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Exposure of stray and hunting dogs to SARS CoV-2 in Campania, southern Italy

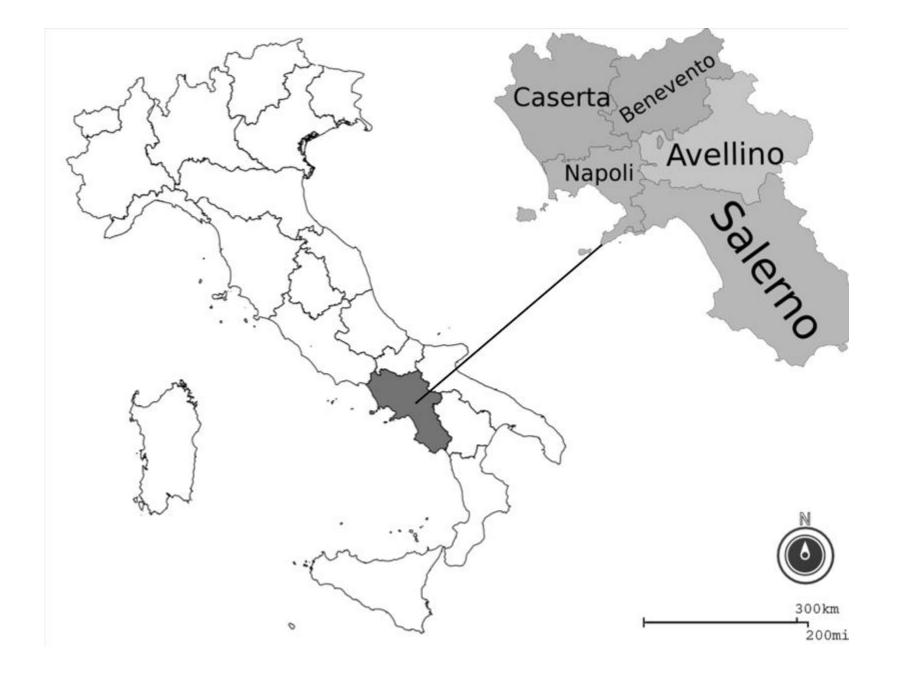
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INTRODUCTION & AIM

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a single-stranded RNA virus responsible for the COVID-19 pandemic in humans. The infection has caused billions of cases worldwide, millions of deaths, as well as huge economic losses. The scientific community was immediately concerned about possible spillovers towards animals. SARS-CoV-2 has been described in cats, dogs, non-human primates, minks, and nowadays in more than 30 animal species (including livestock, wildlife, and zoo animals). Although Sars-CoV-2 prevalence in dogs has been extensively studied in different periods, there have been few studies that evaluate the dynamics of transmission across dogs in various living conditions (for example hunting or stray dogs), as well as the associated risk factors for each. The purpose of this study was to assess the exposure of hunting dogs and stray dogs to SARS-CoV-2 in the Campania canine population of southern Italy, as well as the virus's potential spread in the environment via feces.

METHOD



A total of 112 dogs were sampled (53 hunting and 59 stray). Sampling began in September 2023, when in Italy the main circulating SARS Cov-2 variant was omicron. For each animal, a blood sample was collected in a tube without anticoagulant (for serum) and a stool sample directly from the rectal ampulla. After the collection, all samples were immediately transported to the Department of Veteri-nary Medicine and Animal Production of Naples, maintaining the cold chain. Each sample was accompanied by document containing the animal's data (age, sex, breed, attitude, size, and location). All serum samples were tested for the presence of antibodies directed against the nu-cleocapsid (N) antigen and towards the spike (S) antigen using two ELISAs, respectively ID Screen® SARS-CoV-2 Double Antigen Multi-species ELISA (IDVet) and WANTAI SARS-CoV-2 Ab ELISA (WANTAI). RNA from each fecal sample was extracted using the commercial kit QIAamp® Viral RNA Mini Kit (Qiagen). The extracted RNA was quantified by nanodrop and used as a tem-plate for a single-step-RT-real-time PCR (Norgen's COVID-19 TaqMan RT-PCR Kit N/ORF1ab genes, Norgen) for simultaneous amplification of the N gene and the Open Reading Frame 1ab (ORF1ab).

RESULTS & DISCUSSION

The results of our study highlighted the presence of antibodies against SARS-CoV-2 in 5 out of 112 dogs tested, corresponding to an overall seroprevalence of 4.5%. The only risk factor statistically associated with greater exposure to the virus was the origin, as animals belonging to kennels had a higher prevalence (8.5%) than hunting dogs (0%). All feces from the sampled animals were tested with a one-step RT-real-time PCR protocol for the amplification of two viral genes. No sample tested positive for the two genes investigated. The prevalences we observed are very similar to those of other studies conducted in other geographical areas.

Factor	n	Positive	%	95%CI	χ^2	p
Total	112	5	4.5			
Province						
Avellino	19	0	0			
Benevento	11	1	9.1			
Salerno	36	1	2.8		3.6	0.46
Caserta	35	3	8.6			
Napoli	11	0	0			
Sex						
Male	67	2	3			
					0.85	0.35
Female	45	3	6.7			
Age						
Young	30	0	0			
Adult	55	2	3.6		4.28	0.12
Old	27	3	11.1			
Bred						
Mix	46	4	8.7			
					3.28	0.07
Specific bred	66	1	1.5			

CONCLUSION

Pets have been and continue to be predisposed to exposure to SARS CoV-2 due to their relationship with humans. In this study, the seroprevalence of shelter dogs in a region of southern Italy was evaluated. The results obtained highlight the circulation of SARS CoV-2 in this population of dogs, leading to the hypothesis that contact with infected operators is sufficient to transmit the infection to dogs.

FUTURE WORK / REFERENCES

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