The following are supplemental materials and will be published online only

	Identity		
	Among the Chinese isolates (%)	Between Chinese isolates and the others (%)	Among the European isolates (%)
Whole M CDS sequence	81.4–96.3	71.7–82.8	98–99.99
Whole M AA sequence	92.6–99	92.4–94.5	98.5–99.99
5'UTR NT sequence	95.1–100	88.5–100	96.7–100
Gn NT sequence	82.5–97	81.5–85.3	98.1–100
G2 AA sequence	97.9–100	97.9–98.6	99.3–100
NSm NT sequence	82.4–96.2	79.9–81.6	97.1–99.8
NSm AA sequence	94.8–99.4	89.7–93.1	97.7–100
Gc NT sequence	80.1–96.1	78.8–81.5	97.9–99.8
Gc AA sequence	91.1–98.8	91.1–93.7	98.3–99.9
3'UTR NT sequence	93.7–97.2	93–95.1	97.2–100
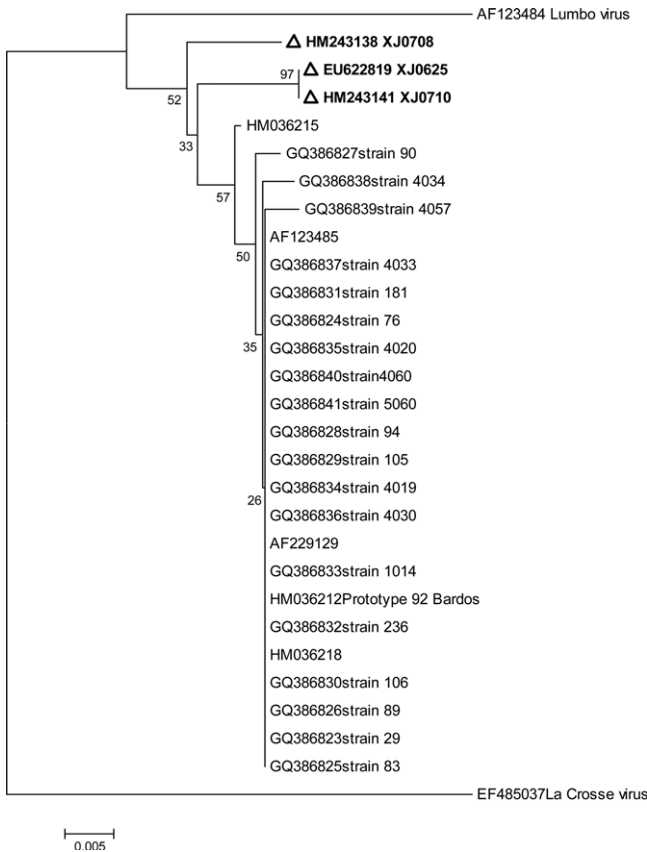
SUPPLEMENTAL FIGURE 1. Phylogenies of Tahyna virus using amino acid sequence of Gn. Distances and groupings were determined by the p-distance algorithm and neighbor-joining method with MEGA version 4 software (www.megasoftware.net). Bootstrap values are indicated and correspond to 1,000 replications. Virus names or isolate designations are listed with GenBank Accession numbers given in parentheses. The tree was rooted by using Bunyamwera virus as the outgroup virus. Scale bars indicate a genetic distance of 0.05-nt substitutions per position.
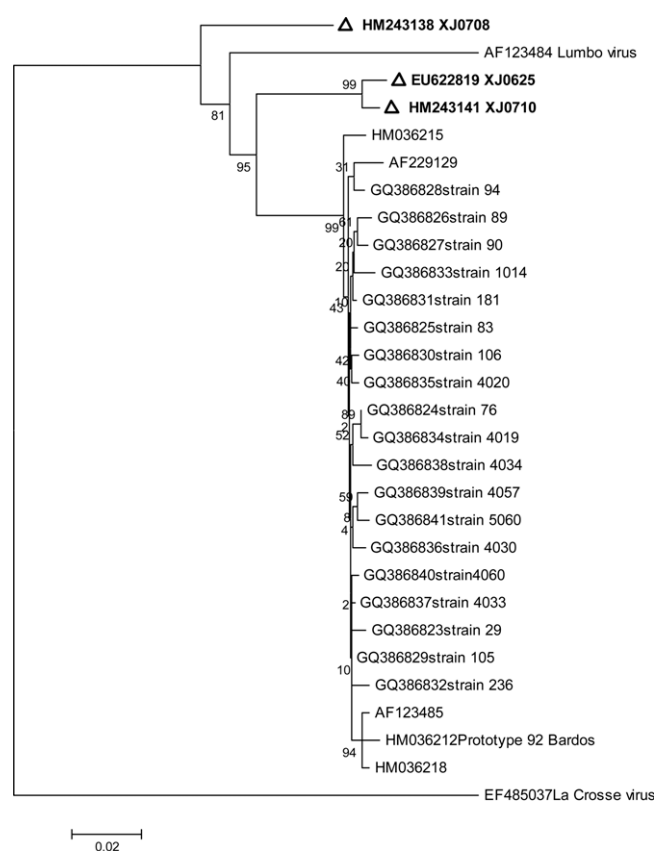
SUPPLEMENTAL FIGURE 2. Phylogenies of Tahyna virus using amino acid sequence of Gc. Distances and groupings were determined by the p-distance algorithm and neighbor-joining method with MEGA version 4 software (www.megasoftware.net). Bootstrap values are indicated and correspond to 1,000 replications. Virus names or isolate designations are listed with GenBank Accession numbers given in parentheses. The tree was rooted by using Bunyamwera virus as the outgroup virus. Scale bars indicate a genetic distance of 0.05-nt substitutions per position.
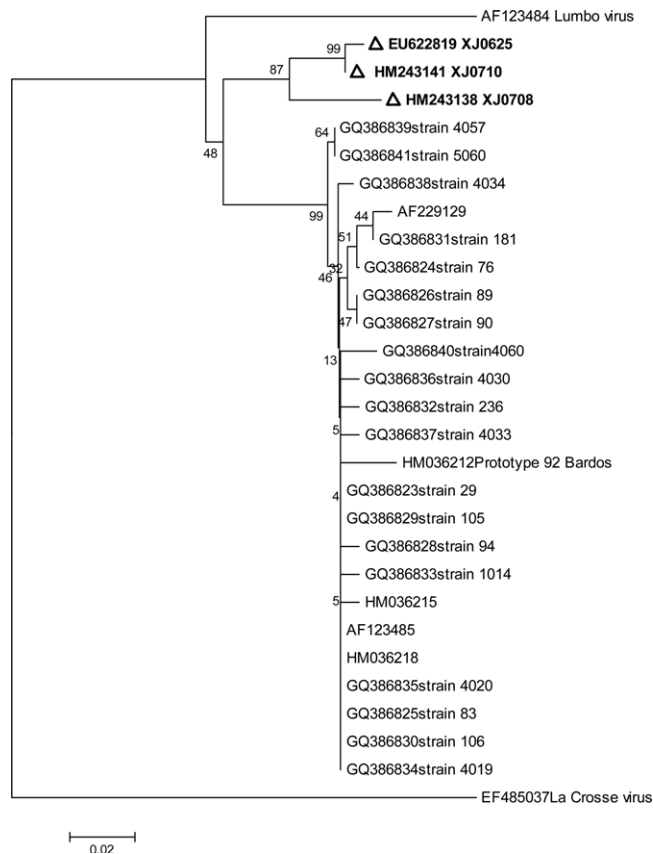
SUPPLEMENTAL FIGURE 3.   Phylogenies of Tahyna virus using amino acid sequence of NSm. Distances and groupings were determined by the p-distance algorithm and neighbor-joining method with MEGA version 4 software (www.megasoftware.net). Bootstrap values are indicated and correspond to 1,000 replications. Virus names or isolate designations are listed with GenBank Accession numbers given in parentheses. The tree was rooted by using Bunyamwera virus as the outgroup virus. Scale bars indicate a genetic distance of 0.05-nt substitutions per position.