

**The Enigma of the Anelloviridae**

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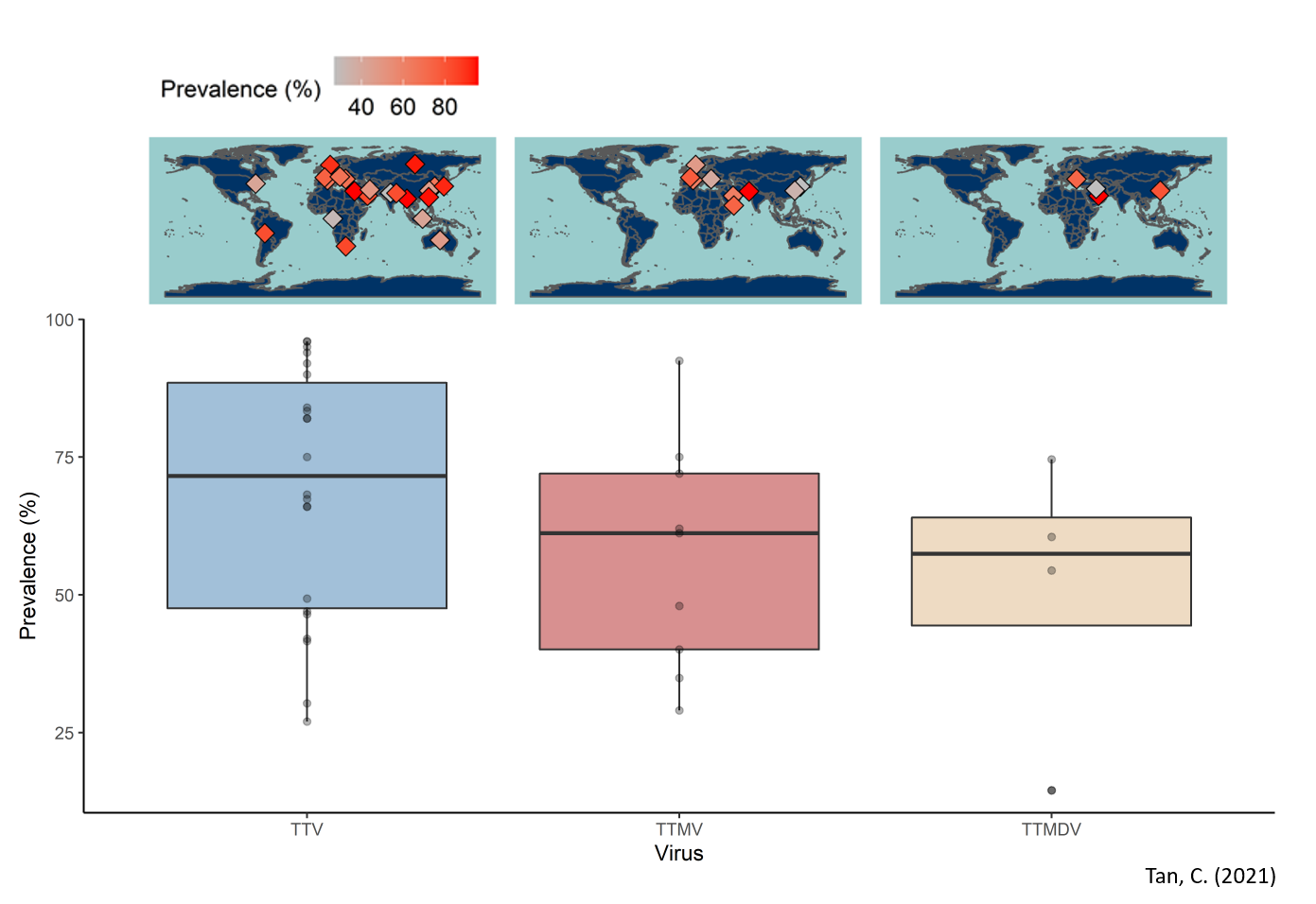
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# Abstract (200 words)

# Introduction (430 words)

The Anelloviridae is a diverse family of small, non-enveloped viruses comprising 14 genera and 76 species as of the 2019 release of the International Committee on Taxonomy of Viruses (ICTV) virus taxonomy (1). The word ‘anello’ is Italian for ‘ring’, which refers to their circular, negative-sense, single-stranded DNA (ssDNA) genomes. As of 20 Oct 2020, there were 1143 complete anelloviruses genomes of length ranging from 1.5-4 kilobases deposited in the *NCBI Virus* database.

Anelloviruses infect a diverse range of hosts, including humans (2), rodents (3), bats (4), and livestock (5,6). The first and most well-studied anellovirus is the human torque teno virus (TTV), which was discovered in the plasma of a hepatitis patient in 1997 (7). The torque teno mini virus (TTMV) and torque teno midi virus (TTMDV) are also known to infect humans. Human anelloviruses are highly prevalent in the human population. Indeed, consolidation of the results from 26 studies found that the prevalence of TTV, TTMV and TTMDV were in the range of 27-96%, 29-92.5%, 14.5-74.6%, respectively (**Figure 1**). Despite this, there has been no convincing evidence thus far implicating human anellovirus infection in disease. The torque teno sus virus (TTSuV) in pigs and chicken anemia virus (CAV) in chicken are also anelloviruses in widespread circulation globally. The former has been associated with postweaning multisystemic wasting syndrome in pigs while the latter has been conclusively found to cause disease (5).



**Figure 1. Global distribution of human anelloviruses**. Prevalence estimates of human anelloviruses in healthy individuals were obtained from 26 independent studies and used to generate this figure. The world maps were generated using the *ne\_countries* function from the *rnaturalearth* package in *R*.

While no anelloviruses have been found to cause disease in humans, the high prevalence and transmissibility of anelloviruses around the world warrants further surveillance. The extensive contact between farm animals or pests and humans facilitates zoonoses or anthroponoses that might result in the emergence of new infectious diseases, which could significantly affect human health or livestock productivity. Indeed, pathogens capable of human-animal transmission are twice as likely to be associated with emerging infectious diseases than those that are not (8). While global health efforts mainly involve post-emergence outbreak control (9), it is prudent to pre-empt and mitigate the emergence of the next infectious disease. This review therefore focuses on the potential of anelloviruses as a pathogen for human and animal hosts. The host range, potential animal reservoirs and evidence for cross-species transmission will be discussed. Additionally, possible mechanisms for the accumulation of genomic diversity in the anelloviridae will be explored. Lastly, an overview of host-virus interactions and pathogenicity will be provided.

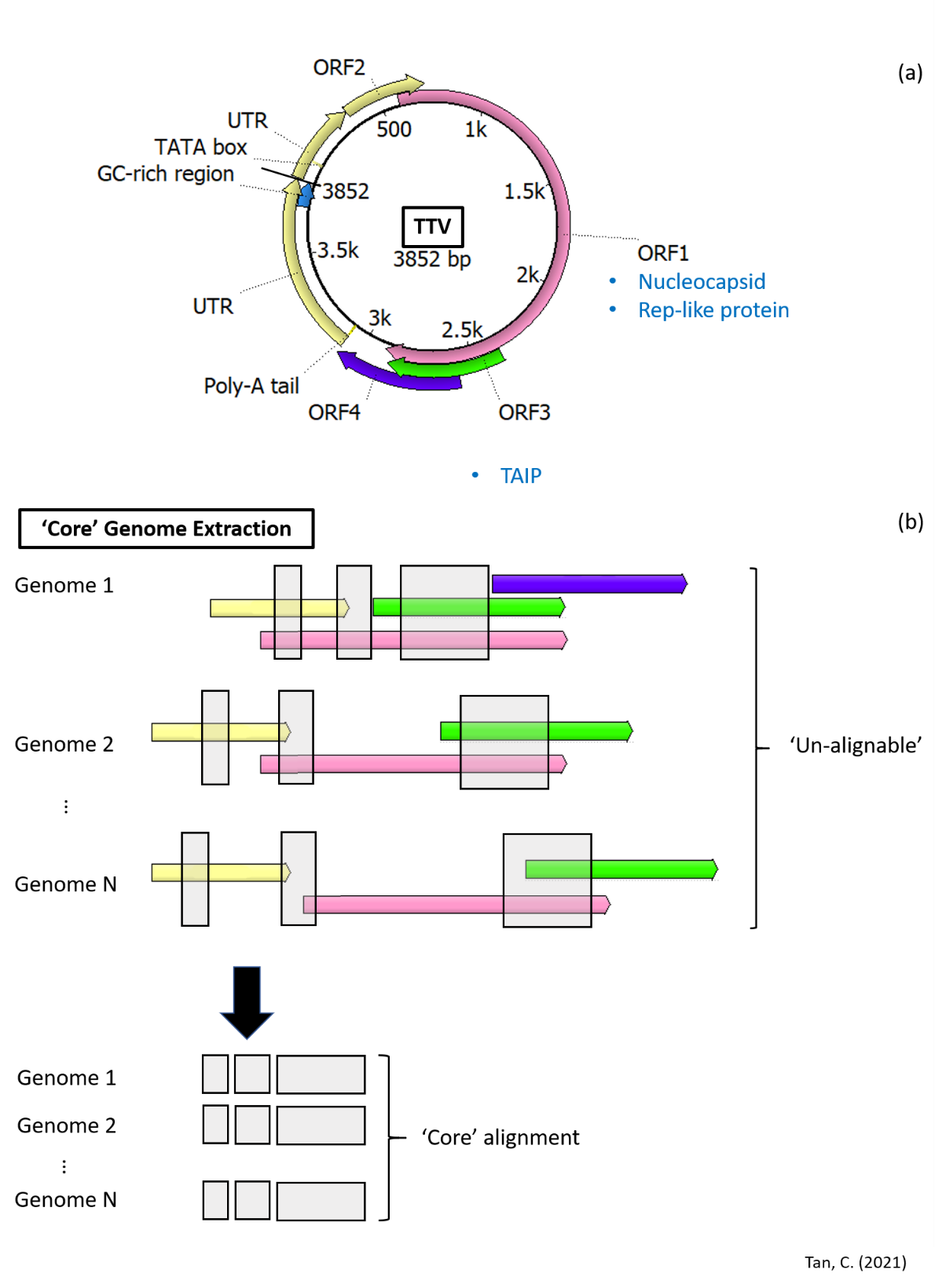
# **Accumulation of Genomic diversity**

## Genome structure and replication (310 words)

Anelloviruses have a largely conserved genome organisation, containing three to four overlapping open reading frames (ORFs) (10) within a coding region demarcated by a TATA-box and poly-A tail sequence. There is also an untranslated region (UTR) containing a GC-rich region (11) (**Figure 2a**). Transfection experiments of human TTV found that at least six proteins are generated by alternative translation initiation (12) on three mRNA species, which were produced by alternative splicing (13). ORF1 putatively encodes the capsid protein that contains an arginine-rich N-terminus(14) and a Rep-like protein that are conserved in circular DNA replicons like plasmids (15). Additionally, ORF2 potentially encodes a phosphatase (16) and ORF3, the TTV-derived apoptosis-inducing protein (TAIP) (17,18).

Currently, the genome replication mechanism of anelloviruses is poorly understood relative to other families of circular ssDNA viruses such as *Geminiviridae* (19) or *Circoviridae* (20). This is largely due to the lack of a stable cell culture system for anelloviruses to date (21,22). Kakkola et al. (23) showed that TTV replication is inhibited by administering the DNA polymerase inhibitor, aphidicolin, suggesting dependency on the host’s replication machinery. In addition to this, the presence of Rep-like motifs and putative stem-loop structures formed by the GC-rich region (24) alludes to a rolling circle mechanism, which is typical of ssDNA viruses (25).

Further investigation into the genome replication of anelloviruses may prove to be useful in the future, especially when developing antiviral therapeutics and strategies. For example, transgenic expression of non-functional viral Rep proteins in plants was shown to interfere with Rep-mediated recruitment of host polymerases for genome replication, inducing resistance to tomato yellow leaf curl geminivirus (26–28). A similar strategy could be explored to reduce the impact of anellovirus-related mortality in livestock.



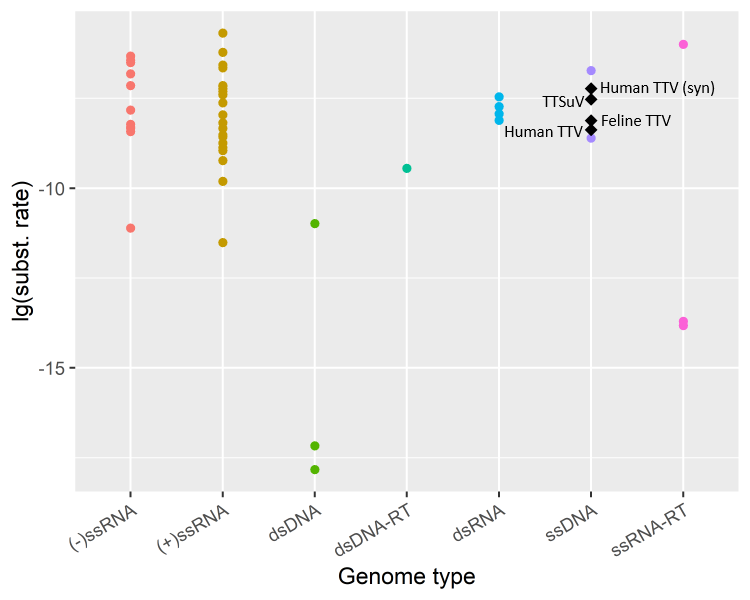
**Figure 2. Genome structure of TTV and ‘core’ genome extraction**. (a) The complete genome of TTV retrieved from NCBI GenBank (NC\_002076.2) was visualised and annotated using UGene (29). (b) Illustration of ‘core’ gene extraction to obtain alignable conserved genomic regions for phylogenetic analysis.

## Genomic diversity (255)

Even though anelloviruses have similar genome structures, there is great sequence divergence within the family. Indeed, the mean genetic distance of aligned amino acid sequences for human TTVs alone is approximately 7.6, 2.2 and 2.1 fold greater than that for hepatitis B virus, human immunodeficient virus-1 and hepatitis C virus, respectively (21). This diversity poses a major challenge for full-genome alignments during the reconstruction of phylogenetic relationships. As such, the ICTV recommends restricting family-wide phylogenetic reconstruction analyses to ORF1 and a 35% nucleotide sequence identity threshold to demarcate viral species (1). Several studies have presented a family-wide phylogeny (10,30–33) in accordance with this. However, doing so does not consider the full-length genomic diversity of the family. Additionally, sequence alignment algorithms are known to have limited accuracy when used for aligning highly divergent sequences (34). As such, alignment-free methods may be more appropriate for future studies investigating the family-wide diversity of the *Anelloviridae*. Notably, many sophisticated methods in population genetics such as those for phylogenetic dating (35) or inferring past population dynamics (36,37) are alignment-dependent. As such, future studies seeking to employ such methods could consider extracting conserved ‘core’ genes or genomic regions from the ‘un-alignable’ viral sequences (**Figure 2b**), which has been previously used on highly divergent members of microbial communities (38) and recently for the family *Coronaviridae* (39). This can be done using gene annotation tools such as *Prokka* (40), *Roary* (41)or *Mauve* (42) and would allow the construction of a sequence alignment that retains a larger proportion of the viral genomes.

## Mutation rates (325)

Understanding how viruses mutate and accumulate genomic diversity has profound practical implications. For example, the emergence of SARS-CoV-2 mutations that putatively aid in immune escape has been of great concern with regards to vaccine efficacy and development (43) in the present COVID-19 pandemic. Additionally, elevating short-term viral mutation rates via mutagen treatment, termed lethal mutagenesis, has been shown to enhance the effectiveness of antiviral treatments (44). Only a few studies to date have provided estimates of the mutation rate of anelloviruses (45–47), which ranges from 2.3-7.3 × 10-4 substitutions/site/year (s/s/y). Cadar et al. (45) reported a substitution rate of 5.4 × 10-4 s/s/y for the TTSuV genomic region containing the UTR, ORF2 and 5’ end of ORF1 sequences sampled from wild boars over six years. Umemura et al. (46) reported a synonymous substitution rate of 7.3 × 10-4 s/s/y for TTV-positive sera over 12 years. Lastly, Bedarida et al. (47) reported a value of ~2 × 10-4 s/s/y for anellovirus sequences obtained from human sera and cat saliva reported over 16 and 6.5 years, respectively. These rates were compared to that of other viruses, which were collated from eight other studies (48–55) (**Figure 3**). The mutation rates of anelloviruses are similar to that of RNA viruses. Additionally, they are discernibly higher than that of double-stranded DNA (dsDNA) viruses, which echoes previous findings that single-stranded viruses mutate faster than their double-stranded counterparts (44). This phenomenon has been suggested to be due to single-stranded viruses being more prone to chemical damage such as oxidative deamination (56).



**Figure 3. Mutation rates of Anelloviridae in the context of other viruses**. The substitution rates of all genomic sites, obtained from the literature and expressed as substitutions/site/year, was visualised in log10 scale for the different human and animal viruses, stratified by their genome types. Anelloviruses are indicated by black diamonds and annotated with their corresponding names. The substitution rate where only synonymous mutations were considered is denoted by “syn”.

## Host-editing and recombination (530)

There have been limited studies to date investigating potential sources of genomic diversity. Given that genome replication is performed by host polymerases (23), which are highly accurate, nucleotide misincorporation may play only a minor role in the accumulation of mutations. Alternatively, host innate antiviral responses may contribute to the genomic diversity. For example, host APOBEC3 proteins are cytidine deaminases that have been found to cause C->T hypermutations in other DNA viruses like human papillomavirus (57,58). While such host-editing by APOBEC3 has not been demonstrated for anelloviruses, *in vitro* experiments found that these proteins preferentially bind ssDNA over dsDNA and may account for higher C->T mutations on the negative-sense strand of HIV reverse transcripts (59). This suggests that negative-sense ssDNA anelloviruses are likely to be subject to host-editing. Investigations of how anelloviruses evade or overcome APOBEC3-mediated editing may prove to be invaluable in our understanding of how viruses evolve.

Recombination also plays a substantial role in shaping the extant genomic diversity of the *Anelloviridae* by generating new genetic combinations that could not have been attained via point mutations alone (60). Indeed, a single recombination event between two viral genomes could generate new combinations of their existing mutations, introducing several nucleotide polymorphisms at a time, which could prevent the accumulation of deleterious mutations (61–63). Using the popular recombination detection tool RDP4 (64), which identifies recombination using an ensemble of different detection methods, Fahsbender et al. (65) found that 89% of torque teno Leptonychotes weddellii virus (TTLwV)-1 and 26% of TTLwV-2 had at least one and one putative recombination event, respectively. They also found that the recombination breakpoints detected in TTLwV-1 tend to fall within the UTR region. This agrees with a previous study (60), which found a significantly higher density of recombination breakpoints outside coding regions and at the edges of genes for almost all of 14 ssDNA viruses spanning 6 families (including TTV and TTMV). Other studies have similarly detected recombination within the different human TTV species (66,67) and within TTSuVs isolated from wild boars and domestic pigs (45). While no studies to date have formally estimated the rate of recombination in anelloviruses, multiple studies have found a high frequency of co-infections of different anellovirus species (68–72), one even reporting a 48% frequency of dual or triple infection of TTV, TTMV and TTMDV in infants. This high frequency of co-infection, together with the strong recombination signals detected by the abovementioned studies, suggest that anelloviruses recombine frequently and that recombination may be a major contributor to the accumulation of genomic diversity. This has significant implications for phylogenetic inference since recombination results in portions of genomes representing different evolutionary histories. This violates the assumption of most phylogeny estimation methods – that a single evolutionary history underlies the sequences analysed (73). In such cases, the resultant phylogeny topologies obtained often differs from the true phylogeny (74), especially when recombination occurs between divergent sequences (73), as in the case of anelloviruses. Future studies attempting phylogenetic estimations should opt for alignment-free methods, which are minimally affected by recombination (34). Alternatively, they may remove putative recombinant segments using breakpoints identified by tools such as GARD (75) or RDP (64,76), which was demonstrated by Cadar et al. (45).

# Transmission routes: anelloviruses can go anywhere (761)

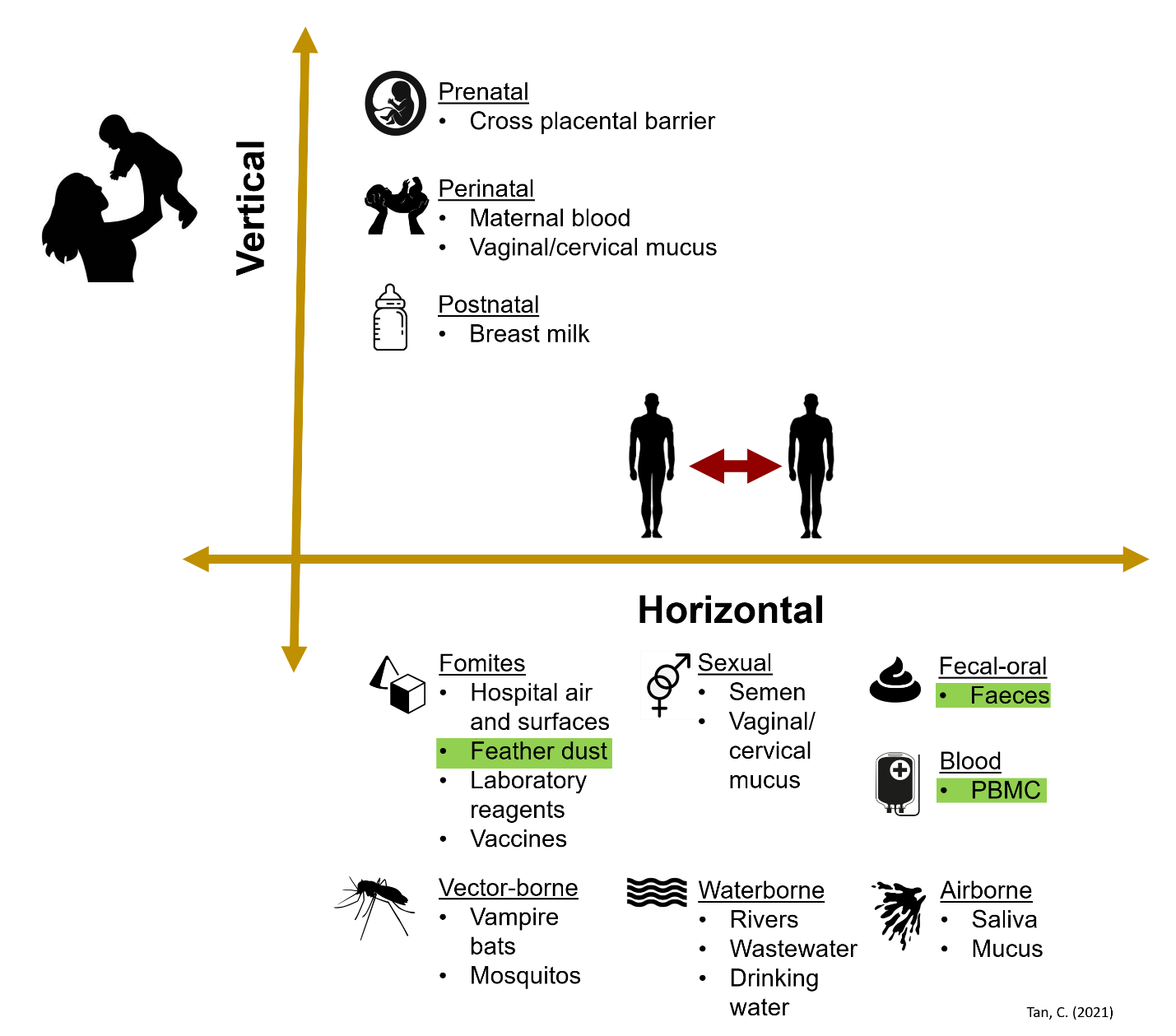
## Horizontal transmission

In line with its high prevalence, anelloviruses may potentially be transmitted via multiple routes, both vertically (*i.e.* from mother to offspring) and horizontally (*i.e.* between organisms not in a mother-offspring relationship) (**Figure 3**). In general, most studies of transmission thus far have employed PCR-based methods of detecting anelloviral DNA. In such methods, PCR with anellovirus-specific primers is used amplify viral genomic fragments, which are then visualised via agarose gel electrophoresis. Suitably sized gel bands corresponding to the length of the PCR target are extracted and subsequently sequenced to confirm that the correct genomic sequences were amplified. Successful amplification of the PCR target is generally regarded as a positive result. However, even if anelloviral DNA is detected, this does not entail that infectious virions are present. Since most studies did not demonstrate the viability of detected anelloviral DNA and its ability to infect naïve hosts, only a few transmission routes have been confirmed (highlighted in green; **Figure 3**). The strength of evidence provided for the different transmission routes will be discussed in this section.

Anelloviral DNA has been detected in bodily fluids like blood, bile, saliva, mucus, semen and faeces (77–83). This suggests that anelloviruses may potentially be transmitted horizontally via sexual, faecal-oral and airborne routes, or via direct contact with bodily fluids. However, since most studies did not confirm the viability of virions in the samples, the presence of viral DNA in samples could have been due to transient shedding of inactivated virus from a distal source that cannot infect a new host. Exceptionally, Itoh et al. showed that mature virions could be extracted from faeces and visualised using electron microscopy, providing stronger evidence for faecal-oral transmission (79). Additionally, anellovirus-positive blood was shown to be able infect cells and proliferate (78,83). Moreover, persistent viremia of TTV and TTMDV from blood donors was found in blood transfusion recipients (84), providing confirmatory evidence for blood as a vehicle of transmission.

Anelloviruses may potentially be transmitted via water or fomites, which are inanimate objects or surfaces that can become contaminated with pathogens (85). Anelloviral DNA has been detected in multiple environmental sources. Studies have demonstrated their persistence in rivers (86–88), wastewaters (89), drinking water (90,91), shed feathers (92), air and surfaces in hospitals (93) or even laboratory reagents (94) and vaccines (95). Of these studies, only one demonstrated the viability of detected anelloviral DNA. Davidson et al. (92) showed that dripping feather shaft extracts obtained from the feathers of CAV-infected chicks into the eyes and mouths of unexposed chicks resulted in infection, confirming that feathers can act as fomites to transmit CAV. However, while confirmation of infectivity is lacking, given the ubiquity and persistence of anelloviral DNA in the environment, the detected viral DNAs are likely to be stably packaged in their capsid protein shells and potentially infectious. Otherwise, ‘naked’ viral DNAs quickly degrade when exposed to the environment. For example, Zhu demonstrated that plasmid DNA in river and ground water is degraded beyond detectable levels after 48-96 h (96). In contrast, the viral load of infectious, encapisdated human adenovirus remains stable even after 40 days in surface waters as quantitated by a plaque assay (97). The relatively higher stability of DNA in infectious virions is likely due to the presence of the viral capsid protein which shields the DNA from degradation by chemical agents, UV irradiation or other means.

Alternatively, anelloviruses may potentially be transmitted via vectors. Shi et al. (98) and Hameed et al. (99) both found that viral sequences extracted from mosquitos and swine of pig farms were phylogenetically interspersed with previously reported TTSuV sequences. The viral sequences extracted from the mosquito samples were therefore likely to have descended from TTSuVs in pigs and may have been acquired during blood-feeding (*i.e.* hematophagy). However, both studies did not confirm that the viral DNA detected in mosquitos were infectious, which may provide stronger evidence for vector-borne transmission. Another study by de Souza et al. found that anellovirus sequences extracted from the liver of a vampire bat (*Desmodus rotundus*) and serum of an opossum (*Didelphis albiventris*) were phylogenetically clustered relative to other species of the *Anelloviridae* (30), suggesting that these anelloviruses are likely to share a common ancestor that was transmitted between the two host types. This is considerable evidence that vampire bats may be a vector of transmission for anelloviruses between the bats’ mammalian hosts.



**Figure 3. Summary of potential transmission routes for anelloviruses**. Transmission routes that are supported by substantial evidence in the literature are highlighted in green.

## Vertical transmission

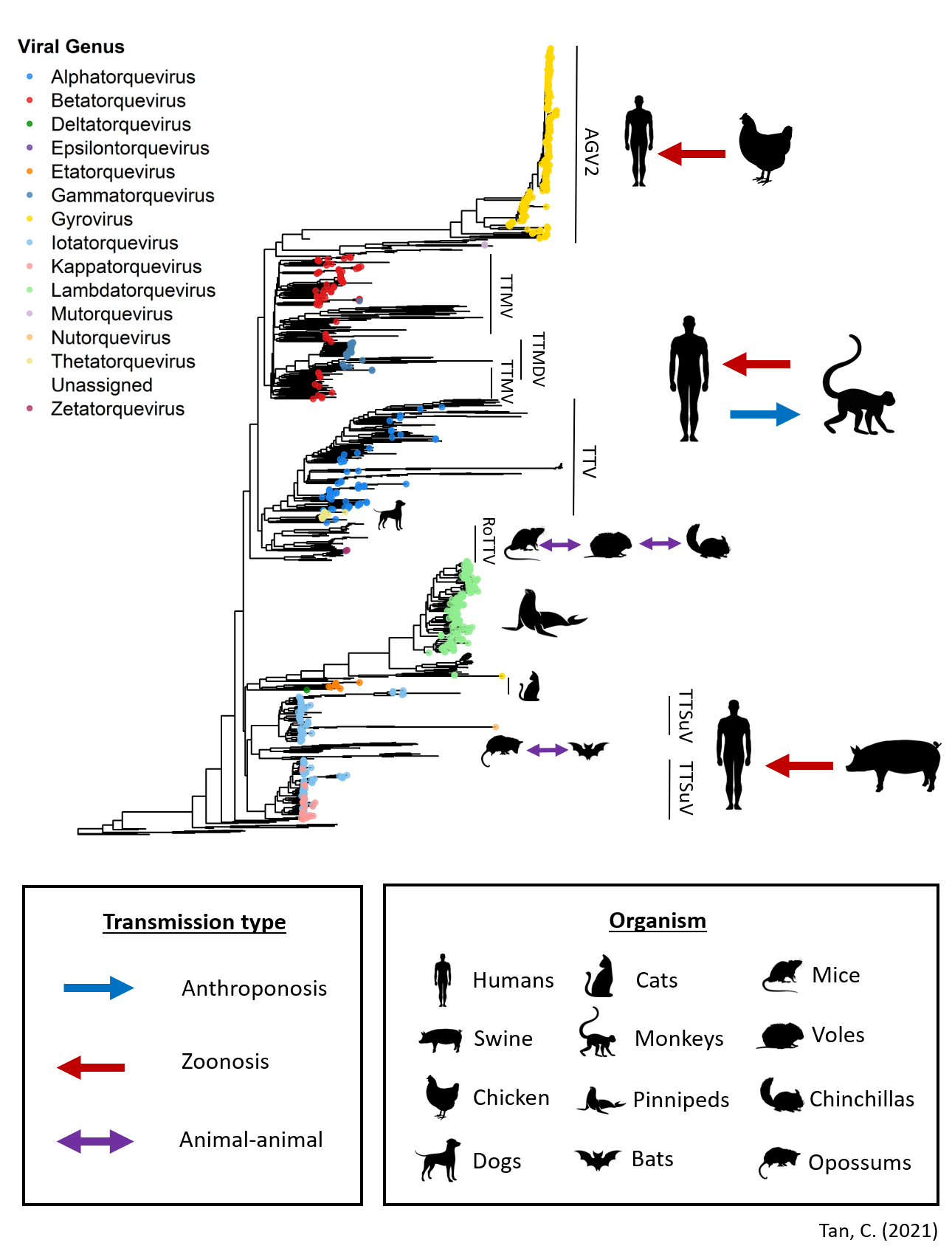
There is strong evidence for vertical transmission of anelloviruses, although the exact route(s) of infection – whether infection occurs before (prenatal), during and immediately after (perinatal), or after birth (postnatal) – is not known. Gerner et al. (100) detected human TTV in human breast milk, and umbilical cord blood. Separately, Matsubara et al. (101) found TTV and TTMV DNA in breast milk, cord blood and amniotic fluid. Both studies employed polymerase chain reaction (PCR) followed by agarose gel electrophoresis to test the fluid samples. PCR amplicons were also sequenced via Sanger sequencing to rule out non-specific amplification. These studies suggest that breastfeeding might be a potential transmission route. However, cross-sample contamination during collection of cord blood or amniotic fluid is difficult to rule out and so these studies may not be sufficient to prove transplacental transmission. In fact, Tyschik et al. (102) did not find TTV in the cord blood from TTV-positive mothers using a highly sensitive quantitative PCR (qPCR) assay that could detect viral loads as low as 1000 viral DNA copies/ml of blood. The authors also detailed stringent measures to prevent cross-contamination, which the previous groups did not do. This suggests that the previous findings could have been due to contamination, which must be accounted for in future studies. Nevertheless, Gerner et al. (100) provided evidence for vertical transmission by showing that follow-up samples taken from infants with TTV-positive cord blood had persistent viremia.

Vertical transmission has also been demonstrated in animals. In particular, Martinez-Guino et al. showed in separate studies that sows, their breast milk and their aborted foetuses (103) or stillborns (104) were PCR positive for TTSuV. They also showed that TTSuV sequences in mother-offspring pairs had nucleotide sequence identities of 91-98%, implying that sample cross-contamination is unlikely. Indeed, it is likely that samples that were cross-contaminated at the point of collection should share identical sequences. As such, these findings may suggest that infections of the foetuses were acquired prenatally and that TTSuV may be transmitted through breast feeding. Vertical transmission of TTSuV through breast milk can be further confirmed in future studies by feeding of TTSuV-positive milk to TTSuV-negative offspring. Separately, human TTMDV was detected in domestic hens and the yolks of their eggs (105), providing evidence for vertical transmission. Confirmation that chicks that developed from TTMDV-positive eggs were also persistently infected would have provided stronger evidence for vertical transmission. Collectively, the studies discussed above provide substantial evidence for vertical transmission of anelloviruses.

# The potential for cross-species transmission:

## Host range: anelloviruses are everywhere (485)

After the discovery of TTV, the first anellovirus, in 1997 (7), multiple studies have detected a diverse range of anelloviruses in humans and animals, including rodents (3), primates, birds, marine mammals (65,106,107), bats (4) and other wild or domesticated animals (30,108–111). An alignment-free phylogeny of 1143 complete anellovirus genomes isolated from at least 43 annotated host species (NCBI Virus; accessed 20 Oct 2020) is presented here (**Figure 4**). The phylogeny demonstrates significant clustering by viral genus and a broad diversity of host types that are segregated by phylogenetically distinct clades (**Figure 4**). Given the extensive sampling of the broad diversity of anelloviruses from a variety of hosts, it may be feasible to investigate the selective pressures involved in viral speciation events (e.g. the emergence of TTMDV from a TTMV lineage; **Figure 4**) or changes to host-specificity. While unexplored in the literature, probing these ideas may yield valuable insights as to how new pathogens can emerge. For example…

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**Figure 4. Genomic diversity of the Anelloviridae and summary of evidence for cross-species transmission**. The genomic diversity of 1143 Anelloviridae genome sequences is represented here as a whole-genome neighbour-joining phylogeny, which was reconstructed using alignment-free Mash distances (112) and rooted with the genome accession MK012481 (see **Appendix**). This phylogeny is annotated with symbols illustrating the host range and cross-species transmission of various viral species.

Studies that have explored the biodiversity of anelloviruses in humans and animals can be non-exhaustively categorised into virus-specific and metagenomic efforts. The former category refers to studies that performed PCR using anellovirus sequence-specific primers, followed by sequencing of the PCR amplicons. For example, Ye et al. characterised the sequences of avian gyrovirus 2 (AGV2) in chickens from live poultry markets (108). Similarly, Singh et al. used TTSuV-specific primers to amplify and subsequently characterise anellovirus sequences in bovine, equine, ovine, canine and elk hosts (109). The latter category refers to studies that do not employ sequence-specific primers but perform metagenomic sequencing, followed by *de novo* assembly (*i.e.* assembly without a reference genome) of sequencing reads. For example, studies have employed this approach for samples obtained from mosquitos (98,99,106), rodents (3,113) and pinnipeds (107,114). To explore the host range and biodiversity of anelloviruses in different animal reservoirs, metagenomic-based approaches appear to yield much more information. Indeed, *a priori* knowledge of viral sequences is required for virus-specific approaches. Given the large sequence divergence within the family, species-specific PCR primers are unlikely to be able to amplify novel anellovirus sequences. In contrast, metagenomic-based approaches do not require *a priori* sequence information and therefore can detect novel anelloviruses. Furthermore, because anellovirus genomes are small, lesser sequencing reads are required for sufficient genomic coverage to produce reliable genome assemblies. This entails that while the genomic fragments retrieved via virus-specific PCR is restricted by the amplicon length, longer or even full-length genomic sequences can be assembled via metagenomics-based approaches. In short, metagenomics may capture more genomic information from a larger proportion of the anelloviral diversity.

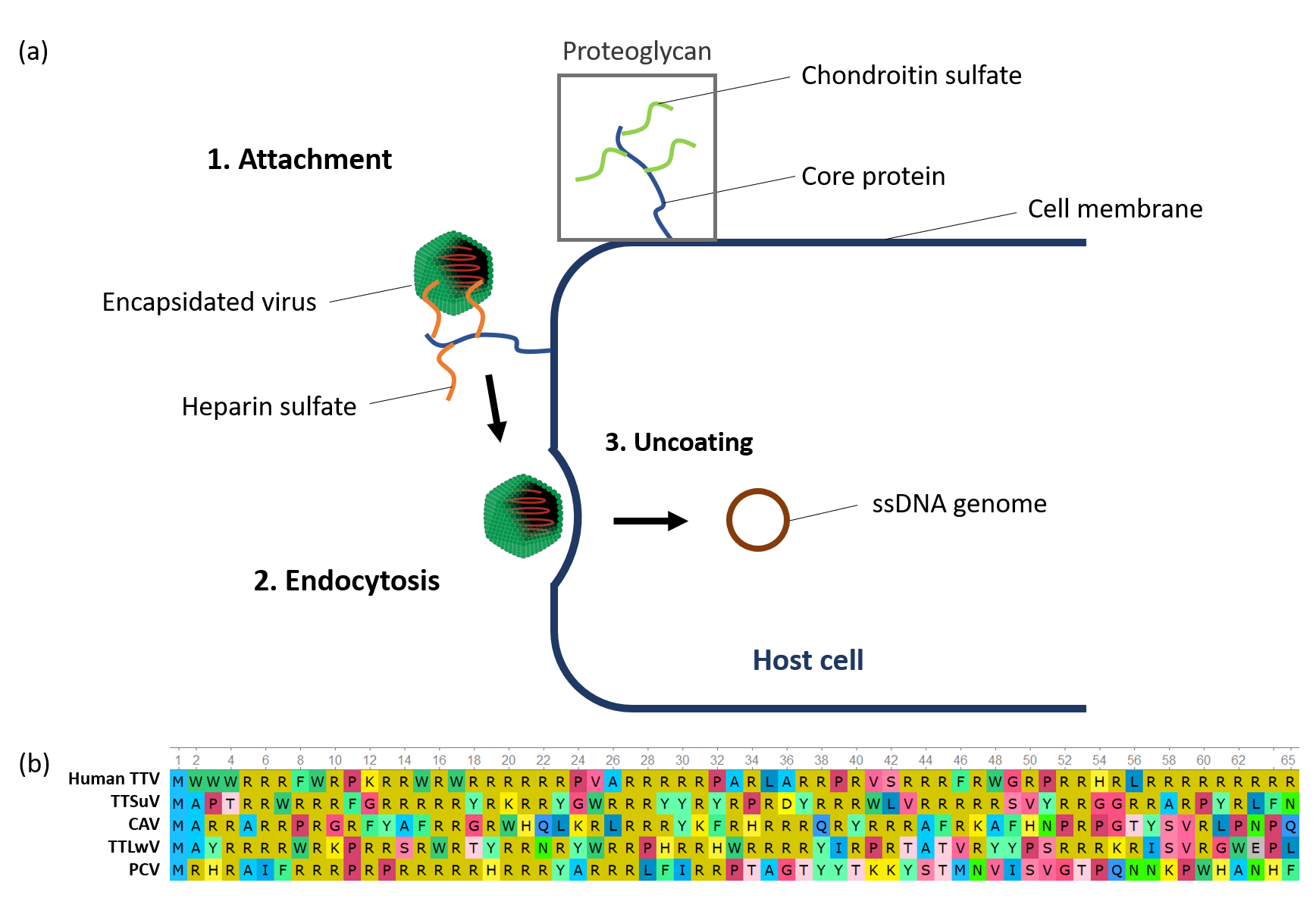
## Animal reservoirs (267)

The broad host range of anelloviruses suggest that there may be multiple animal reservoirs where zoonotic spillover may occur, especially those in frequent contact with humans. Animal reservoirs are groups of animals that harbour viral pathogens, some of which may be transmitted to humans (*i.e.* zoonoses), resulting in the emergence of novel human infectious diseases. A study of 415 viruses found that the number of zoonotic viruses is proportional to the number of viral species maintained by each animal reservoir (115). If true, the diversity of anelloviruses in different animals may be a risk factor for zoonotic spillover. Indeed, metagenomic-based studies often detect different species of anelloviruses, sometimes from different viral genera. For instance, a survey of anelloviruses in civets (*Paguma larvata*) found viral species from at least four genera (116), while that in rodents spanned at least two viral genera (113). Another risk factor for zoonotic spillover is extensive contact between humans and the reservoir. This is intuitive given that there must be ample opportunity for host-specific adaption of the virus to jump into humans (117). Further, a minimum of 20% geographical overlap was suggested to be necessary for viral sharing (resulting from cross-species transmission) (118) and the probability of sharing increases with overlap up till a 50% overlap (119). This implies that livestock and wildlife such as bats or rodents that are in reasonably close contact with humans are potential animal reservoirs. A meta-analysis of the vast amount of metagenomic sequencing data from bats (120–122), rodents (123,124) and livestock (125–127) may yield valuable insights on the diversity of anelloviruses in these potential reservoirs.

## Animal-animal transmission, zoonoses and anthroponoses

There has been considerable evidence supporting the broad host-specificity of single anelloviruses. Singh and Ramamoorthy (109) detected both TTSuV and human TTV sequences in canine, bovine, ovine, equine, and elk sera using species-specific PCR primers. They further detected TTSuV-specific antibodies in bovine, ovine and equine samples using enzyme-linked immunoabsorbant assays (ELISA), confirming the presence of productive TTSuV infection in these animals. Notably, the authors did not find TTSuV-specific antibodies in elk and canine samples despite the presence of TTSuV DNA, suggesting that either the magnitudes of antibody responses were below the limit of detection for the ELISA assay used, or that viral replication was insufficient to trigger the production of TTSuV-specific antibodies. The former possibility implies considerable variability in the strength of adaptive immune responses to anellovirus infection while the latter suggests that TTSuV may not be adapted for efficient replication in said hosts. Nonetheless, these findings provide strong evidence for the ability of TTSuV to infect multiple animal hosts and possible cross-species transmission of both TTSuV and human TTV. Additionally, as mentioned previously, de Souza et al. (30) found two phylogenetically similar anelloviruses in a vampire bat and an opossum. A third anellovirus sequence obtained from the frugivorous (i.e. fruit-eating) bat, *Carollia perspicillata*, was also clustered with these two viral sequences (30). The node where the three sequences diverged from the other anelloviruses had a high bootstrap support value, suggesting that their evolutionary relationships can be confidently inferred. A likely explanation for these observed relationships is the cross-species transmission of anelloviruses between mammalian species whose habitats overlap, which underscores the ability of anelloviruses to infect different hosts. Rodent TTVs have also been shown to infect a broad range of hosts. A large metagenomic surveillance study on rodent samples collected from 20 provinces in China found that rodent TTV lineages were present in multiple hosts from the same family, or even hosts from three different families (*Circitidae*, *Muridae* and *Chinchillidae*) (113). These studies suggest that anelloviruses, or at least those associated with mammalian hosts, tend to be ‘generalists’ that have retained the ability to infect a broad range of hosts.

Understanding how anelloviruses are internalised by cells during infection may account for the broad host range of anelloviruses. However, the exact mechanism for viral entry is currently unknown. Generally, non-enveloped viruses, which include anelloviruses, enter host cells by the binding of capsid proteins to cell surface (128). These viruses subsequently penetrate the cell membrane and release their genomes into the host cell where it proliferates. A comparison of anelloviruses to porcine circovirus (PCV) – a circular ssDNA virus of the family *Circoviridae* – suggests that proteoglycans are potential candidates for such extracellular receptors. Proteoglycans are macromolecules found on the surface of cells. They consist of a core protein chain that is covalently attached to several glycosaminoglycan chains such as heparin sulfate or chondroitin sulfate (**Figure Xa**). Visualisation of PCV and anellovirus capsid protein sequences showed that there is an arginine-rich region at their N-termini (**Figure Xb**). The arginine-rich region in PCV has been shown to act as a cell-penetrating peptide (CPP) that triggers endocytosis and hence uptake of its cargo into the cell (129). Further, PCV has been shown to use proteoglycans such as heparin sulfate proteoglycans (HSPG) and chondroitin sulfate-B (CSPG) for viral entry (130). While a direct interaction between the N-terminal sequence of the PCV capsid and proteoglycans has not been described, most CPPs are understood to allow the translocation of macromolecules into cells by binding to proteoglycans (131,132). Interestingly, PCVs were found to be able to infect cells lacking both HSPGs and CSPGs (130). Additionally, inhibition of major endocytotic pathways such as clathrin-mediated endocytosis or macropinocytosis was found to reduce uptake of PCV-derived N-terminal sequences (129). These findings suggest that multiple cellular pathways are involved in PCV viral entry. This, in addition to the fact that HSPGs are expressed on the surface of most animal cells, (133) may explain why PCV can infect multiple cell types and host species (134). Similarly, the promiscuous cell- (136) and host-specificity of anelloviruses points to the involvement of common host cell receptors during viral entry. Future studies may consider investigating whether the anellovirus-derived N-terminal capsid sequences can function as CPPs to probe the mechanism(s) of viral entry. Arguably, with a better understanding of viral entry mechanisms, it may be possible to estimate the potential for cross-species transmission of anelloviruses.



**Figure X. Potential mechanism of viral entry** (a) Schematic of a possible mechanism of viral entry for anelloviruses, modelled off that of PCVs. (b) UGene (29) visualisation of the first 65 amino acid residues in the capsid protein of Human TTV (QHS01920.1), TTSuV (YP\_003587901.1), CAV (AYN79688.1), TTLwV (YP\_009388631.1) and PCV (YP\_009315911.1). A meaningful alignment of these sequences could not be produced.

Notably, a study of 162 zoonotic viruses found that 63% of zoonotic viruses can be found in hosts from at least two different taxonomic orders (137), which suggests that broad host-specificities may be a risk factor for zoonotic emergence. Additionally, the authors presented a network analysis of the number of viruses shared between different hosts. Wild rodents and domestic animals such as dogs, pigs, cats and cattle were centrally located and highly connected in the network, suggesting that such animals may serve as vectors that facilitate the transmission of viruses between humans and wild-animal reservoirs. If so, the ‘generalist’ nature of animal anelloviruses may warrant closer surveillance of the anelloviral diversity in livestock or other animals that humans are frequently in contact with.

Several studies have also provided evidence for the potential of anelloviruses to infect humans, which might result in zoonotic spillovers and the emergence of new human infectious diseases. Using a PCR-based method, AGV2 was detected in the blood of 4/301 (138) , 2/178 (108) and 3/352 (139) human samples in three independent studies.

Whilst the focus of infectious disease research has traditionally been on zoonoses, the importance of anthroponotic transmission was brought to the forefront in the recent COVID-19 pandemic. Indeed, there has been great concern that anthroponotic transmission of SARS-CoV-2 into animal populations that can sustain transmission may result in the formation of animal reservoirs (140,141). These reservoirs in turn serve as vectors of transmission between humans. Further, upon successful anthroponosis, there is evidence for rapid viral adaptation to its new host, contributing to the extant genomic diversity of the virus (142).

Anthroponosis might also result in mortality in livestock.

* Zoonosis

1. TTSuV
2. Avian Gyrovirus
3. simian TTV, TTMDV

* Anthroponosis as mechanism for creating animal reservoirs

1. TTV and TTMV in captive chimps
2. TTV in swine and cattle
3. Human TTV in swine, bovine and simian sera

* High prevalence in livestock and humans

1. Potential for emergence of recombinant strains (cf. human adenovirus from recombinant Chimp and Bonobo viruses)

* Seem to be generalists (like Coronaviruses)
* Broad host range is risk factor for emergence
* (<https://royalsocietypublishing.org/doi/abs/10.1098/rstb.2001.0889>)
* We find that the fraction of pathogens shared between two hosts decreases with the phylogenetic distance between them. Our results suggest that host phylogenetic similarity is the primary factor for host‐switching in pathogens. (liam)
* Ability to infect multiple hosts, ‘generalist’ nature is risk factor for disease emergence in humans and wildlife, at least 1.29 fold more likely to emerge
* Pathogens that also infected wildlife species are 1.96 fold more likely to emerge (Cleaveland)
* Instead, the number of human-infecting viruses increases proportionately to the total number of viruses maintained by each reservoir group (Mollentze)

# Host-virus interactions (1000 words)

* TTV has no stable cell culture or animal model so it is difficult to study
* Mechanisms for regulation of innate immunity
* Mechanisms for regulation of cell-mediated immunity
* All proteins are antigenic <https://www.sciencedirect.com/science/article/pii/S0042682208005928#bib28>
* Higher viral loads associated with disease. Competes with immune system

# Pathogenicity (1000 words)

* Suspected cause of death in pinnipeds (discuss Koch’s postulates)
* Synergistic co-infection causing fatal postweaning multisystemic wasting syndrome in pigs
* Chicken anemia virus causes atrophy of thymus and bone marrow
* No evidence for pathogenicity to humans; studies have only shown that TTV is marker of immune status
* However, we cannot rule out that human anelloviruses can alter disease progression or severity

1. **Conclusion (500 words)**

* If anelloviruses are arguably not pathogenic to humans, why should we care?

1. Kills livestock
2. Generalist nature potentiates cross-species transmission and possibly the emergence of pathogenic strains

* Stress importance of viral surveillance in animal reservoirs

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# Appendix

**Table 1. Summary of evidence for cross-species transmission of anelloviruses**.

|  |  |  |  |
| --- | --- | --- | --- |
| **Study** | **Information about host range** | **Transmission type** | **Notes** |
| De Souza et al. (30) | * Anelloviruses found in: * rodents (Criticidae) * bats (Molossidae, Phyllostomidae) * opossums (Didelphidae) * Bat and opossum viruses clustered phylogenetically with strong bootstrap support. Possible transmission via hematophagy. | Animal-animal | * Bat virus found in kidney and liver samples. Likely to be viable. |
| Nishiyama et al. (3) | * RoTTV1 and RoTTV2 found in: * wood mice (Apodemus sylvaticus) * field voles (Microtus agrestis) * bank voles (Myodes glareolus) | Animal-animal | * Absent in mus musculus |
| Du et al. (113) | RoTTV lineages found to infect hosts from one to three families (Circritidae, Muridae, Chinchillidae). | Animal-animal |  |
| Ng et al. (106) | * Mosquito TTV sequences phylogenetically clustered with TTSuVs. | Animal-animal | * Low bootstrap support * Viability of virions not confirmed |
| Shi et al. (98) | * TTSuV1-like viruses detected in mosquitos using TTSuV1-specific PCR primers. * Phylogenetically interspersed with TTSuV1 viruses isolated from pigs. | Animal-animal | * Viability of virions not confirmed |
| Singh et al. (109) | * TTSuV detected in: * Bovine * Equine * Ovine * Canine * Elk | Animal-animal |  |
| Ssemadaali et al. (143) | * Transfection of TTSuV1 genomes into human PBMCs resulted in viral proliferation. * TTSuV DNA detected in both human and swine sera samples. 27 of 40 human blood samples and twelve of 20 swine samples | Zoonotic |  |
| Ye et al. (108) | * 98.3-100% pairwise nucleotide sequence identities for AGV2 amplicons of 10/54 chicken feather samples and 2/178 human blood samples. | Zoonotic |  |
| Ninomiya et al. (144) | * 73 of 74 chimpanzees in capitivity tested positive for human TTV and TTMV * Coinfection of human TTV, TTMDV and simian TTMDV in one healthy human subject. * Chimpanzee TTV/TTMV phylogenetically clustered with human TTV/TTMV | Zoonotic/Anthroponotic |  |
| Iwaki et al. (145) | * Simian-associated TTVs found in 10.5% of a samples from a Japanese cohort * Phylogenetically distinct from human TTVs. | Zoonotic |  |

# Checklist

1. good use of figures and appropriate use of legends and references
2. “general-to-specific” structure
3. Understandable to the non-specialist
4. Introduction with relevance of the review topic, aims and roadmap present
5. Logical transitions between topics
6. Conclusions and perspectives present
7. Highlights limitations / challenges / questions in field.
8. Provides (few) directions for future experimental work based on the limits and challenges mentioned
9. Clear and relevant figures