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## Studying *Rotavirus* zoonosis/interspecies transmission by whole genome sequencing of viral strains

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*Rotavirus-A* (RVAs) are a major cause of severe viral diarrhea in the young of humans and animals. RVAs are zoonotic pathogens. Since all 11 segments of the RVA genome are susceptible to reassortment events, analyses of the antigenically significant RVA outer capsid protein VP7 and VP4 encoding genes may not be sufficient to obtain conclusive data on RVA zoonosis/interspecies transmission and reassortment events, necessitating whole genomic analysis of RVAs. During the last eight years, we have performed whole genome sequencing on several RVA strains detected in a wide variety of host species (humans, pigs, cattle, goats, horses and monkeys) from different countries, including developing countries (Bangladesh, India, Indonesia, Kenya, Thailand, Venezuela and West Indies). Whole genomic analyses of these RVAs yielded a plethora of conclusive, crucial and/or first-time data on zoonosis/interspecies transmission and reassortment events of RVAs, such as first conclusive evidence for simian-to-human and porcine-to-simian interspecies transmission of RVAs, interspecies transmission of RVAs from cattle and pigs to humans, detection of human RVAs possessing caprine RVA-like gene segments on a human RVA genetic backbone, common evolutionary pathways of typical human RVA strains with bovine and porcine RVAs, interspecies transmission of RVAs from pigs and cattle to horses, complex animal-human and animal-animal RVA reassortment events, and identification of novel RVA genotypes. Taken together, our findings provided vital insights into *Rotavirus* zoonosis/interspecies transmission and animal-human reassortment events, especially in developing countries where humans live in close proximity to animals with implications on public health.

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## Molecular epidemiology of *Theileria annulata* in bovine of three different temporal regions of Pakistan

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Tropical theileriosis is a tick-borne hemoparasitic disease caused by *Theileria annulata*, which negatively affects the immune physiology of the livestock and hence make them more prone to a number of serious health maladies. A study was conducted in three temporal zones of Khyber Pakhtunkhwa (KPK) province of Pakistan, to monitor the prevalence of *T. annulata* and the associated risk factors in bovine at molecular level. A total of 900 blood samples were collected from 479 cows and 421 buffaloes. The overall prevalence of *T. annulata* was found 18.88%. The central zone showed the highest prevalence i.e., 21.66% (49/300), followed by southern and northern zone with 18.66% (65/300) and 16.33% (56/300) prevalence, respectively. Cows were found significantly more susceptible as compared to buffalo population. The univariate analysis of risk factors like temporal zone, specie, breed, sex, age, management system, tick infestation, previous tick history, tick control, type of acaricide used and interval of acaricide usage showed a significant ( $p < 0.05$ ) association with prevalence of *T. annulata* in bovine of the three zones. Previous history, tick infestation and breed of animals especially in cows were found as the most potential risk factor of tropical theileriosis. The results revealed here will help in developing more effective control strategies in future for dairy farmers in Pakistan.

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