

Co-evolution between parvovirus and wild and domestic carnivore hosts

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We want to investigate the complete VP2 gene of CPV type 2 variants isolated from several wild carnivore species in the Serengeti ecosystem, northern Tanzania, and domestic dogs, to determine the prevalence and phylogenetic relationship among variants currently circulating in the carnivore guild. We consider this research will provide a unique opportunity to look at co-evolution between host species and parvovirus variants. The prevalence of co-infection in wild carnivore species will be assessed using quantitative PCR through viral screening of tissue and faecal samples. Variants will be identified through cloning of viral DNA and sequencing. We will establish whether (1) variants infect different carnivore species at random or whether specific variants are adapted to infect particular hosts; (2) infection with different CPV type 2 variants in different carnivore species can be explained by the binding properties of the TfR-receptor in these species. Banked, deep frozen tissue samples of intestinal epithelium tissue from several focal species are available at the IZW.