Cryptic Invasion and Transmission Dynamics of Peste des Petits Ruminants Virus, Europe, 2024–2026

Claire Guinat, Samia Guendouz, Olivier Kwiatek, Eva Connilhere, Antoni Exbrayat, Aikaterini Kirtzalidou, Maria Gianniou, Corina Ancuceanu, Mona Ghiță, Anna Zdravkova, Iliyan Kostov, Emilia Ivanova, Florica Bărbuceanu, Konstantia E. Tasioudi, Peter Malik, Adrienn Örkényi, Erga Shkodra, Armend Cana, Ivana Lojkić, Andreja Jungić, Antun Beljan, Marina Prišlin-Šimac, Dragan Brnić, Ljupka Maltar, Žaklin Acinger-Rogić, Martina Rubin, Ivana Lohman Janković, Michaela Stätter, Daniel Polzer, Susanne Koethe, Arnaud Bataille

Peste des petits ruminants (PPR) disease has spread in southeastern Europe since July 2024. Virus sequence analyses and field investigations covering 7 countries affected through January 2026 suggest that eastern Romania was the point of introduction and source of regional viral dissemination in the region. Cross-border transmission inferred from genetic data was strongly associated with official records of live animal trade; outbreak investigations indicate additional roles for illegal trade and indirect transmission. Important temporal gaps in the phylogeny suggest that PPR virus has been circulating undetected in multiple areas in southeastern Europe, as noted by the high variability of clinical signs in infected animals. Those findings highlight a real risk for continued spread across Europe. Increased awareness of the difficulty in detecting the disease, coordinated cross-border surveillance, timely data sharing, and integrated control measures are needed to stop the spread of PPR into Europe.

Since July 2024, the sheep and goat disease called peste des petits ruminants (PPR) has reemerged in Europe (*1*) (Figure 1). After a limited incursion in Bulgaria in 2018, Europe is experiencing its largest recorded PPR epizootic in 2026. Listed as a category A animal disease within the European Union (EU), PPR requires immediate implementation of eradication mesures in infected holdings. During July 2024–January 2026, a total of 183 outbreaks, corresponding to small ruminant holdings with ≥1 laboratory-confirmed case, were officially reported across Greece, Romania, Bulgaria, Hungary, Albania, Kosovo, and Croatia, resulting in the mass culling of hundreds of thousands of sheep and goats. Infections with PPR virus (PPRV; *Morbillivirus caprinae*) are usually characterized by high rates of illness, including clear clinical symptoms such as including nasal discharge, mucosal erosion, and diarrhea (*2*), and deaths. In Europe, the clinical picture in is highly variable; many outbreaks are associated with lower mortality rate (0%–10%) and few or no clinical signs (e.g., limited nasal or ocular

Author affiliations: University of Toulouse ENVT INRAE IHAP, Toulouse, France (C. Guinat); ASTRE University of Montpellier, CIRAD, INRAE, Montpellier, France (S. Guendouz, O. Kwiatek, E. Connilhere, A. Exbrayat, A. Bataille); Directorate of Veterinary Center of Athens, Ministry of Rural Development and Food, Athens, Greece (A. Kirtzalidou, K.E. Tasioudi); Ministry of Rural Development and Food, Athens (M. Giannou); Institute for Diagnosis and Animal Health, Bucharest, Romania (C. Ancuceanu, M. Ghiță, F. Barbuceanu); Bulgarian Food Safety Agency, Sofia, Bulgaria (A. Zdravkova); Republic of Bulgaria Ministry of Agriculture and Food, Sofia (I. Kostov); National Diagnostic and Research Veterinary Medical Institute, Sofia (E. Ivanova), Faculty of Veterinary Medicine, Bucharest (F. Bărbuceanu); National Food Chain Safety Office, Budapest, Hungary (P. Malik, A. Örkényi); Food Safety and Veterinary Institute, Tirana, Albania (E. Shkodra); Kosovo Food and Veterinary Laboratory, Pristina, Kosovo (A. Cana); Croatian Veterinary Institute, Zagreb, Croatia (I. Lojkić, A. Jungić, A. Beljan, M. Prišlin-Šimac, D. Brnić); Ministry of Agriculture, Forestry and Fisheries, Zagreb (L. Maltar, Ž. Acinger-Rogić, M. Rubin, I.L. Janković); Austrian Agency for Health and Food Safety, Mödling, Austria (M. Stätter, D. Polzer, S. Koethe)

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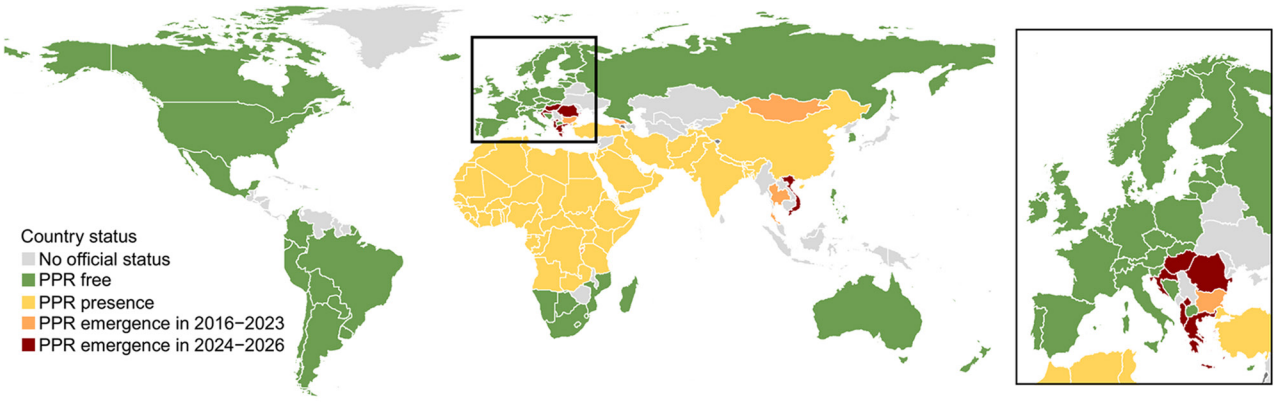


Figure 1. Global distribution of PPR since 2016. Emergence in 2024–2026 is highlighted in Asia, particularly Vietnam, and in Europe (inset) in Greece, Romania, Hungary, Albania, Kosovo, and Croatia. Data source: World Organisation for Animal Health (https://www.woah.org). PPR, peste des petits ruminants.

discharge, abortions) and are easily mistaken for other diseases or overlooked, which can delay detection of infections. Despite control measures that included movement restrictions, enhanced surveillance, and culling of infected herds, the disease continues to spread, highlighting the challenges in the early detection and containment of the disease in Europe. The situation is of particular concern considering the scale of small-ruminant production in Europe; ≈67 million sheep and goats are raised primarily in Spain, Greece, Romania, France, and Italy (*3*,*4*).

PPR is endemic in large parts of Africa, Asia, and the Middle East, where it represents a major disease in small ruminant production (Figure 1). Current evidence supports that other susceptible animals, such as wild ruminants, play a limited role in PPR epidemiology (*5*). PPR affects more rural and marginalized communities because goats and sheep in those regions are often raised by smallholder farmers or nomadic populations with limited resources. Consequently, PPR not only affects animal health but also exacerbates poverty and livelihood insecurity (*6*,*7*). The resulting economic losses are substantial, US $1.5–2 billion annually (*8*). The severe impact of PPR on vulnerable populations has led the Food and Agriculture Organization of the United Nations (FAO) and the World Organisation for Animal Health to launch a global eradication program for PPR, aiming to eradicate the disease by 2030 through coordinated surveillance and targeted vaccination strategies (*8*), using vaccines that are efficient against all 4 existing PPRV genetic lineages (*9*). Despite those efforts, several hundred PPR outbreaks have continued to be reported since 2016, including newly affected areas (Figure 1); the widespread PPRV lineage IV plays a major role in those emergences (*10*).

In this context, disentangling the epidemiologic links and transmission routes underlying introduction and spread of PPR in Europe is critical for informing surveillance and control strategies. Here, we performed phylodynamic analyses of PPRV circulating in Europe during 2024–2026. We leveraged a timely virus whole-genome sequence dataset generated by the EU Reference Laboratory for PPR (EURL-PPR, https://eurl-ppr.cirad.fr) in collaboration with national reference laboratories and included the results of epidemiologic investigations conducted by veterinary authorities of the affected countries. Our objectives were to identify the likely geographic origins of viral introductions into the affected countries, quantify viral spread between countries, and assess the role of live small-ruminant trade in shaping spatial transmission dynamics. Our findings provide a detailed picture of the ecology and spread of PPRV during its recent emergence in Europe, with direct implications for surveillance, prevention, and control.

Methods

Data Collection and Processing

We retrieved PPR outbreak data in small ruminant farms in Europe from January 2015–January 2026 from national reference laboratories and veterinary services and completed with the Global Animal Disease Information System database of the FAO (https://empres-i.apps.fao.org) as of January 28, 2026. No ethics approval was required for this study; all samples used were collected by the competent veterinary authorities within the frame of official investigations concerning outbreaks of a category A disease (PPR).

The EURL-PPR generated whole-genome sequences of PPRV circulating in small ruminant holdings in Europe during July 2024–December 2025, as described previously (*10*). We replaced the library preparation

steps with the Illumina Stranded Total RNA Prep kit with ligation with Ribo-Zero Plus (https://www.illumina.com). That procedure obtained nearly complete genomes from samples with a relatively low viral load (cycle threshold <30) and from complex matrices like blood. The National Reference Laboratory of Austria generated a genome sequence from quarantined sheep in Romania after amplification of 9 overlapping amplicons with primers designed in PrimalScheme (*11*) using Illumina paired-end sequencing. Those sequences originated from samples collected in the first infected farms identified in each affected country, as well as from additional farms in newly affected regions, or when new epidemiologic contexts were suspected via outbreak investigations. We assembled genomes from raw sequencing data using an in-house bioinformatic pipeline (*12*). We obtained nearly complete genomes (>95% coverage) for all samples (Table). We inspected and trimmed sequences as described previously (*13*), then aligned them using Geneious version 10.2.6 (https://www.geneious.com) with a selection of reference PPRV genomes of the lineage IV North-East Africa clade (*12*), previously shown to be the most closely related to the strains circulating in Europe (*10*). We inferred maximum-likelihood phylogenies from the resulting alignment using RAxML-NG (*14*) under a

Table. Characteristics of peste des petits ruminants virus samples after genomic sequencing in study of transmission dynamics of the virus, Europe, 2024–2026*

Country	Locality	Outbreak date	Sample ID	Sample type	Host	Coverage, %	Mean depth	GenBank accession no.
Albania	Bulqize	2025 Jun 9	D4870	Nasal swab	Goat	99.4	136	PZ271097
	Diber	2025 Jun 9	D4867	Spleen	Goat	99.2	151	PZ271098
	Shkoder	2025 Jun 4	D4861	Lung	Goat	98.3	7	PZ271096
Austria	Horn	2025 Feb 27	842–48	Nasal swab	Sheep	95.5	6000	PZ271138
Croatia	Bogdanovici	2025 Dec 13	11	Vaginal swab	Sheep	99.4	11390	PZ271099
Greece	Aitoloakarnania	2024 Aug 22	2356	Blood	Sheep	99.3	256	PZ271101
	Aitoloakarnania	2024 Aug 22	2532	Nasal swab	Sheep	99.4	369	PZ271100
	Attiki	2024 Jul 29	612	Nasal swab	Sheep	99.4	1121	PZ271102
	Crete	2024 Aug 1	836	Lung	Sheep	99.5	423	PZ271103
	Karditsa	2024 Aug 2	862	Nasal swab	Sheep	98.2	7.5	PZ271104
	Korinthia	2024 Jul 27	376	Nasal swab	Sheep	98.6	9.4	PZ271105
	Korinthia	2024 Aug 5	838	Rectal swab	Sheep	99.2	18.5	PZ271106
	Larissa	2024 Jul 24	163	Lung	Sheep	99.6	8759	PZ271107
	Rodopi	2024 Sep 3	2458	Blood	Sheep	84.1	4.5	PZ271108
	Kalambaka	2024 Jul 11	72A	Lung	Sheep	97.9	18.8	PZ271109
Hungary	Zala	2025 Jan 31	6393	Nasal swab + lung	Sheep	98.9	13.1	PZ271110
Kosovo	Prizren	2025 Jul 2	205	Nasal swab	Goat	99.3	2165	PZ271111
	Prizren	2025 Sep 26	450	Nasal swab	Goat	94.2	7.9	PZ271112
Romania	Babadag	2024 Jul 22	34	Pool organs	Sheep	90.0	4.1	PZ271114
	Babadag	2024 Jul 23	128	Pool organs	Sheep	98.5	1048	PZ271116
	Babadag	2024 Jul 24	53	Pool organs	Sheep	99.5	98	PZ271115
	Babadag	2024 Jul 31	14	Pool organs	Sheep	98.9	16.5	PZ271113
	Baia	2024 Jul 31	15	Nasal swab	Sheep	99.1	35	PZ271118
	Baia	2024 Aug 10	3	Nasal swab	Sheep	99.3	18.9	PZ271117
	Bihor	2025 Mar 5	203	Pool organs	Sheep	99.0	24	PZ271119
	Constanta	2024 Jul 23	1	Nasal swab	Sheep	99.3	93	PZ271120
	Haidar	2024 Aug 2	11	Nasal swab	Sheep	99.3	28.3	PZ271121
	Lalomita	2024 Aug 4	5	Nasal + ocular swab	Sheep	99.2	20.2	PZ271122
	Macin	2024 Jul 30	122	Pool organs	Sheep	99.0	8.7	PZ271123
	Stejaru	2024 Jul 26	77	Pool organs	Sheep	99.5	190.8	PZ271127
	Stejaru	2024 Jul 26	80	Nasal swab	Sheep	99.3	59.8	PZ271128
	Stejaru	2024 Jul 26	81	Pool organs	Sheep	95.5	6.5	PZ271129
	Stejaru	2024 Jul 26	93	Pool organs	Sheep	99.4	16953	PZ271130
	Stejaru	2024 Jul 26	96	Nasal swab	Sheep	99.3	52	PZ271131
	Stejaru	2024 Jul 26	98	Nasal swab	Sheep	99.3	264	PZ271132
	Stejaru	2024 Aug 2	6	Nasal swab	Sheep	98.2	8.6	PZ271126
	Stejaru	2024 Aug 2	7	Nasal swab	Sheep	99.3	1563	PZ271125
	Stejaru	2024 Aug 2	8	Nasal swab	Sheep	99.3	151	PZ271124
	Timis	2024 Jul 26	57	Pool organs	Sheep	99.0	27276	PZ271133
	Timis	2024 Aug 24	224	Ocular swab	Sheep	98.9	1428	PZ271134
	Timis	2024 Aug 30	357	Ocular swab	Sheep	98.3	230.9	PZ271135
	Timis	2024 Sep 2	612	Nasal swab	Sheep	99.4	1121	PZ271136
	Vulturu	2024 Aug 8	4	Nasal swab	Sheep	99.4	10672	PZ271137

*Outbreak date is date of laboratory confirmation; mean depth, mean number of sequencing read per genome position in the reference PPRV genome used for the alignment. Pool organs indicates that multiple organs (lung, spleen, lymph nodes) were pooled. Data corresponding to the 4 sequences from Romania, Greece, and Bulgaria previously published (*10*) are not included.

general time reversible nucleotide substitution model with gamma distributed among site rate variation. We assessed temporal signal by examining the relationship between genetic divergence and sampling dates.

We retrieved live small ruminant trade data between the study countries in Europe from the Food and Agriculture database of the FAO (https://www.fao.org/faostat) as of February 11, 2026; the most recent available data were from 2024. We aggregated trade data into a matrix summarizing the total number of live sheep and goats transported between each pair of countries in 2023 and 2024, expressed as number of heads.

Phylodynamic Analysis

To quantify PPRV transmission dynamics between countries, we inferred time-calibrated phylogenies and viral migration parameters with a Bayesian phylodynamic framework implemented in BEAST version 2.7.5 (*15*). We performed analyses using the same substitution model (*16*), an uncorrelated lognormal relaxed molecular clock model (*17*), and a Bayesian structured coalescent skyline model (*18*). To visualize PPRV diffusion in space and time, we conducted complementary analyses in BEAST version 1.10.4 (*19*), using similar substitution and molecular clock models but assuming a Bayesian exponential coalescent model and a relaxed random walk model (*20*). We extracted spatiotemporal information embedded within the posterior phylogenies using the seraphim package (*21*). We ran analyses for 100 million Markov chain Monte Carlo steps, sampling phylogenies and model parameters every 10,000 steps. We assessed convergence and mixing properties using Tracer version 1.7.2 (*22*). After discarding the first 10% of samples as burn-in, we generated maximum clade credibility phylogenies using TreeAnnotator version 1.10.4 (*15*,*19*) and annotated using the ggtree package (*23*). To assess whether live animal trade was associated with viral transmission between countries, we evaluated the relationship between the number of inferred migration events and the number of live sheep and goat movements between countries pairs, using a Mantel test based on Spearman rank correlation with 999 permutations and a significance threshold of $p<0.05$. We conducted analyses in R version 4.2.2 (The R Project for Statistical Computing, https://www.r-project.org).

Results

Genomic Surveillance of PPR Outbreaks in Europe

Among the 183 PPR outbreaks, most occurred in the more abundant sheep holdings and encompassed a wide range of production types, from smallholder backyard systems to large collection centers of >50,000 sheep, which aggregate animals from smaller farms for international export. Most outbreaks were reported in Greece (86/183 [47%]) and Romania (67/183 [37%]) during July–October 2024 (Figure 2, panel A). Some outbreaks in Greece could be identified after tracing animal trade movements from Romania to different regions of Greece. We observed sporadic detections in Hungary (3/183 [2%]), Bulgaria (1/183 [1%]), and Romania (1/183 [1%]) during November 2024–March 2025. The first outbreak in Hungary was linked to importation of animals from the western part of Romania, near the border with Hungary, although no outbreak had been reported from Romania since September 2024. During official controls in February 2025, the virus was detected in sheep transported from a collection center in western Romania to a slaughterhouse in Austria for direct slaughter. That collection center was subsequently confirmed as infected in March 2025. Of interest, sheep inspected in the truck at arrival in Austria showed clear clinical signs and some deaths, whereas no sheep in the collection center showed clinical signs despite being confirmed positive by PCR. Outbreaks were then reported in Albania (17/183[9%]) and Kosovo (2/183 [1%]) in summer, June–September 2025, and in Croatia (6/183 [3%]) in winter, December 2025–January 2026. Field investigations in Kosovo suggested that the emergence was related to the illegal purchase of animals from Albania. The origin of the introduction in Romania, Bulgaria, Albania, and Croatia has not yet been identified, although illegal trade is also thought to be involved.

We analyzed a total of 47 PPRV whole-genome sequences from 7 countries, 42 obtained for this study and 4 in a previous study (*10*) by the EURL-PPR. Most were from Romania (n = 27) and Greece (n = 11), followed by Albania (n = 3), Kosovo (n = 2), Hungary (n = 1), Bulgaria (n = 1), and Croatia (n = 1) (Table). We obtained 1 additional sequence in Austria from quarantined imported sheep originating from Romania. The spatiotemporal distribution of the 47 Europe sequences broadly reflected the reported outbreak dynamics (Figure 2, panel B).

Europe Clustering and Regional Spread

We examined the phylogenetic structure of PPRV genome samples during the 2024–2026 Europe outbreaks. Maximum-likelihood phylogeny inference showed that the 47 sequences formed a single well-supported monophyletic cluster (bootstrap support >95%) nested within the Northeast Africa clade of lineage IV (*12*) (Figure 3; Figure 4, panel A). That

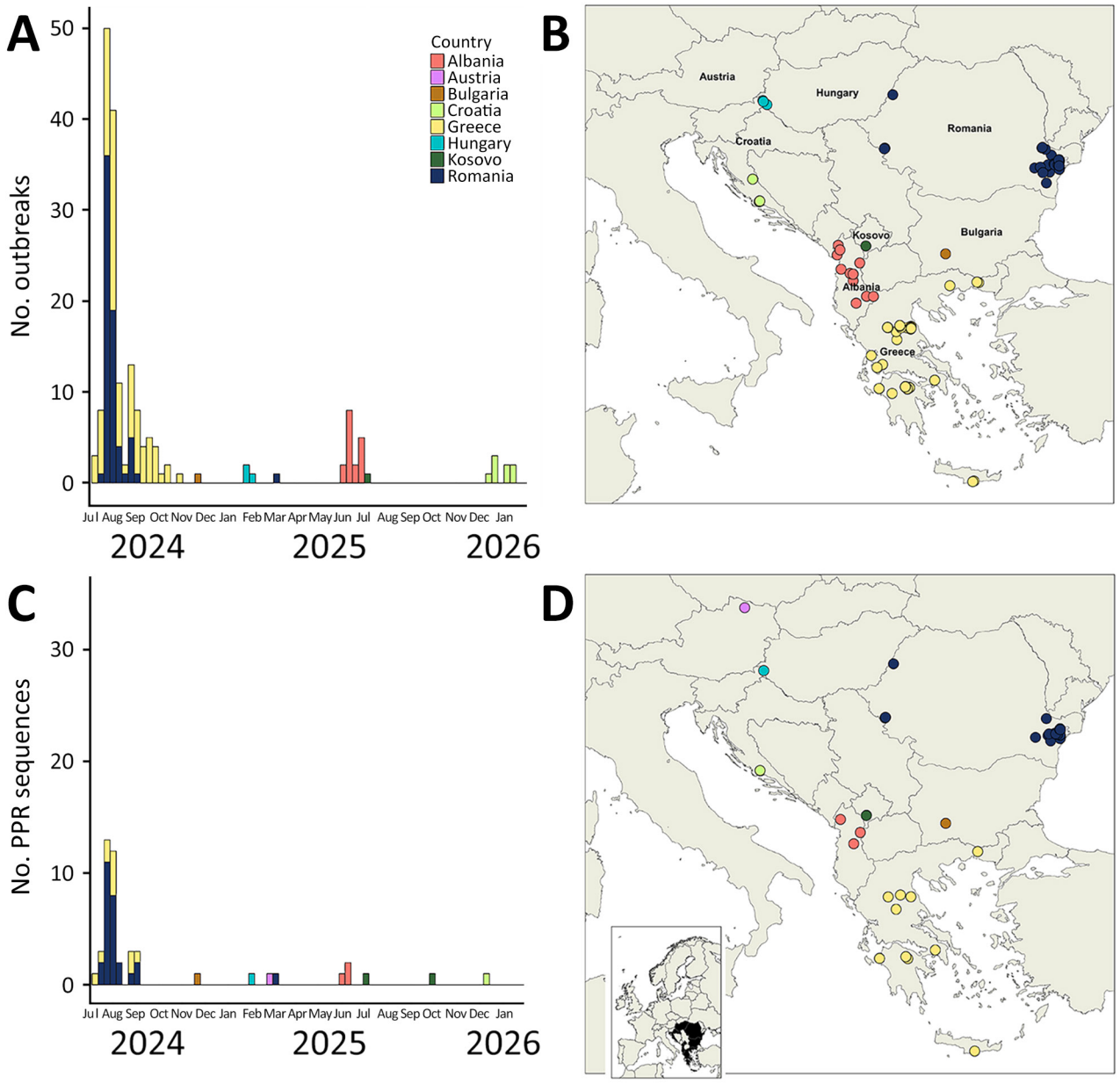


Figure 2. Spatiotemporal epidemiology and sequencing efforts of PPR in Europe, 2024–2026. A) Distribution over time of 183 PPR outbreaks in Europe. B) Geographic locations of those outbreaks. Data source: Global Animal Disease Information System (https://empres-i.apps.fao.org). C) Distribution over time of 47 sequences obtained from the outbreaks. D) Geographic sources of those sequences. Inset shows outbreak area within Europe. Data source: European Union Reference Laboratory for PPR (https://eurl-ppr.cirad.fr). PPR, peste des petits ruminants.

clustering was consistent with previous reports (*10*,*24*) and suggested that the emergence in Europe had a common origin followed by regional spread. The phylogeny also showed that sequences sampled in Romania and Greece occupied basal positions and sequences from both countries formed several closely related groups, suggesting sustained and multiple transmission events between the 2 countries (Figure 3). Sequences from Albania, Kosovo, and Hungary formed a well-supported monophyletic group (bootstrap support >95%), suggesting a common origin for the spread into those countries. In contrast, sequences from Croatia and Bulgaria were scattered across the phylogeny, pointing toward independent introductions to those countries. As expected, the sequence obtained in Austria from quarantined sheep imported from Romania was highly similar to the sequence from the associated outbreak in an infected collection

center in the Bihor province in western Romania. However, those 2 sequences did not group with any other sequences from 2025, suggesting no direct link with the introduction into other countries.

Repeated Cross-Border Transmission Events and Silent Spread

We next aimed to approximate the chains of cross-border transmission linking affected countries. Root-to-tip regression analysis revealed a strong positive correlation between genetic divergence and sampling dates among the European sequences (r = 0.82), indicating progressive accumulation of genetic substitutions over time and confirming the suitability of the dataset for phylodynamic inference using molecular clock models (Figure 4, panel B). Bayesian phylodynamic analyses showed that most internal nodes of the time-calibrated phylogeny belong to Romania (posterior probability [PP] >0.75), suggesting Romania acted as the primary source of regional viral

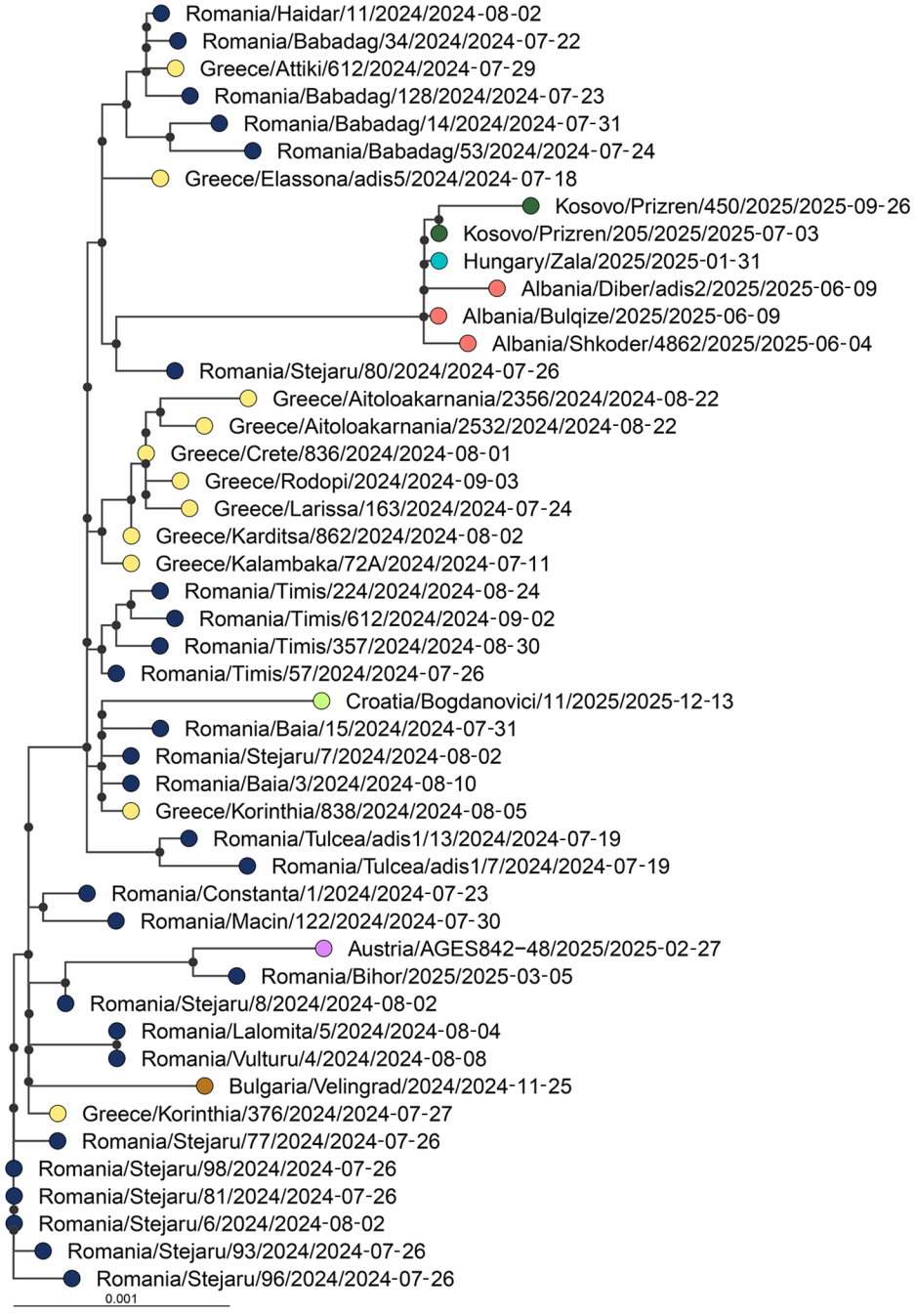


Figure 3. Maximum-likelihood phylogeny of peste des petits ruminants virus genomes identified in study of transmission dynamics of the virus, Europe, 2024–2026. Node color indicates sampling country. Black internal nodes indicate bootstrap support values >0.75. Scale bar indicates substitutions per site.

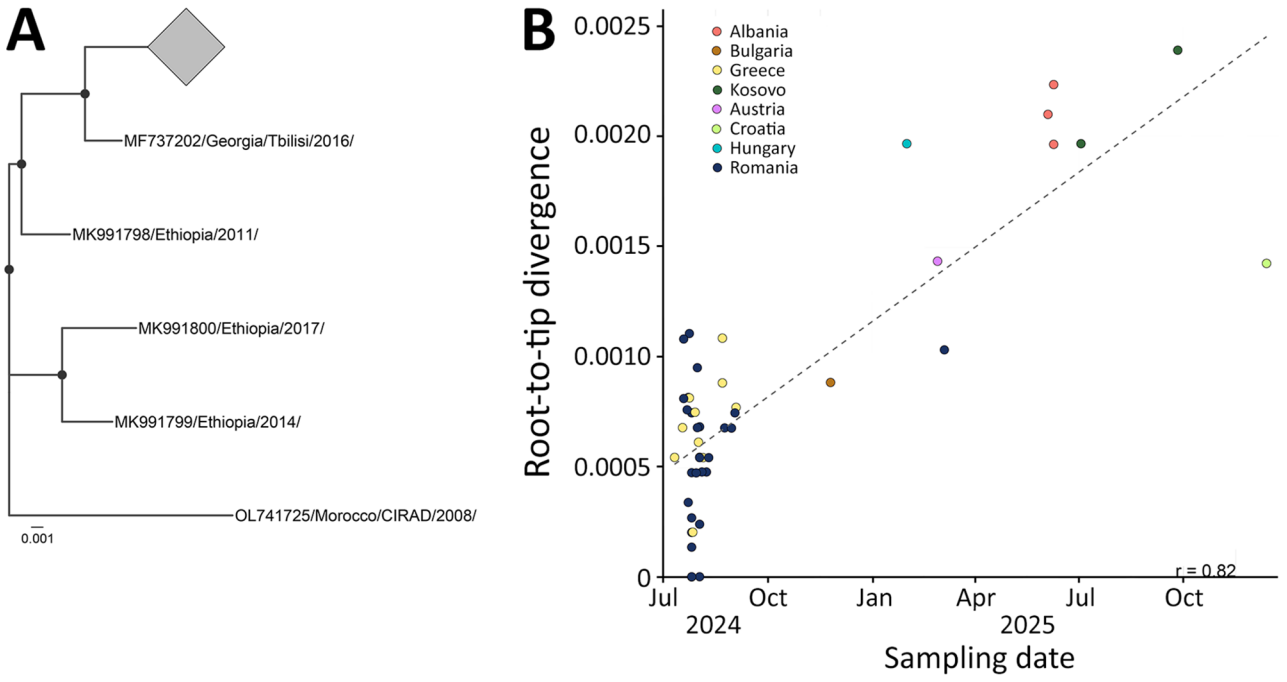


Figure 4. Molecular phylogenetics of peste des petits ruminants virus genomes identified in study of transmission dynamics of the virus, Europe, 2024–2026. A) Maximum-likelihood phylogeny of virus genomes. Gray diamond indicates the location of the European clade (Figure 3) within lineage IV. Scale bar indicates substitutions per site. Black internal nodes indicate bootstrap support values >0.75. B) Root-to-tip regression of genetic divergence between sequences from Europe against sampling dates.

spread (Figure 5). Sampling bias toward Romania might have affected those results and should be interpreted cautiously. Nevertheless, Romania was associated consistently with the highest median number of inferred viral migration events as a source country (Figure 6, panel A), in particular from Romania to Greece (median = 5 [95% highest posterior density interval 1–8]) (Figure 6, panel A), reflecting repeated transmission events from Romania (in particular, eastern Romania) to several provinces of Greece (including Thessaly, Peloponnese, and Central Greece), and from Thessaly to Crete (Figure 5; Figure 6, panel B). Field investigations supported that pattern, showing virus transmission through live-animal trade. Beyond the initial Romania–Greece transmission period, we inferred eastern Romania as the likely origin of detections in Bulgaria and Croatia (PP >0.75) (Figure 5; Figure 6, panel A), as well as in 2 different areas in western Romania (Timiş and Bihor provinces) (Figure 5; Figure 6, panel B). The detection in Timiş province in 2024 could be directly related to the legal movement of animals from eastern Romania before implementation of movement restrictions, but the origin of the infections in Bihor province in 2025 could not be traced to other outbreaks in Romania. Eastern Romania was also inferred as a likely source of separate introductions into Hungary and Albania, with subsequent transmission from Albania to Kosovo (PP >0.75) (Figure 5). Field investigation traced the Hungary outbreak back to animal movements from a live animal market in western Romania; however, we lacked sufficient data to connect that specific market with eastern Romania. Several long branches in the phylogeny separated sequences from different countries, particularly sequences from Croatia (December 2025) and Romania (August 2024), indicating substantial unsampled diversity with large temporal gaps; those gaps might represent outbreaks not detected during that period.

Contribution of Live Small Ruminant Trade to Regional Spread

The patterns of cross-border transmission and previous studies from Africa and Asia suggest that trade of live small ruminants might be an important source of cross-border PPR transmission (*25*–*26*; S. Gao et al., unpub. data, https://doi.org/10.22541/au.159646793.37101393). We investigated the potential role of live small ruminant trade in shaping regional viral spread. Bayesian phylodynamic analyses estimated an average wavefront velocity of 10.8 km/wk over the study, along with a period of rapid expansion; we observed the highest weekly peak, 153.1 km/wk, in May 2024. Those estimates should be

interpreted cautiously because undetected regional circulation could affect velocity calculations; rapid, long-distance spread is inconsistent with local diffusion alone and suggests human-mediated movements, such as trade of live animals. To further explore the hypothesis, we retrieved the official records of live small ruminant (sheep and goats) movements between the study countries in 2023 and 2024. In both years, the highest volumes of trade were from Romania to Greece (≈500,000–1 million animals), followed by Romania to Croatia (≈115,000–170,000 animals), and Romania to Bulgaria (≈78,000–150,000 animals) (Appendix Figure, https://wwwnc.cdc.gov/EID/article/32/12/26-1012-App1.pdf), which mirrored the main directions of viral migration inferred from the phylodynamic analyses. We recorded smaller volumes from Romania to Austria (≈10,000–27,000 animals). Trade connections potentially underlying transmission from Romania to Hungary, Albania, and Kosovo were less clear. Although Romania was the main source of small ruminants to Hungary in both years (≈9,000–47,000 animals), livestock supplied to Albania originated from multiple sources, including Romania (≈19,000–71,000 animals), Serbia (≈39,000–65,000 animals), and Greece (≈11,000–12,000 animals), and limited official trade between Hungary and Albania or between Albania and Serbia. However, in both years, the total number of live small ruminants traded was overall positively associated with the average number of inferred migration events between countries ($p = 0.001$; Mantel statistic = 0.82–0.92), indicating a strong correspondence between official small ruminant trade to the regional spread of PPR in Europe. Seasonal increases in demand for lamb and sheep during religious celebrations might have influenced those patterns, enabling some of the observed transmission events.

Discussion

PPR disease is spreading in Europe, raising growing concern. Although the risk for PPR introduction into Europe from Turkey or other endemic regions had

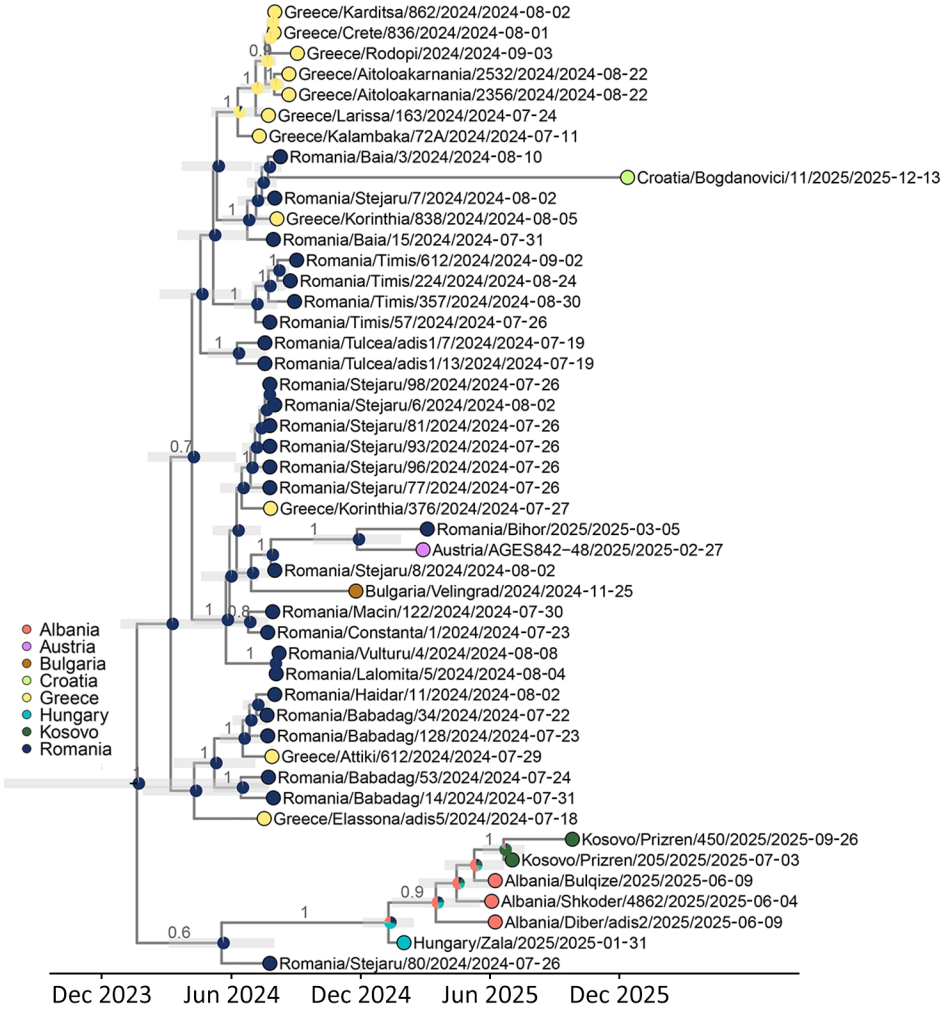


Figure 5. Maximum clade credibility phylogeny of of peste des petits ruminants virus genomes identified in study of transmission dynamics of the virus, Europe, 2024–2026. Clade was inferred under a structured coalescent skyline model. Node color indicates sampling country. Branch labels indicate posterior probability values. Internal node colors indicate posterior location probabilities distribution. Gray bars indicate 95% highest posterior density intervals reflecting uncertainty about internal node dates.

been acknowledged at least since 2016 (*27*,*28*), the emergence across southeastern Europe in 2024 was unexpected because it started in an area not considered directly at risk. Genetic and field investigations point toward an initial introduction into Romania, although the exact origin of the introduction remains unresolved. Romania is one of the most important exporters of sheep, especially within Europe and to regions where the disease is circulating (e.g., northern Africa, Middle East) (*29*,*30*). That extensive role of a hub for small ruminant trade, along with potential illegal movement of animals or vehicles from infected regions to Romania is suspected to have contributed to the introduction and spread of the disease.

Delays in reporting PPR suspicions in infected herds enabled spread of PPR disease because of limited awareness in affected regions distant from PPR disease–endemic countries; another reason is the low death rate and mild or absent clinical signs that followed textbook patterns of PPR infection in naive populations. The observation that animals from the same infected herd showed no clinical signs in a collection center in Romania but had clear signs at arrival in a quarantine area in Austria suggests that the variable outcome of PPR infection is related to animal health and stress level, although that hypothesis requires further investigation.

Once PPR outbreaks are suspected in Europe, animal movement restrictions and other control measures are implemented within a restricted zone of several kilometers. Despite implementation of swift and adequate measures after EU legislation, detection delays and removal of movement restrictions once an outbreak appeared to have ended enabled legal trade to play a major role in the viral spread. Overall, cross-border transmission was positively associated with official records of legal trade of live small ruminants. Combining genetic and trade data, our results suggest that eastern Romania acted as the main source of regional viral dissemination, with multiple introductions to Greece, sporadic introductions to Bulgaria and Croatia, movements from eastern to western Romania reaching Austria, and spread into southeastern Europe, including Albania, Hungary, and Kosovo. Although the whole-genome sequence dataset we developed in this study is one of the most comprehensive, it remains small (47 genomes) and represents only 21% of officially reported outbreaks, with a bias toward Romania (27/47 genomes). Therefore, phylodynamic analysis results regarding regional dissemination must be interpreted with caution when not backed by field investigations. Expanding sequencing efforts for additional genomic data from countries

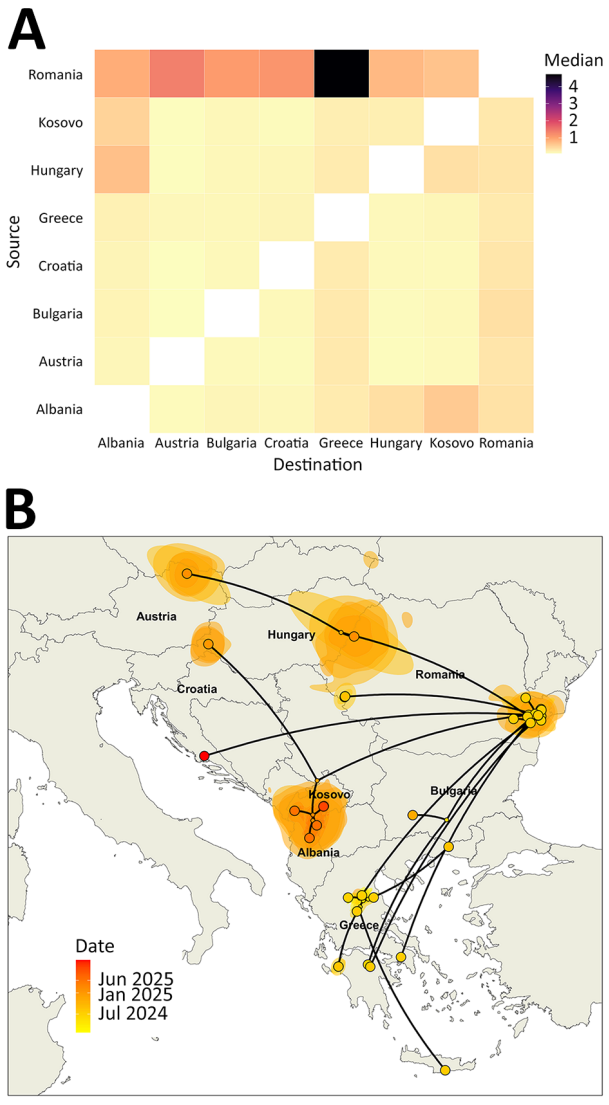


Figure 6. Phylodynamics of peste des petits ruminants virus in study of transmission dynamics of the virus, Europe, 2024–2026. A) Heatmap indicating the median number of migration events between location pairs inferred under a structured coalescent skyline model. B) Spatiotemporal diffusion of the Europe virus genomes inferred under an exponential growth coalescent model and relaxed random walk model. Phylogeny branches are arranged in space by the known locations of tip nodes and inferred locations of internal nodes as visualized in Figure 5. Shaded regions indicate 95% highest posterior density regions of internal nodes. Node colors indicate time.

where PPRV is circulating would enhance phylodynamic power, enabling a more precise understanding of transmission dynamics.

Outbreak investigations also indicate a role of illegal trade in PPRV transmission. For example, the spread from Albania to Kosovo likely involved illegal purchase of animals after PPR emergence and price reductions. Moreover, other reports of spread with no

direct contact between animals indicate a role of indirect transmission. A secondary outbreak in Hungary was traced to hay moved from a primary infected holding, suggesting transmission from virus particles carried on the vehicle, food, or staff. Although PPRV is thought to have limited environmental persistence, the potential for indirect transmission has not been fully assessed and warrants further investigation and implementation of strict biosecurity measures in areas at risk (*31*).

Despite large control efforts in agreement with EU legislation, PPRV appeared to have continued circulating unreported in Romania after the last notification in September 2024, likely because of the lack of clinical signs of the disease; our phylodynamic analyses revealed that it potentially seeded outbreaks in other countries in Europe. Infections in new countries despite animal movement restrictions suggest that early transmission in 2024 occurred before their implementation and that transmission in late 2024 and 2025 occurred after some restrictions were lifted. The lack of phylogenetic links between some of the 2025 outbreaks and the large temporal and spatial gaps observed in the phylogeny point toward unsampled diversity that is unlikely to be explained only by missing sequences from official outbreaks, mostly from Romania and Greece in 2024. Overall, our analysis shows that PPR has been and is probably still currently circulating undetected in multiple countries in southeastern Europe and that the risk for further spread to other countries in Europe and beyond remains real. New outbreaks notified in Romania, Croatia, and Albania support that conclusion. It seems clear that early-detection and control strategies based largely on clinical surveillance are not adequate in the context of PPR circulation in Europe, where infections with limited clinical signs occur; awareness of the limitations to detection should be disseminated widely across the veterinary sector. Critical surveillance elements to incorporate include reinforcing live animal trade traceability, testing animals originating from affected or at-risk areas with or without clinical signs, and systematically sampling holdings on the basis of risk factors such as trade intensity (legal and illegal), epidemiologic links with currently or previously infected areas, and biosecurity levels in place. Strong regional collaboration is needed to rapidly share information and harmonize control and prevention measures.

Our findings highlight the importance of cross-border cooperation, coordinated surveillance, and timely data sharing to prevent further dissemination of PPR in Europe and reduce its effects on national and regional economy and food security. The support of the EU will be paramount in the success of such collaborative effort, in agreement with European Animal Health Law.

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All raw sequencing reads were deposited in the National Center for Biotechnology Information Sequencing Read Archive (https://www.ncbi.nlm.nih.gov/sra; accession no. PRJNA717034) and genome sequences were deposited into GenBank (accession nos. PZ271096–138). Outbreak data are available from the Global Animal Disease Information System (EMPRES-i) database of the FAO (https://empres-i.apps.fao.org). Live small ruminant trade data in Europe are available from the Food and Agriculture (FAOSTAT) database of the FAO (https://www.fao.org/faostat). Codes and analysis files are available via the GitHub repository p (https://github.com/ClaireGuinat/ppr_europe_phylo.git).

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About the Author

Dr. Guinat is a research scientist at INRAE in spatial and molecular epidemiology of animal infectious diseases. Her research focuses on investigations the transmission dynamics of zoonotic and animal infectious diseases to improve control.

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Address for correspondence: Arnaud Bataille, CIRAD Departement Systemes biologiques, TA-A117/E, Campus International de Baillarguet, Montpellier, Languedoc-Roussillon 34398, France; email: arnaud.bataille@cirad.fr