

Combining genomics and epidemiology to investigate rabies outbreaks in the Philippines

P2-B6

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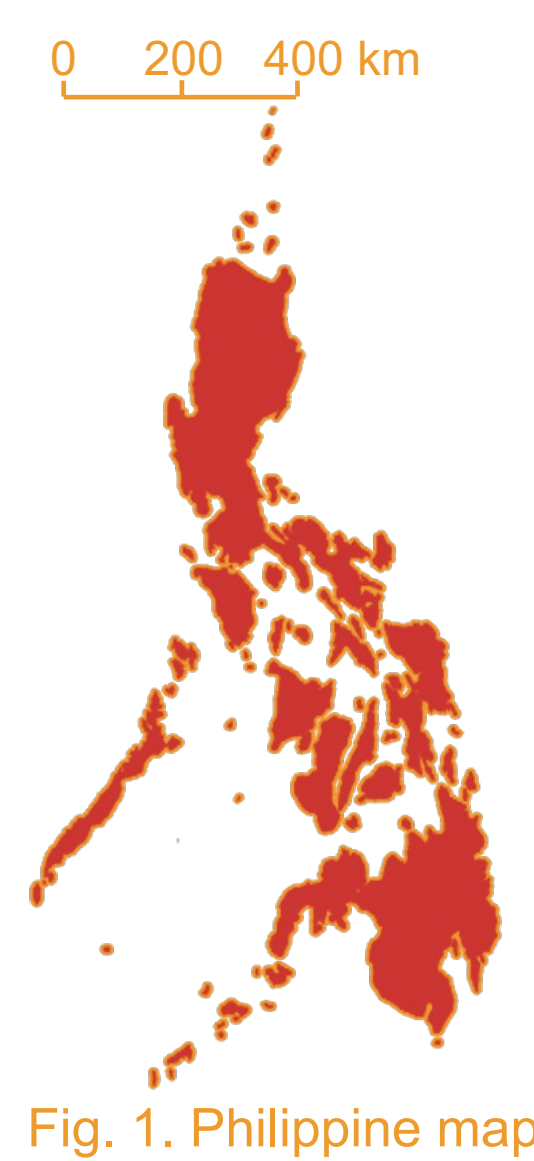
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Enhanced surveillance through Integrated Bite Case Management (IBCM) and genomic sequencing enabled us to detect a canine rabies outbreak in a rabies-free island in the Philippines, which we traced from at least 3 separate introductions from other provinces.

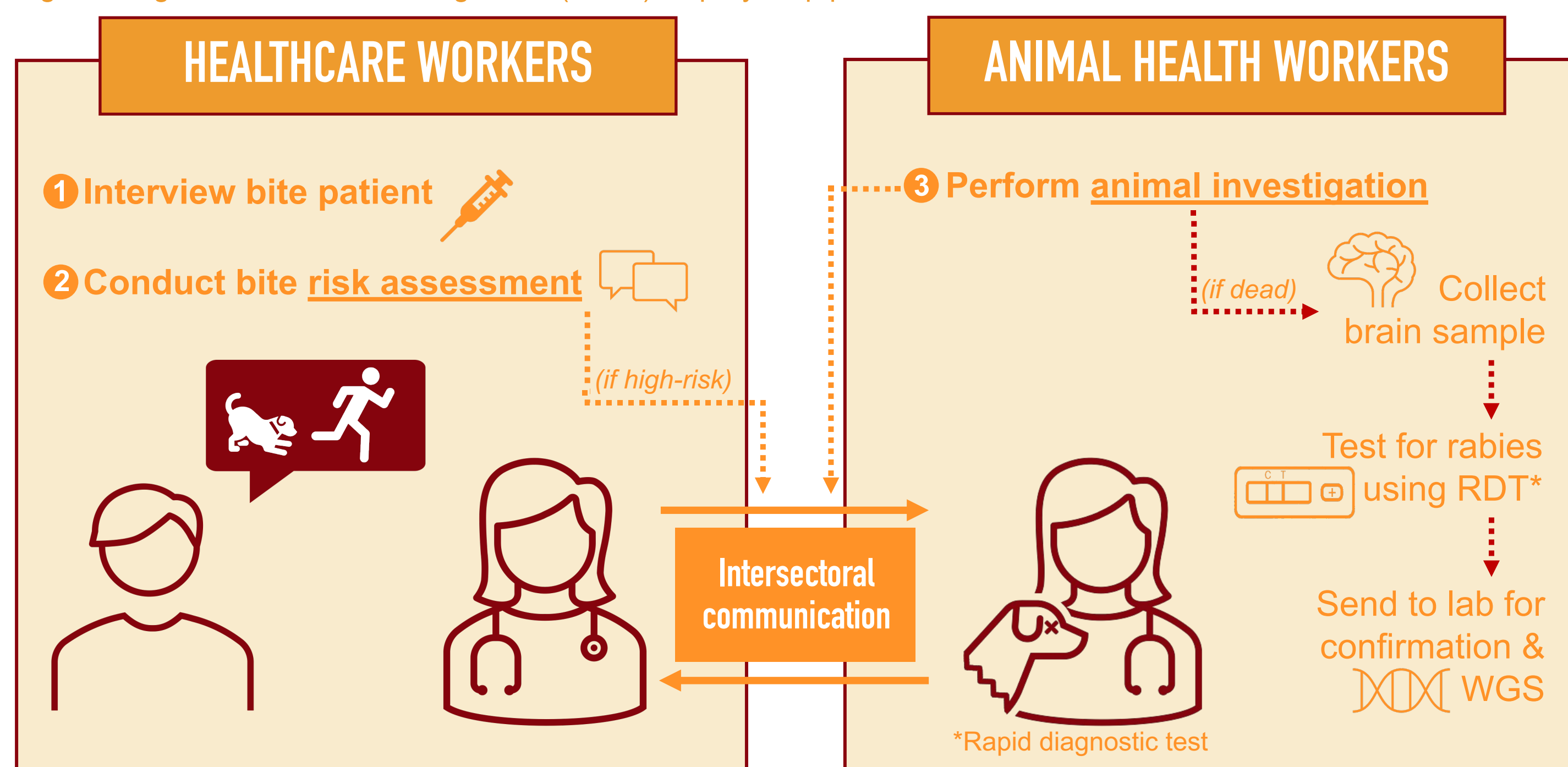
BACKGROUND

Rabies kills 200-300 people in the Philippines (Fig. 1) annually, and is mainly transmitted by dogs. The province of Romblon was declared rabies-free in 2019, but through Integrated Bite Case Management (IBCM) and whole genome sequencing (WGS), we investigated the transmission dynamics of a local outbreak in late 2022, demonstrating the value of using a One Health approach for tracking rabies outbreaks in real time.



METHODS

Fig. 2. Integrated Bite Case Management (IBCM) step-by-step process

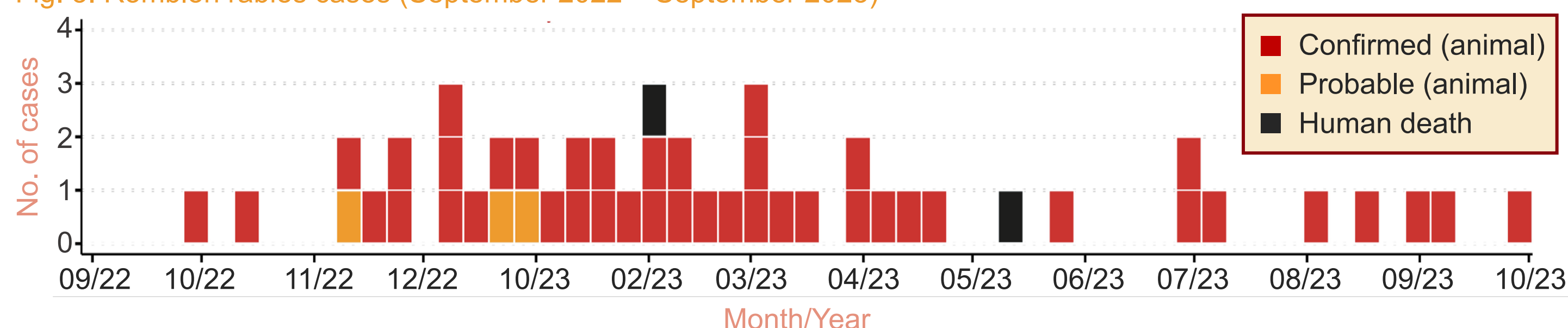


Rabies surveillance data have been collected since the implementation of IBCM in 2020. Epidemiological data collected from human exposures and animal investigations (Fig. 2) increased case detection, enabling whole genome sequencing of confirmed rabies-positive samples using an established sample-sequence-interpretation workflow. 48 consensus sequences were obtained, supplemented by publicly available data (n=664), and an ongoing Philippine-wide sequencing study (n=162). Phylogenetic analysis, including tree dating and ancestral character reconstruction, was conducted to estimate the dates and locations of geographic dispersal events. Transmission trees for the Romblon outbreak were reconstructed, ensuring consistency with phylogenies.

RESULTS

43 dog rabies cases were confirmed in Tablas Island from September 2022-2023. Despite increased case detection by IBCM, considerable transmission went undetected, resulting in two human deaths (Fig. 3).

Fig. 3. Romblon rabies cases (September 2022 – September 2023)



Rabies cases were reported in all except one municipality in Tablas Island (Fig. 4). An estimated 75 undetected cases occurred on average and detection delays ranged from 4-14 months. Integrating human bite cases and animal investigations in conjunction with viral genome data vastly improved transmission chain resolution, revealing orphaned cases and unsampled transmission chains indicative of undetected cases in locations where transmission was occurring. Phylogenetic analysis showed at least three independent introductions to Tablas Island based on three clusters of lineages (Fig. 5). The resulting cases were found to be closely related to lineages from northern provinces, implying human-mediated movement of dogs into Romblon as the likely source of the outbreak, facilitated by pandemic-induced lapses in dog vaccination from 2020 to 2021.

Fig. 4. Rabies outbreak in Tablas Island, Romblon. Grey polygons indicate municipalities.

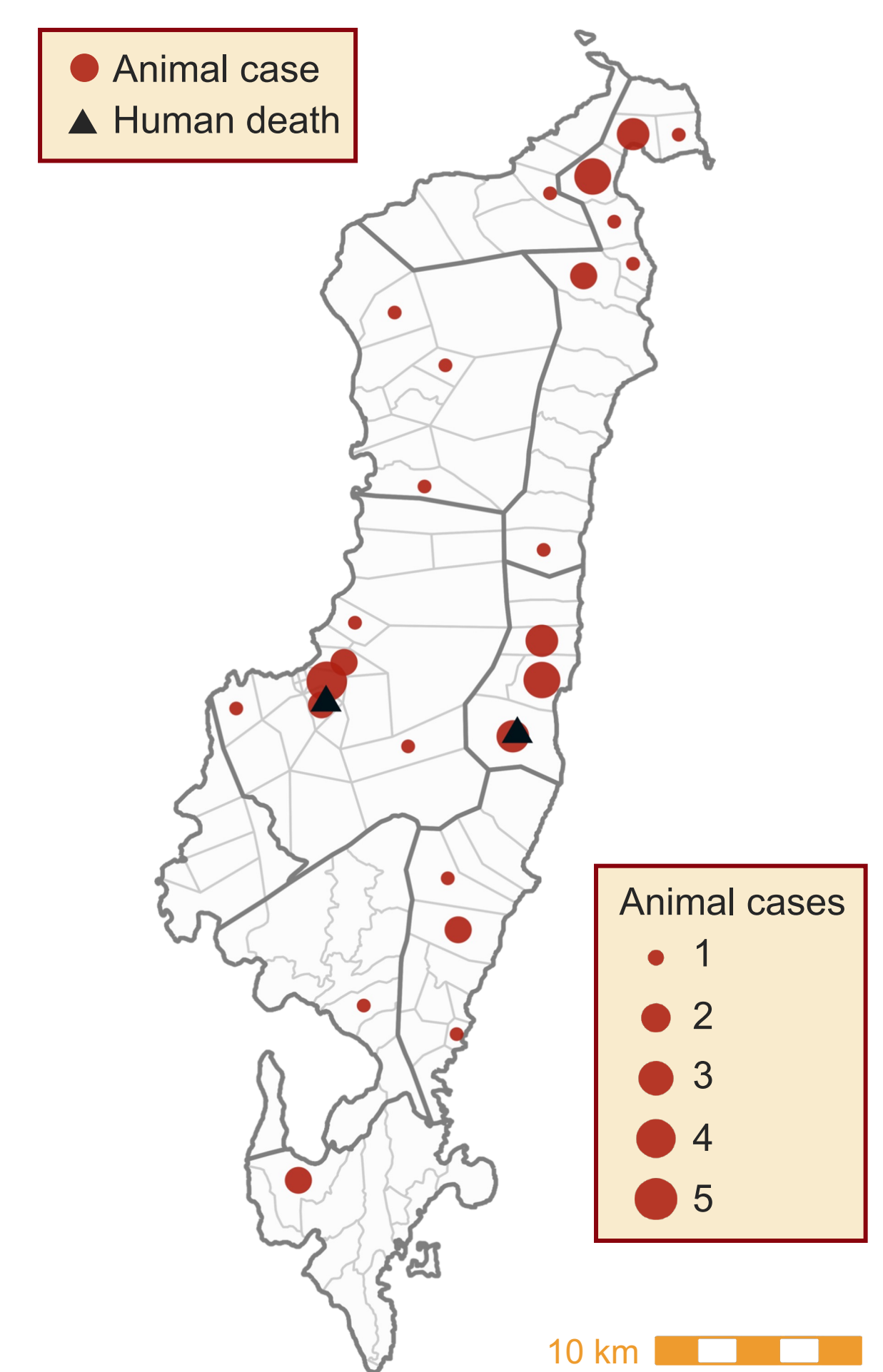
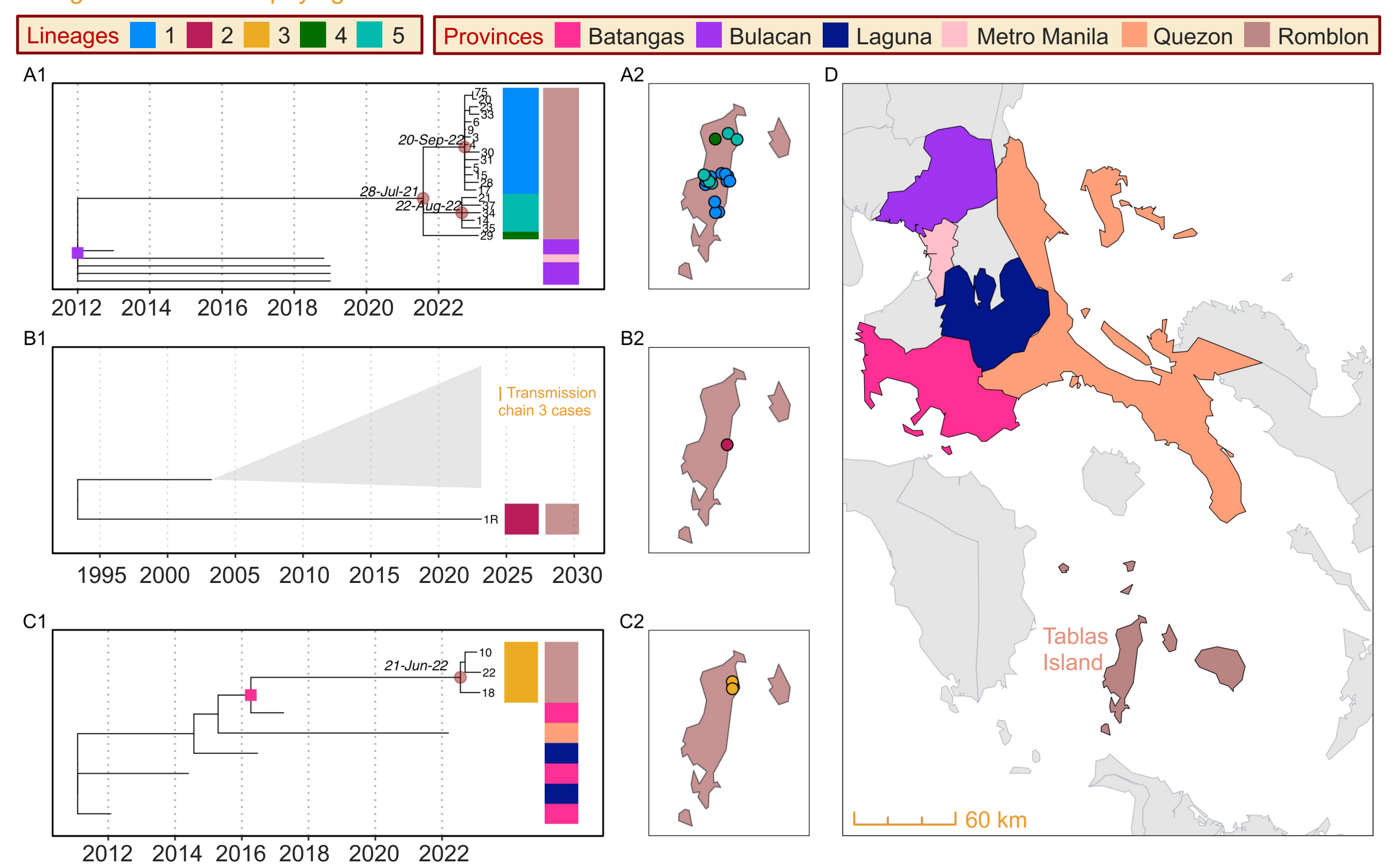


Fig. 5. Time-scaled phylogenetic subtrees from the current outbreak



CONCLUSION

Our results indicate that human-mediated introductions to geographically isolated areas occur frequently and maintaining dog vaccination coverage together with strict border control will limit incursions. This investigation demonstrates the value of IBCM, WGS and RDTs for inferring the source and spread of rabies outbreaks.

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