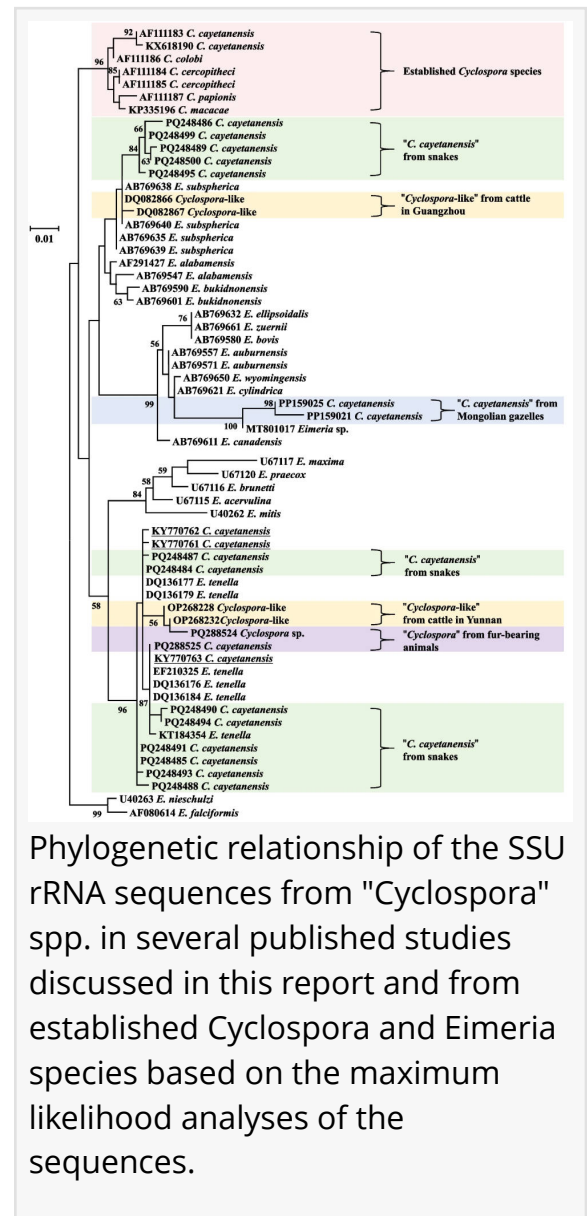


Genetic reanalysis redraws China's Cyclospora risk map

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A review of genetic evidence from China is challenging assumptions about whether animals serve as reservoirs for the human diarrheal parasite *Cyclospora* *cayetanensis*. By reassessing epidemiological reports and DNA sequences from humans, animals, fresh produce, and water, the authors found that several detections of the parasite in animals were probably misidentifications involving closely related *Eimeria* parasites. The review also shows that human *C. cayetanensis* populations in China have distinctive genetic patterns that may aid disease surveillance and outbreak investigations. Together, the findings refine current understanding of cyclosporiasis epidemiology and provide a practical framework for more reliable surveillance, source tracing, food-safety assessment, and One Health prevention without treating every positive animal test as evidence of zoonotic spread.

Cyclosporiasis can cause prolonged watery diarrhea and other gastrointestinal symptoms, while outbreaks are frequently associated with contaminated fresh produce or water. Although *C. cayetanensis* is generally regarded as human-specific, polymerase chain reaction (PCR) surveys have reported the parasite in cattle, monkeys, pets, fur-bearing animals, snakes, and wildlife. Many tests target the small-subunit ribosomal RNA (SSU rRNA), a region in which *Cyclospora* and *Eimeria* can be highly similar. Cross-reacting primers, unsuitable reference sequences, and incomplete phylogenetic comparisons may therefore misidentify a related parasite to an apparent zoonotic threat and distort public-health priorities. Because of these challenges, deeper investigation of *Cyclospora* host specificity and its true transmission routes is needed.



review was conducted by researchers from the College of Veterinary Medicine at South China Agricultural University. The team examined *Cyclospora* epidemiology and genetic diversity in China, reassessed reports from animal and environmental samples, and evaluated whether existing molecular evidence supports zoonotic transmission of *C. cayetanensis* across different host species.

The researchers searched PubMed and the China National Knowledge Infrastructure ([CNKI](#)), without language restrictions, for studies published through 2025. They compiled prevalence findings from human populations and reviewed reports involving nonhuman primates, cattle, companion animals, fur animals, snakes, fresh produce, sewage, and water. Published sequence data were then re-evaluated, with particular attention to SSU rRNA identity, reference-sequence validity, and phylogenetic placement.

Across PCR-based human studies, *C. cayetanensis* was detected in 111 of 13,703 people, an overall prevalence of 0.8%, although individual estimates ranged from 0.2% to 10.0%. Infection patterns varied with residence, season, and clinical or immune status, while many cases occurred during warmer months. Multilocus sequence typing (MLST), whole-genome sequencing (WGS), and mitochondrial analyses indicated that Chinese isolates form geographically distinctive populations.

Animal evidence was less convincing. Macaques were mainly infected with the host-adapted species *Cyclospora macacae*. Reanalysis of published data suggested that a "Cyclospora-like" parasite reported in cattle was probably *Eimeria subspherica*, while several sequences attributed to *C. cayetanensis* in cattle, fur animals, Mongolian gazelles, and snakes clustered more closely with known *Eimeria* species. Limited detections of *C. cayetanensis* in lettuce, sewage, wastewater, and macaque-associated lake water nevertheless reinforce the need to monitor environmental routes, particularly irrigation water that may contaminate crops.

The authors said the central message is not that animal or environmental surveillance should be reduced, but that unexpected detections require stronger and more transparent evidence. They said a single PCR result or close SSU rRNA match cannot reliably establish a new host when related *Eimeria* species may be present. Microscopy, validated reference sequences, and confirmation across multiple genetic markers can distinguish genuine transmission signals from analytical error. This distinction matters because overstating zoonotic risk may misdirect public-health resources, while underestimating contaminated produce or water could leave important exposure routes insufficiently controlled.

The review provides a diagnostic roadmap for laboratories, veterinarians, food-safety agencies, and outbreak investigators. Suspected *Cyclospora* infections in unexpected hosts should be verified by microscopy, including examination of oocyst size, shape, and sporulation, rather than by PCR alone. Sequence analysis should include validated references from both *Cyclospora* and *Eimeria* and should be followed by multilocus confirmation. The authors also recommend combining SSU rRNA analysis with markers such as the cytochrome c oxidase subunit I (COI)

gene. More accurate identification could improve outbreak source attribution, strengthen surveillance of irrigation water and fresh produce, distinguish true hosts from mechanical carriers, and support targeted cyclosporiasis prevention without exaggerating evidence for cross-species transmission.

References

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