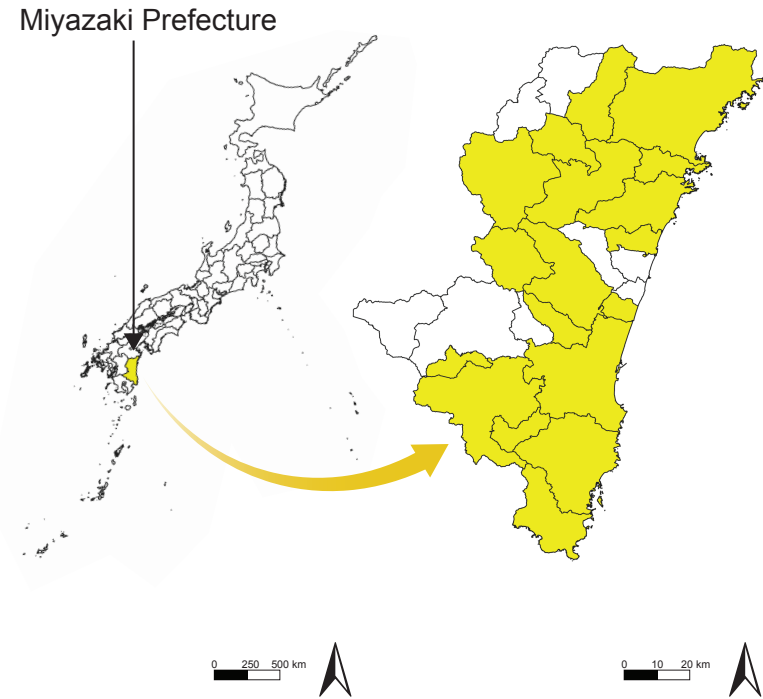
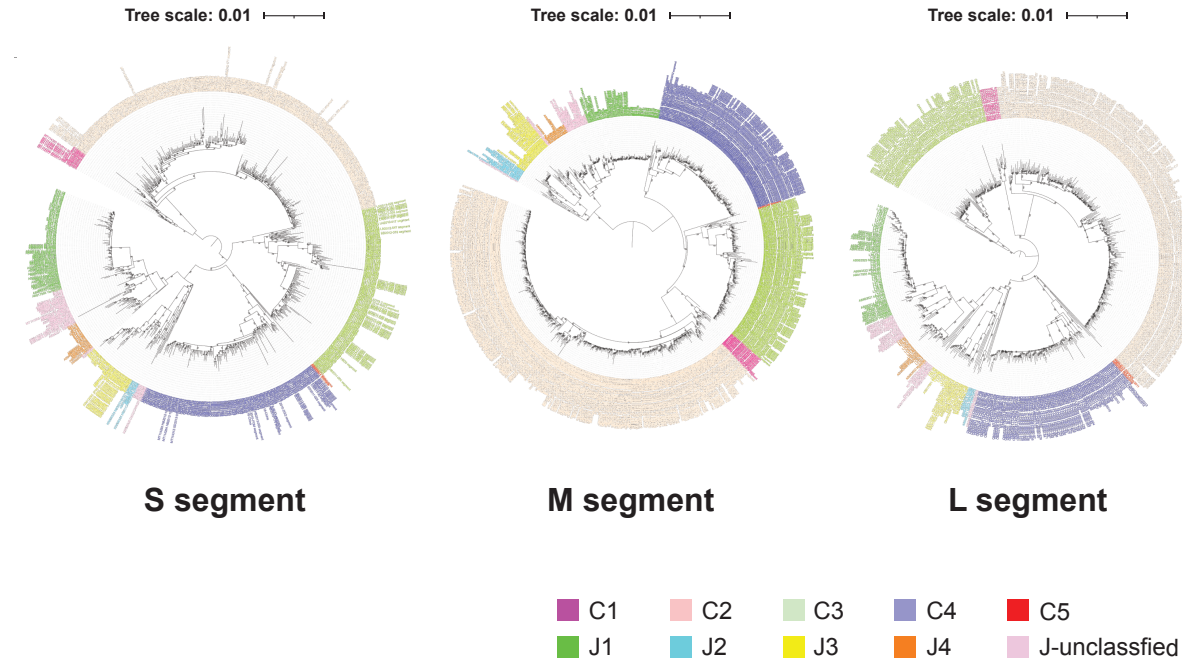


SFTS cases in Miyazaki Prefecture (2012–2023)



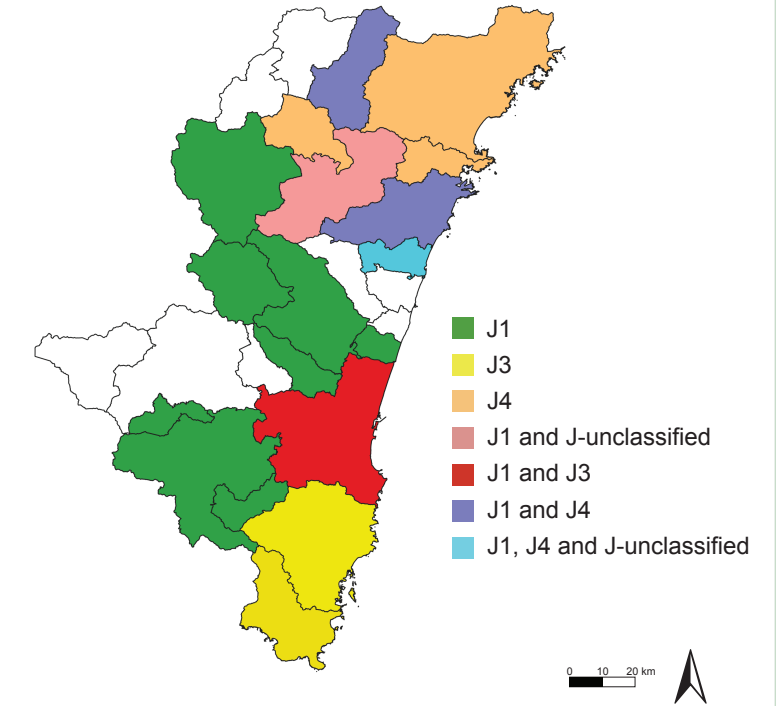
- 107 confirmed SFTS cases (~10% of Japan)
- Presumed infections in 18/26 regions

Whole-genome analysis of SFTSV



- S, M, and L segments sequenced (Illumina iSeq100 and Nanopore MinION/GridION)
- Phylogenetic tree creation (ML and NJ methods) with global comparison (Japan, China, and Korea)

Geographic regionality of SFTSV genotypes



- Four genotypes detected: J1, J3, new J4, and J-unclassified
- Distinct spatial clustering within Miyazaki Prefecture

Key findings

- ✓ New genotype identified: J4 (Japanese Clade)
- ✓ Regional distribution: J1 (central), J3 (south), J4 (north), and J-unclassified near J1 and J4

- ✓ Genetic reassortment: detected in 3 strains
- ✓ Genetic recombination confirmed in M segment, including strains from distant regions (Miyazaki–Nagasaki, ~174 km)
- ✓ No association between genotype and patient outcome ($p = 0.9714$)

SFTS: severe fever with thrombocytopenia syndrome; SFTSV: SFTS virus; ML: maximum likelihood; NJ: neighbor joining; S, M, and L: small, medium, and large

Genotypes of SFTSV in Miyazaki Prefecture show strong regionality with a newly identified genotype J4, informing local epidemiology and prevention strategies