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Wild Mice and Shrews as Natural Reservoirs of Emerging Tickborne Yezo Virus, Hokkaido, Japan, 2023–2025

Appendix

Appendix Table 1. Nucleotide sequence identities of nucleoprotein genes of Yezo virus isolates in Japan compared with those identified in this study

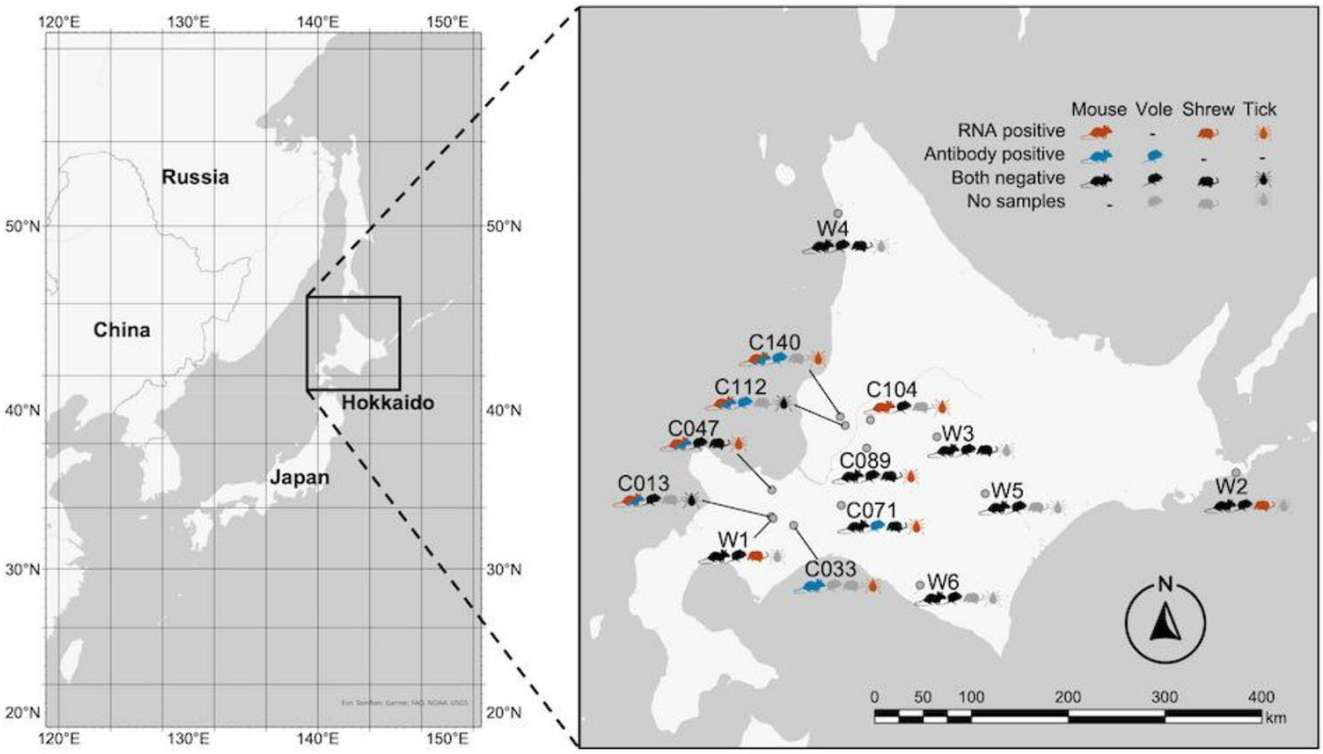
			Sequence identity (%)								
Study	Source	Isolate	HAs25–107	HAs25–201	HAa25–262	HSg23–005	HSc23–012	HSg23–013	HSg23–067	HIpe24–390	HIpe25–192
This study	Mouse	HAs25–107	-	93.5	93.4	99.8	99.9	93.4	93.4	93.5	93.4
		HAs25–201	93.5	-	99.2	93.6	93.6	99.5	99.4	100.0	99.3
		HAa25–262	93.4	99.2	-	93.4	93.5	99.2	99.1	99.2	99.1
	Shrew	HSg23–005	99.8	93.6	93.4	-	99.9	93.4	93.5	93.6	93.4
		HSc23–012	99.9	93.6	93.5	99.9	-	93.5	93.6	93.6	93.5
		HSg23–013	93.4	99.5	99.2	93.4	93.5	-	99.5	99.5	99.5
		HSg23–067	93.4	99.4	99.1	93.5	93.6	99.5	-	99.4	99.4
	Questing ticks	HIpe24–390	93.5	100.0	99.2	93.6	93.6	99.5	99.4	-	99.3
		HIpe25–192	93.4	99.3	99.1	93.4	93.5	99.5	99.4	99.3	-
Kodama et al. (*1*)	Human	HH001–2019	99.3	93.8	93.7	99.3	99.4	93.7	93.8	93.8	93.7
		HH003–2020	93.4	99.3	99.1	93.4	93.5	99.5	99.4	99.3	100.0
		HH007–2016	97.3	93.8	93.7	97.4	97.4	93.7	94.0	93.8	93.7
		HH008–2017	93.3	99.3	99.1	93.4	93.4	99.3	99.2	99.3	99.1
		HH009–2017	99.7	93.5	93.3	99.8	99.8	93.3	93.4	93.5	93.3
		HH011–2020	97.3	93.8	93.7	97.4	97.5	93.6	94.0	93.8	93.6
Yamaguchi et al. (*2*)	Human	HH074–2023	93.4	99.5	99.2	93.4	93.5	99.7	99.5	99.5	99.5
		HH080–2023	99.1	93.4	93.3	99.2	99.3	93.4	93.4	93.4	93.3
		HH081–2023	93.5	99.5	99.2	93.6	93.6	99.7	99.5	99.5	99.5
		HH083–2024	93.4	99.5	99.2	93.5	93.6	99.7	99.5	99.5	99.5
	Tick from human	HH073T-2023	93.6	99.8	99.1	93.6	93.7	99.4	99.3	99.8	99.4
Nishino et al. (*3*)	Tick from bird	BT-1821	93.2	99.4	98.7	93.2	93.3	99.1	98.9	99.4	98.9
		BT-1826	93.2	99.6	98.9	93.3	93.4	99.3	99.1	99.6	99.1
		BT-1844	93.4	99.6	98.9	93.4	93.5	99.2	99.1	99.6	99.2
		BT-1864	93.3	99.3	99.1	93.4	93.4	99.3	99.2	99.3	99.1
		BT-1968	93.4	99.9	99.2	93.4	93.5	99.5	99.4	99.9	99.3
		BT-2135	93.4	99.9	99.2	93.4	93.5	99.5	99.4	99.9	99.3
		BT-2155	93.4	99.7	99.1	93.4	93.5	99.3	99.3	99.7	99.3

Appendix Table 2. Nucleotide sequence identities of glycoprotein precursor genes of Yezo virus isolates in Japan compared with those identified in this study

Study	Source	Isolate	Sequence identity (%)					
			HAs25–107	HAa25–262	HSc23–012	HSg23–013	HSg23–067	HIpe24–390
This study	Mouse	HAs25–107	-	97.4	99.5	97.2	97.3	97.2
		HAa25–262	97.4	-	97.5	98.9	99.0	98.9
	Shrew	HSc23–012	99.5	97.5	-	97.2	97.3	97.3
		HSg23–013	97.2	98.9	97.2	-	99.2	99.1
		HSg23–067	97.3	99.0	97.3	99.2	-	99.2
	Questing tick	HIpe24–390	97.2	98.9	97.3	99.1	99.2	-
Kodama et al. (*1*)	Human	HH001–2019	98.5	98.0	98.4	97.8	97.9	97.8
		HH003–2020	97.2	98.9	97.3	99.2	99.3	99.1
		HH007–2016	98.9	97.6	98.8	97.3	97.5	97.4
		HH008–2017	97.3	99.0	97.4	99.2	99.3	99.2
		HH009–2017	99.3	97.3	99.3	97.2	97.2	97.1
		HH011–2020	98.9	97.6	98.8	97.3	97.5	97.4
Yamaguchi et al. (*2*)	Human	HH074–2023	97.4	99.0	97.4	99.6	99.4	99.3
		HH080–2023	99.2	97.7	99.2	97.5	97.5	97.5
		HH081–2023	97.2	98.9	97.3	99.6	99.2	99.1
		HH083–2024	97.3	99.0	97.3	99.2	99.3	99.5
	Tick from human	HH073T-2023	97.1	98.7	97.1	99.0	99.1	99.5
Nishino et al. (*3*)	Tick from bird	BT-1821	97.2	98.8	97.2	99.1	99.2	99.3
		BT-1826	97.2	99.0	97.3	99.2	99.3	99.4
		BT-1844	97.3	98.9	97.3	99.2	99.3	99.4
		BT-1864	97.4	99.1	97.4	99.3	99.4	99.3
		BT-1968	97.3	98.9	97.3	99.2	99.3	99.7
		BT-2135	98.2	97.7	98.1	97.5	97.5	97.5
		BT-2155	97.3	98.9	97.3	99.2	99.3	99.4

Appendix Table 3. Nucleotide sequence identities of RNA-dependent RNA polymerase genes of Yezo virus isolates in Japan compared with those identified in this study

Study	Source	Isolate	Sequence identity (%)					
			HAs25–107	HSg23–005	HSc23–012	HSg23–013	HSg23–067	HIpe24–390
This study	Mouse	HAs25–107	-	99.4	99.4	97.3	97.4	97.3
	Shrew	HSg23–005	99.4	-	100.0	97.2	97.3	97.3
		HSc23–012	99.4	100.0	-	97.2	97.3	97.3
		HSg23–013	97.3	97.2	97.2	-	99.1	99.1
		HSg23–067	97.4	97.3	97.3	99.1	-	99.3
	Questing tick	HIpe24–390	97.3	97.3	97.3	99.1	99.3	-
Kodama et al. (*1*)	Human	HH001–2019	98.3	98.2	98.2	97.3	97.5	97.4
		HH003–2020	97.3	97.3	97.3	99.1	99.3	99.4
		HH007–2016	99.1	99.0	99.0	97.4	97.5	97.5
		HH008–2017	97.2	97.1	97.1	98.8	98.9	98.9
		HH009–2017	99.5	99.4	99.4	97.3	97.4	97.4
		HH011–2020	99.1	99.0	99.0	97.4	97.5	97.5
Yamaguchi et al. (*2*)	Human	HH074–2023	97.3	97.2	97.2	99.6	99.2	99.1
		HH080–2023	99.2	99.2	99.2	97.4	97.5	97.5
		HH081–2023	97.2	97.2	97.2	99.6	99.1	99.1
		HH083–2024	97.2	97.2	97.2	99.6	99.1	99.1
	Tick from human	HH073T-2023	97.3	97.3	97.3	99.1	99.2	99.6
Nishino et al. (*3*)	Tick from bird	BT-1821	97.2	97.1	97.1	99.0	99.1	99.1
		BT-1826	97.2	97.1	97.1	99.0	99.1	99.1
		BT-1844	97.2	97.1	97.1	99.0	99.1	99.1
		BT-1864	97.2	97.1	97.1	98.8	98.9	98.9
		BT-1968	97.4	97.3	97.3	99.2	99.3	99.7
		BT-2135	97.3	97.3	97.3	99.1	99.3	99.6
		BT-2155	97.2	97.1	97.1	99.0	99.1	99.1



Appendix Figure. Study sites where small mammals and ticks were collected, Hokkaido, Japan, 2023 –2025. Hokkaido is the northernmost island prefecture of Japan. In the right panel, labels (e.g., W4 and C140) indicate site IDs. Icons under the site ID represent mice, voles, shrews, and ticks from the left. Orange icons indicate sites where Yezo virus RNA were detected and blue icons indicate sites where anti-Yezo virus antibody-positive animals were identified. Black icons represent sites where all collected samples were negative for both RNA and antibody, while gray icons denote sites where no samples of that taxonomic group were collected. The basemap images were provided by Esri.

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