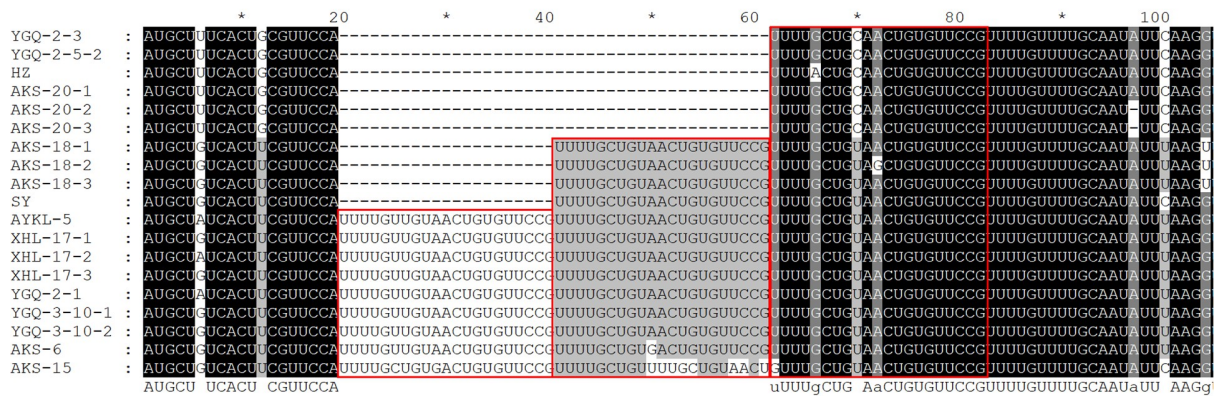


**Figure S1.** Stem-loop structures formed by the conserved nucleotides at 5' and 3' termini of jujube yellow mottle-associated virus (JYMaV) RNAs.



**Figure S2.** Multiple alignment of nucleotides at the 3' un-translation region (3'UTR) of RNA1 sequences of jujube yellow mottle-associated virus (JYMaV) amplified from Aksu jujube samples and the corresponding sequence of a reported isolate SY. The 21-bp repeat sequences were highlighted with red boxes. Each sequence was labeled with a sampling field ID followed with a location number and a clone number.

```

          *      20      *      40      *      60      *
AKS-5 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
AKS-6 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
AKS-9 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
AKS-18 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
AKS-20 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
AYKL-5 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
GS : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
HZ : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
XHL-5 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
XHL-6-1 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
XHL-17-1 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
XHL-20 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUGUAAUACAAUGAA
YGQ-2-3 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
YGQ-3-7 : AACCAUACCAAACUUAACAUA AAAAUG-----AGUAUUUGUAAUACAAUGAA
SY : AACCAUACCAAACUUAACAUA AAAAUGAGUAUUUGUAAUACAAUGAAGCAUAAAAUAAGUAUUUGUAAUACAAUGAA
      AACCAUACCAAACUUAACAUA AAAAUG      AGUAUuGUAAUACAaUGAA

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**Figure S3.** Multiple alignments of nucleotides at the 5' UTR of RNA3 sequences of jujube yellow mottle-associated virus (JYMaV) amplified from Aksu jujube samples and the corresponding sequence of a reported isolate SY. Each sequence was labeled with a sampling field ID followed with a location number and a clone number.

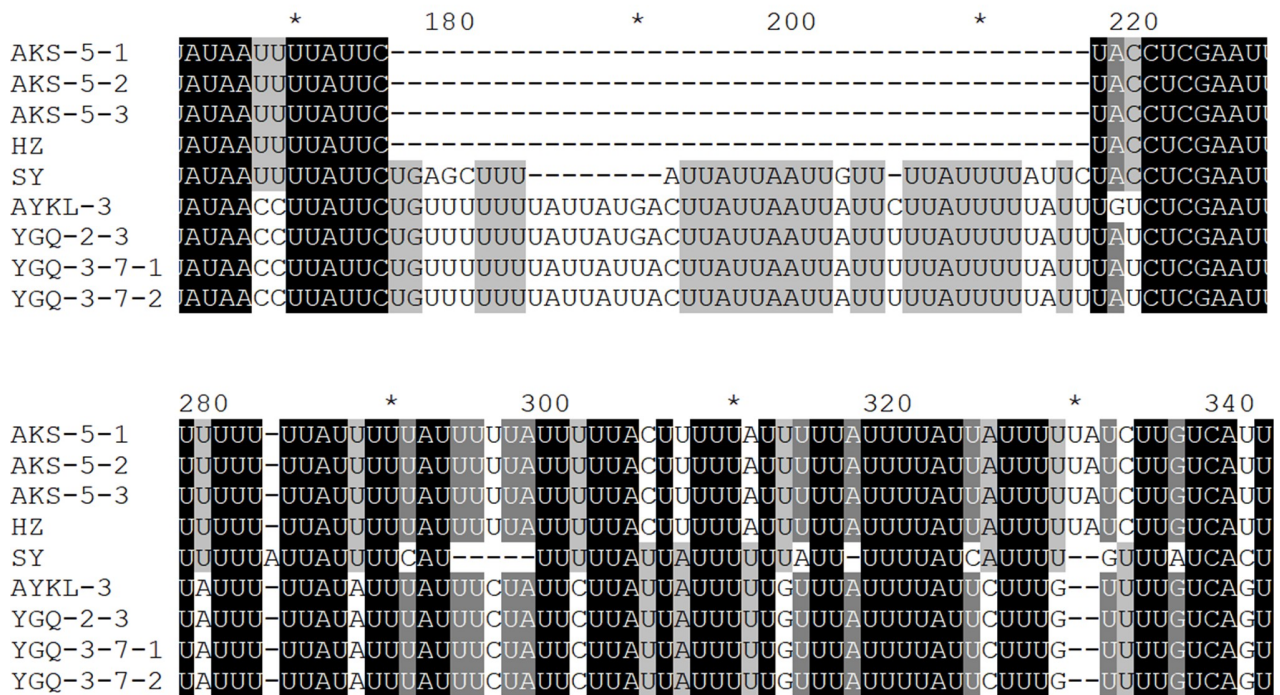
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*          20          *          *          100          *          120
YGQ-2-3-1 : GAGCGAAGAUAAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
YGQ-2-3-5 : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
YGQ-2-3-6 : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
YGQ-2-3-7 : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
YGQ-3-7-1 : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
YGQ-3-7-2 : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
HZ          : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
HZ-1       : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
HZ-2       : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
HZ-3       : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
HZ-4       : GAGCGAAGAU GAUU-----GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
AKS-15     : AAGCGAAGACA AUUGAAACUUA GUAUCA AUGU?   AUCAUAAG-----UUUUUAU
SY         : GAGUGAAGAAA AUUGUAGCUUA GUAUGCAUGU?   AUCAUAAGUAUUUUUAUUUUUUUAUUUUUUUAUUUUUAU

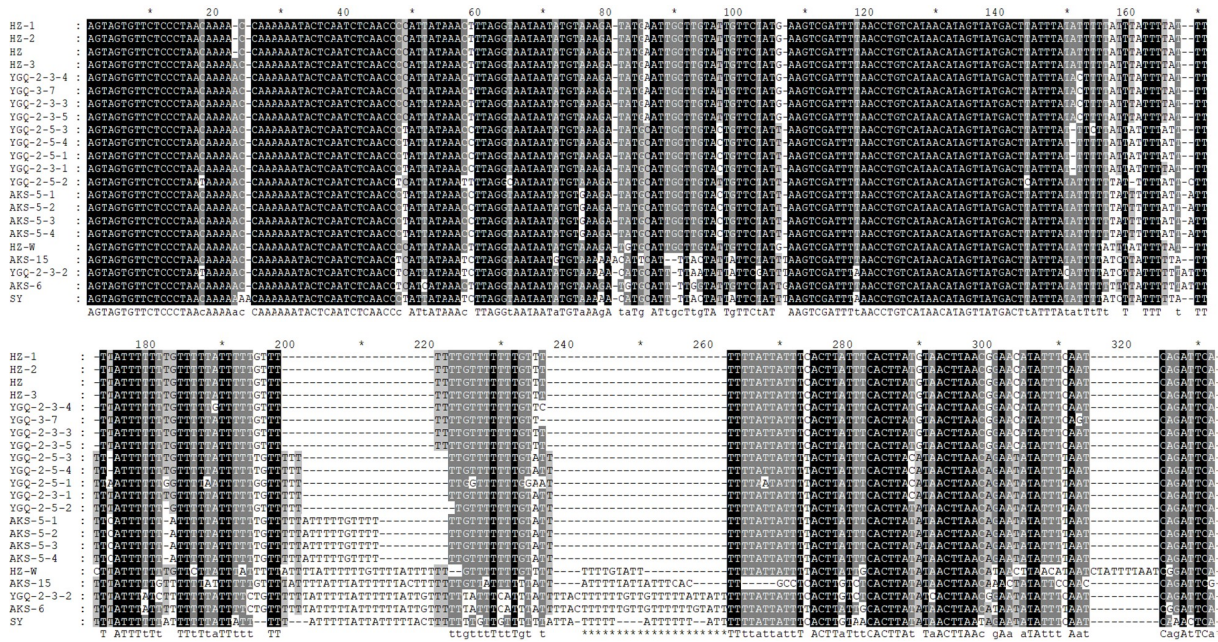
          180          *          200          *          220          *
YGQ-2-3-1 : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUGAUCA
YGQ-2-3-5 : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
YGQ-2-3-6 : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
YGQ-2-3-7 : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
YGQ-3-7-1 : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
YGQ-3-7-2 : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
HZ          : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
HZ-1       : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
HZ-2       : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
HZ-3       : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
HZ-4       : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUUUAACCA
AKS-15     : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUGAUCA
SY         : UUUAAUAUUU-----UUAUCUUGAUAAU-----UUAUGAUCA
          UUUAAUAUUU          UUAUCUUGAUAAU          UUAUUUAACCA

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**Figure S4.** Multiple alignments of nucleotides at the 5' UTR of RNA4 sequences of jujube yellow mottle-associated virus (JYMaV) amplified from Aksu jujube samples and the corresponding sequence of a reported isolate SY. Each sequence was labeled with a sampling field ID followed with a location number and a clone number.



**Figure S5.** Multiple alignments of nucleotides at the 5' UTR of RNA5 sequences of jujube yellow mottle-associated virus (JYMaV) amplified from Aksu jujube samples and the corresponding sequence of a reported isolate SY. Each sequence was labeled with a sampling field ID followed with a location number and a clone number.



**Figure S6.** Multiple alignments of nucleotides at the 5' UTR of RNA6 sequences of jujube yellow mottle-associated virus (JYMaV) amplified from Aksu jujube samples and the corresponding sequence of a reported isolate SY. Each sequence was labeled with a sampling field ID followed with a location number and a clone number.

**Table S1** Primers designed for amplification of the ORF4 and ORF5 of jujube yellow mottle-associated virus (JYMaV) isolate HZ

ORF	Primer	Sequence <sup>a</sup> (5'-3')	Position (nt)	Product size (bp)
ORF4	P4-F	<u>AAAAAGCAGGCTCCATGAAAATATTTCAAGTATATT</u>	1317-1392	1155
	P4-R	<u>AGAAAGCTGGGTC</u> CAATGCTATCTTAGACATATC	265-285	
ORF5	P5-F	<u>AAAAAGCAGGCTCCATGAAAGTTATCAAGGCTTAC</u>	1131-1151	861
	P5-R	<u>AGAAAGCTGGGTC</u> ATCATTATAATGTATGGAC	318-336	

a: The artificially added nucleotides used for recombination reactions were underlined.

**Table S2.** Contigs derived samples HZ by small RNA sequencing (sRNA-seq) and matched proteins of raspberry leaf blotch virus (RLBV), a member of the genus *Emaravirus* as analyzed against database available in NCBI GenBank

<b>Matched protein</b>	<b>No. of contig</b>	<b>Length (bp)</b>	<b>aa identity (%)</b>
P1	51	51-287	48.4-90.8
P2	12	56-180	51.6-70.8
P3	12	56-190	59.4-88.2
P4	13	55-350	46.8-91.3
P8	1	73	69.2



**Table S3** Contigs derived from samples AKS-6 and AKS-15 by RNA-seq and identity with the genomic RNAs of jujube yellow mottle-associated virus (JYMaV) isolate HZ

Sample	RNA	Contig ID	No. of reads	Size (bp)	Position (nt)	Identity (%)
AKS-6	RNA1	contig_364	280980	7134	31–7160	92.2
	RNA2	contig_489	90265	2221	1–2221	95.9
	RNA3	contig_60	298358	1225	1–1224	98.3
	RNA4	contig_255	65443	1312	168–1483	91.6
	RNA5	contig_309	109523	1260	11–1274	88.9
	RNA6	contig_66	116627	991	1–991	90.1
AKS-15	RNA1	contig_177	370602	7151	13–7159	92.4
	RNA2	contig_70	93402	2221	1–2221	93.7
	RNA3	contig_107	601278	1228	1–1228	98.0
	RNA4	contig_184	86128	1488	2–1488	95.8
	RNA5	contig_914	79172	1239	2–1239	97.9
	RNA6	contig_305	99406	975	1–975	87.9

**Table S4** RT-PCR detection of jujube yellow mottle-associated virus (JYMaV) using the three pair of primers in jujube plants grown in Xinjiang Uygur Autonomous region of China and Shanxi Province

Origin	Variety	Sample ID <sup>a</sup>	Tissue <sup>b</sup>	Symptom <sup>c</sup>	RT-PCR <sup>d</sup>		
					RNA3	RNA5	RNA6
Xinjiang	Huizao	AKS-1	L	CRS	+	+	+
		AKS-3	L	CRS	-	-	-
		AKS-5	L	B, CS	+	+	+
		AKS-9	L	M, MF	+	+	+
		HZ-1	L	CRS, MF, B	+	+	+
		XHL-17	L	CS, MF, M	+	+	+
		XHL-18	L	CS, MF, M	+	+	+
		XHL-19	L	CS, MF, M	+	+	+
		XHL-20	L	CS, MF, M	+	+	+
		YGQ3-1	L	CS, MF, M	+	+	+
		YGQ3-2	L	CS, MF, M	+	+	+
		YGQ3-3	L	CS, MF, M	+	+	+
		YGQ3-4	L	CS, MF, M	-	-	-
		YGQ3-5	L	CS, MF, M	+	+	+
		YGQ3-6	L	CS, MF, M	+	+	+
		YGQ3-7	L	CS, MF, M	+	+	+
		YGQ3-8	L	CS, MF, M	+	+	+
		YGQ3-9	L	CS, MF, M	+	+	+
		YGQ3-10	L	CS, MF, M	+	+	+
		YGQ3-11	L	CS, MF, M	+	+	+
		YGQ3-12	L	CS, MF, M	+	+	+
		YGQ3-13	L	CS, MF, M	+	+	+
		YGQ3-14	L	CS, MF, M	+	+	+
		YGQ3-15	L	CS, MF, M	+	+	+
		YGQ2-7	L	CS, MF, M	+	+	+
		YGQ2-8	L	CS, MF, M	+	+	+
		KEL-1	L	N	-	-	-
		AKS-8	L	B, CS	+	+	+
		AKS-10	L	N	-	-	-
		AKS-11	L	N	-	-	-
		AKS-12	L	CS, B	+	-	-
		AKS-14	L	CS, B	+	+	+
		AKS-15	L	CS, MF	+	+	+
		AKS-16	L	CS, B	+	+	+
AKS-17	L	CS, B	+	+	+		
AKS-18	L	M, B	+	+	+		

		AKS-19	L	CS, B	+	+	+
		AKS-20	L	M, B	+	+	+
		XHL-1	L	CS, MF, M	+	+	+
		XHL-2	L	CS, MF, M	+	+	+
		XHL-3	L	CS, MF, M	-	+	+
		XHL-4	L	CS, MF, M	+	+	+
		XHL-5	L	CS, MF, M	+	+	-
		XHL-10	L	CS, MF, M	+	+	+
		YGQ2-1	L	CS, MF, M	+	+	-
		YGQ2-2	L	CS, MF, M	-	-	-
		YGQ2-3	L	CS, MF, M	+	+	+
		YGQ2-4	L	CS, MF, M	+	+	+
		YGQ2-5	L	CS, MF, M	+	+	+
		YGQ2-6	L	CS, MF, M	+	+	+
		KEL-2	L	N	-	-	-
	<i>Z. jujube</i>	AKS-2	L	CRS	+	+	+
	var. spinosa	AKS-4	L	CRS	+	+	+
		AKS-6	L	CRS	+	+	+
		XHL-6	L	CS, MF, M	+	+	+
		XHL-7	L	CS, MF, M	+	+	+
		XHL-8	L	CS, MF, M	-	-	-
		XHL-9	L	CS, MF, M	-	+	-
		AYKL-1	L	CS, MF, M	+	+	+
		AYKL-2	L	CS, MF, M	+	+	+
		AYKL-3	L	CS, MF, M	+	+	+
		AYKL-4	L	CS, MF, M	+	+	+
		AYKL-5	L	CS, MF, M	+	+	+
	Jixinzao	AKS-7	L	B, MF, CS	+	+	+
	Unknow	WS-1	L	N	-	-	-
		WS-2	L	N	-	-	-
		WS-3	L	N	-	-	-
		WS-4	L	N	-	-	-
		WS-5	L	N	-	-	-
		WS-6	L	N	-	-	-
		WS-7	L	N	-	-	-
		WS-8	L	N	-	-	-
		WS-9	L	N	-	-	-
		WS-10	L	N	-	-	-
	Dongzao	AKS-13	L	CRS	+	+	+
Shanxi	Hupingzao	SX-1	L	N	-	-	-
		SX-2	L	N	-	-	-
		SX-3	L	N	-	-	-

SX-4	L	N	-	-	-
SX-5	L	N	-	-	-
SX-6	L	N	-	-	-
SX-7	L	N	-	-	-
SX-8	L	N	-	-	-
SX-9	L	N	-	-	-
SX-10	L	N	-	-	-
Total			55	56	53

a: samples were collected from five different locations in Xinjiang Uygur Autonomous region of China as indicated by the first letters (AKS, XHL, YGQ3, YGQ2, and AYKL) in the sample names.

b: L, leaf

d: M, mosaic; B, blotch; MF, malformation; CS, chlorotic spot; CRS, chlorotic ringspot; N, symptom unknown.

d: +, positive; -, negative; N, not tested.