinga-Ondémé et al., 2012). While in the region surrounding Tai National Park no SFV infections have been detected in humans, serological evidence gives indications that there is exposure (M. Peeters, unpublished data; Ali et al., 1996). The human T-lymphotropic virus type 1 (HTLV-1) strains found in humans living in West Africa almost all belong to the subtype A, which is a strain that seems to be restricted to humans (i.e. no evidence for zoonotic

transmission). Interestingly, unlike in most of West Africa, in the villages around Tai National Park, of the 14 HTLV-1 strains identified in humans, six belonged to NHP STLV-1 strains. Surprisingly, these six strains were not all the same, but five were likely from sooty mangabeys, while one likely stemmed from a red colobus monkey, suggesting there were multiple spillover events from the NHP in Tai into the human population (Calvignac-Spencer et al., 2012a; Mossoun et al., 2017). Similarly, the SIV strain infecting sooty mangabeys has been transmitted to humans on multiple occasions and gave rise to the large HIV-2 epidemic (one of the two major species infecting humans: Santiago et al., 2005; Ayouba et al., 2013). The strains infecting red colobus and olive colobus monkeys have been found in chimpanzees but not in the human population. While the SIV strain infecting sooty mangabeys has repeatedly made the interspecies jump into humans, this strain is conspicuously absent from chimpanzees.

Several host mechanisms for SIV/HIV resistance have been described, including variation in host receptors (e.g. CCR5; Samson et al., 1996) and restriction factors (e.g. APOBEC3 G, TRIM5a, tetherin, reviewed in Malim & Beniasz, 2012). SIV/HIV viruses also appear to have developed mechanisms for evading this resistance, with several antiviral host restriction factors now described (e.g. Vif, Vpr, Vpu, Nef, reviewed in Kirchhoff, 2010). One reason that red colobus SIV strains may not infect Tai National Park chimpanzees is the interaction of host APOBEC3 G and the lentiviral viral integration factor (Vif). APOBEC3 G is an intracellular cytidine deaminase that can restrict retroviruses survival by hypermutating their genomes – in essence, APOBEC3 G allows the host to make most SIV genomes produced during the infection non-functional. Retroviruses can defend themselves from APOBEC3 G with Vif, which uses the host's cellular cleaning machinery to promote the degradation of APOBEC3 G, rendering the human cells helpless to defend themselves. Across all cercopithecine monkeys, the site where Vif binds APOBEC3 G to target it for destruction is conserved (Compton & Emerman, 2013).

In contrast, the site where Vif binds colobine APOBEC3 G has shifted, likely because of an insertion in the colobine APOBEC3 G sequence, which meant that Vif needed to change to target this new APOBEC3 G (Compton & Emerman, 2013). As a result of this evolutionary arms race between colobines and their SIV strains, colobine SIVs are easily degraded by non-colobine NHP APOBEC3 G, which cannot be bound by their Vif. Human APOBEC3 G, which is strictly identical to chimpanzee APOBEC3 G at the Vif binding site (Compton & Emerman, 2013), cannot be bound by colobine Vif, presumably preventing these SIV strains from propagating in chimpanzees or humans, despite the extremely high exposure to SIV in red colobus meat. Given that the sooty mangabey SIV strain efficiently inhibits human APOBEC3 G, allowing this virus to enter the human population, the lack of sooty mangabey SIV transmission into the Taï chimpanzee population could be a result of the extreme prey preference for red colobus, meaning they are almost never exposed to the SIV of sooty mangabeys. Humans, on the other hand, are much less specific in the NHP they eat and bush meat market analyses suggest that nearly all NHP species found in Taï National Park are regularly consumed (Refisch & Koné, 2005). Humans may have broken the long-standing traditions and prey preferences of their ancestors and, as a result, have been exposed to this devastating HIV virus.

22.3 Conclusion

The aforementioned highlights important insights into the ecology and evolution of Taï chimpanzee microbial communities that have been made, but also highlights avenues of future research. We have begun exploring the viral and bacterial components of these microbial communities in this wild chimpanzee community, but a large part of these microbial communities consists of fungi, bacteriophages (viruses of bacteria), viruses of viruses, archaea and microbial eukaryotes. These have all shown a potential to impact the host and other microorganisms in profound ways; for example, by

serving to reduce the abundance of certain microbes and maintaining diversity (Ventura et al., 2011; Mills et al., 2013), changing evolutionary processes by promoting the exchange of genetic material between microbes (Roberts & Kreth, 2014) and even being used by the host as an extension of their immune system (Barr et al., 2013). For example, receptors in the mucous membranes appear to be able to bind specific bacteriophages, thereby creating a protective barrier of bacteriophages that reduce the concentrations of detrimental bacteria in these mucous membranes which may serve as a sort of non-host-derived immune system (Barr et al., 2013). It appears that epithelial layers may even facilitate the transmission of bacteriophages across them, so that these phages can then be found circulating within the host, waiting to destroy any bacteria that may cross these barriers (Nguyen et al., 2017). Neither these bacteriophages nor the host's genetic factors facilitating such binding or transmission across epithelial layers have been studied at Taï.

Little work has yet explored the function of these microbial communities, either viral or bacterial. Beyond a few pathogens (e.g. human respiratory diseases, anthrax, Ebola), we know surprisingly little about the impact of most of the microbes present in the Taï chimpanzees on health. The long-term nature of the research conducted in Taï, including faecal samples collected from known individuals for the last 15 years, provides exciting opportunities to look at fitness implications of some aspects of these microbial communities. Beyond direct measures of fitness, there are exciting opportunities to use markers of health that are measurable in wildlife (such as neopterin) to relate the microbiome to chimpanzee health (Behringer et al., 2017).

Unfortunately, the population size of the Taï chimpanzee community continues to decline (Oksanen et al., 2016). Changes in group sizes and concurrent changes in behaviour have been observed elsewhere as well, and such fluctuations may reflect a mix of anthropogenic disturbances (e.g. climate change and disease) and normal fluctuations of populations; such changes are predicted to impact these microbial communities (Gogarten et al., 2014b, 2015). It is important

to understand how these reductions in group sizes and population sizes are impacting these microbial communities and how these changes may be impacting chimpanzee health and ultimately their conservation.

22.4 Acknowledgements

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Box 22.1 Personal Insight

Jan: As an early-career scientist diving into the world of primate-associated bacterial and viral communities, I became intrigued with the idea that organisms might be best considered as holobionts (i.e. the host with all of its associated microorganisms) and hologenomes (i.e. the sum genetic information of the host and all of its microbiota). The rather intriguing hologenome theory of evolution considers the holobiont as one of the units of selection in evolution (Zilber-Rosenberg & Rosenberg, 2008); while considerations of the individual as a holobiont are not new, the technological advances allowing us to consider these ideas empirically are. Working with wild communities of non-human primates, particularly of our closest living relatives, provides exciting opportunities to think about these ideas and begin to test hypotheses. An understanding of how these communities assemble and evolved is only possible when one considers primates in their natural environments; captive primates have significantly altered bacterial microbiomes (Amato et al., 2013) and potentially even bacterial phages (Dutilh et al., 2014). In fact, evidence of resistance to medical and veterinary antibiotics used locally were found in wild primate gut bacteria (Goldberg et al., 2007), suggesting humans already influence wild primate microbiomes that may obscure evolutionary signals, highlighting the time-sensitivity of this research. The Taï primate community provides exciting opportunities to test phenomena critical to the hologenome theory of evolution: that symbiotic microorganisms are transmitted between generations, that the association between host and symbionts affects the fitness of the holobiont, that variation in the hologenome can be brought about by changes in either the host or the microbiota genomes, and that these changes may allow the symbiotic microbial community to rapidly change and potentially adapt the host to a new environment. There is a lot of exciting work to be done.

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