Costa Rica Wildlife Disease Reporting System for Preventive Medicine and Disease Control

#916

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Introduction

SARS-COV-2 pandemic evidence that the impact of new zoonotic diseases can be on both social and economical levels. Since such agents are originated from wildlife reservoir communities, there's a need for more active actions to be taken in case of jeopardizing public health's situation. The first step is establishing a routinary reporting data system of wildlife diseases by implementing a local surveillance system able for monitoring the presence of endemic and possible new agents. In countries like Costa Rica, which are very diverse not only in fauna but also in macro-microparasites. It's highly recommended to set up an early warning system for zoonotic agents detection.

The aim of this project undertook to evaluate the feasibility of establishing a passive surveillance system where selected infectious agents would be monitored. The focus was on obtaining information on pathologies of terrestrial mammals and birds in the wild suspected of disease sent for investigation in two years.

Materials & Methods

Pathological assessment: Several vertebrate species admitted were submitted to laboratories by either the National Wildlife Service (SINAC), National Animal Health Service (SENASA) or other NonProfit wildlife organizations (Wildlife Rescue Centers). A total of 67 mammals and 9 birds were suitable for a postmortem analysis process (macroscopic and histopathological). Extra samples were taken and submitted for further investigation. Other analyses were performed or identification methods were carried out to establish the etiological agents (fig. 1).

Geo/coding: Data such sex, species, location (GPS position) and possible cause of death were recorded. All this data was coded into shapefile, and we generated maps of the cases by location and species.

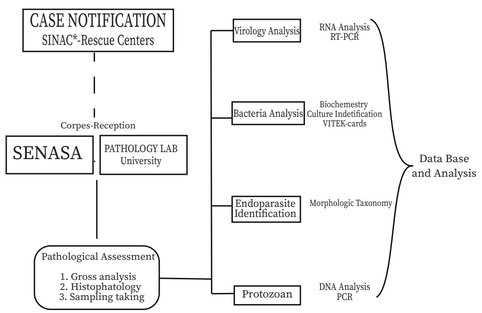

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Figure 1. Flowchart of the admission and process of pathogen determination

Results

Between 2018 to 2020 a total of 76 animals were admitted for examination. Most affected systems were gastrointestinal gastrointestinal (71.6%) and, respiratory systems (68.6%) the most affected systems in mammals. Being pyogranulomatous ileocolitis associated to *P. elegans* (fig 2) and mononuclear interstitial pneumonia associated to Distemper virus, the most common lesions observed respectively. In birds, the gastrointestinal system was affected with a 55% of the cases, being hemorrhagic ventriculitis associated to *Contracaecum* spp. the most prevalent lesion observed. Distribution of taxonomic group and affected systems are shown in fig. 3. Forty six percent (35 out of 76) showed infectious malady with zoonotic potential. The total distribution of agents are shown the Table 1.

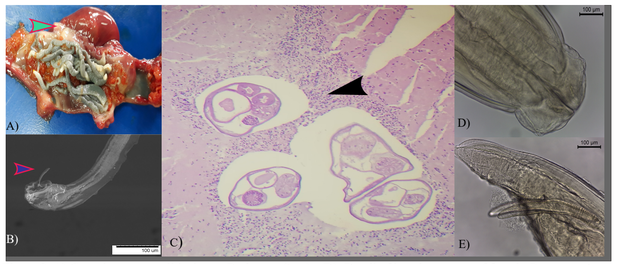
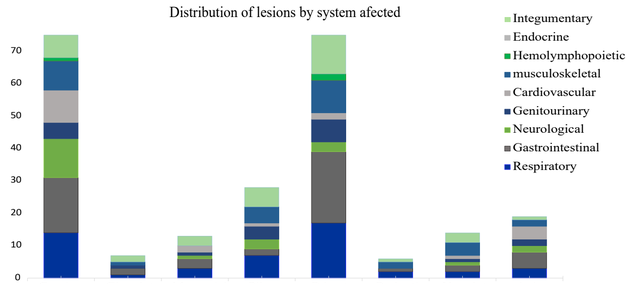
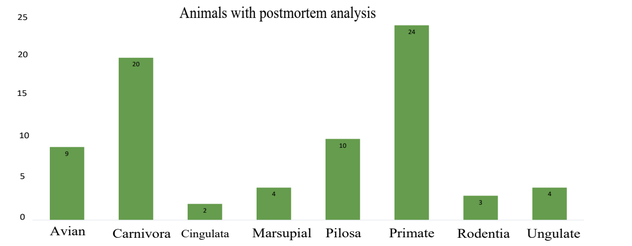


Figure 2. A) Granulomatous colitis due to *P. elegans* ( ) D) Detail of bucal structure of female *B. procyonis.* B) Spicule and folded bursa feature for specie recognition ( ) E) Spicule of male *B. procyonis.* C) Eosinophilic meningoencephalitis with presence of *A. costaricensis* ( )

	ETIOLOGICAL AGENT		TAXONOMIC GROUP							
			Carnivora	*Cingulata*	*Marsupial*	*Pilosa*	*Primate*	*Rodentia*	*Ungulate*	*Avian*
VIRAL DISEASES	Distemper	Analyzed	10	0	0	1	0	0	0	NA
		Positive	7	0	0	0	0	0	0	NA
	Flavivirus-Alphavirus	Analyzed	1	0	0	1	4	0	1	3
		Positive	0	0	0	0	0	0	0	2
	Influenza	Analyzed	0	0	0	0	4	0	0	9
		Positive	0	0	0	0	0	0	0	0
	Newcastle	Analyzed	NA	NA	NA	NA	NA	NA	NA	9
		Positive	NA	NA	NA	NA	NA	NA	NA	0
	Rabies	Analyzed	17	2	3	10	24	3	4	NA
		Positive	0	0	0	0	0	0	0	NA
BACTERIAL DISEASES	*Clostridium perfringes*	Analyzed	0	1	0	4	8	2	2	1
		Positive	0	0	0	0	0	0	1	0
	Escherichia coli	Analyzed	0	1	0	4	8	2	2	1
		Positive	0	0	0	0	1	0	0	0
	Klebsiella Pneumoniae	Analyzed	0	1	0	4	8	2	2	1
		Positive	0	0	0	0	1	0	0	0
	Mycobacterium spp.	Analyzed	0	0	0	0	13	0	1	0
		Positive	0	0	0	0	0	0	0	0
	Salmonella spp.	Analyzed	0	1	0	4	8	2	2	1
		Positive	0	0	0	0	0	0	0	0
	Staphylococcus aureus	Analyzed	0	1	0	4	8	2	2	1
		Positive	0	0	0	1	1	0	0	0
PROTOZOAN DISEASES	*Leishmania* spp.	Analyzed	0	2	0	4	0	1	0	0
		Positive	0	0	0	0	0	0	0	0
	Sarcocystis spp.	Analyzed	2	0	1	0	0	0	3	0
		Positive	1	0	0	0	0	0	1	0
	Toxoplasma gondii	Analyzed	0	0	0	0	2	0	0	0
		Positive	0	0	0	0	2	0	0	0
	Trypanosoma spp.	Analyzed	7	0	4	0	1	1	0	0
		Positive	0	0	0	0	0	0	0	0
MACROPARASITIC DISEASES	*Angiostrogylidae*	Present	4	0	1	0	0	0	0	0
	Ascaridida	Present	1	0	0	0	0	0	0	2
	Diphyllobothriidae	Present	2	0	0	0	0	0	0	0
	Filarioidea	Present	5	0	0	1	5	0	1	0
	Gnathostomidae	Present	0	0	1	0	0	0	0	0
	Oligacanthorhynchidae	Present	5	0	0	0	10	0	0	0

Table 1. Determination of infectious agents by taxon.





Figuras 3. Shown the distribution of differentes variable and region by percentaje of cases

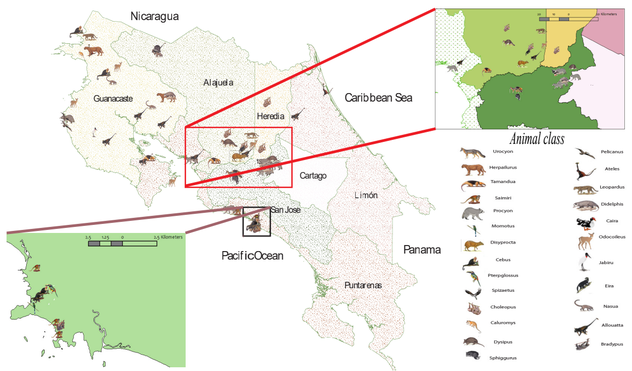


Figure 4. Geo-coding by points and registered vertebrate species

Discussion

The microparasitic pathological agents identified are mainly vector-borne agents (filariae, alphaviruses and flaviviruses), this stresses the role of some of these vertebrates are the reservoir of infectious agents with a high risk of causing epidemics in tropical regions. Which is consistent with studies of predictive models of emerging diseases in Latin America [1].

Concerning infectious agents of direct transmission, the detection of *Klebsiella pneumoniae* is of great relevance. *K. pneumoniae* strains with an hypermucoviscosity phenotype, associated with epizootics of high mortality in non-human primates and are considered an emerging disease in humans. The finding of many bacterial species (Table 1) that also cause infections in humans, shows a latent risk of penetrating the wild animal-human interface [2].

The wild carnivores (mainly Procyonid) showed a high prevalence of Distemper virus, all the cases were from peri-urban and had neurological symptoms and high mortalities. Due to the active and proximity between pets and wildlife in urban, such events should be closely monitored to assess the potential risk and impact on animal conservation. Even when all the specimens tested negative for the Rabies virus, the high prevalence of animals with neurological symptoms highlights the urgency of monitoring diseases with neurological symptoms which could impact public health [3].

The pathogen *Leishmania* spp. and *Trypanosoma* spp. were not detected, possibly associated with the fact that we did not examine specific reservoir hosts, only some sloths from non-endemic areas. However, protozoa such as *Toxoplasma gondii* and *Sarcocystis* spp., agents associated with foodborne and waterborne diseases, were detected. This makes it important to determine if water sources close to infection areas are used for consumption, mainlyin in poor populations, which could facilitate infection of susceptible people [4].

Macroparasites of public health concern were determined, such as *A. costaricensis, B. procyonis* and *P. elegans*, presented a high prevalence over susceptible specimens. The results in our study stressing the needs for more monitoring these parasites in highly populated areas (fig. 4). Mainly because in Costa Rica there's a high prevalence of gastrointestinal parasites in children, which is associated with eating habits [5-6].

Conclusions

Our findings demonstrate:

1. Some pathogens and Public Health related agents were circulating in wildlife species in Costa Rica.
2. There is a need for developing an integrated wildlife disease surveillance and monitoring system for the management of diseases in free-ranging wildlife from Costa Rica.
3.The infrastructure and know-how are also available so a cooperative surveillance system involving the main animals' authorities and the school veterinary medicine could be set up.

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