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 TABLE 1

Nucleotide and amino acid identity within M segment of Chinese and European TAHV isolates



0.005

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.



tutions per position.

- AF123484 Lumbo virus

- △ EU622819 XJ0625

Δ HM243141 XJ0710

HM036215

- AF229129

- GQ386826strain 89

- GQ386827strain 90

GQ386825strain 83

GQ386830strain 106

GQ386835strain 4020

- GQ386838strain 4034

GQ386836strain 4030

GQ386840strain4060

- GQ386823strain 29

GQ386824strain 76

- GQ386833strain 1014



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.