

Supplemental Table I. Characteristics of PCR markers and respective primersPolymorphic PCR markers in parental genotypes *S. arcanum* accessions LA2157 and LA392.

| Marker name | Marker type | Primer name | Primer sequence | T _m (°C) ^a | PCR product size (bp) | Restriction enzyme |
|--------------|-------------|--------------------|------------------------------------------------------------------|----------------------------------|------------------------------------------------------|--------------------|
| CT119 | Codominant | CT119-F CT119-R | 5'- TCAGGTATCGAACCAAAACC -3' 5'- TAAAAGGTTTCATCCTAATAC-3' | 55 | 450 ^b | <i>MseI</i> |
| <i>Cf-2</i> | Codominant | CF2-F CF2-R | 5'- CTAGGCAGCGATTTCCATTT -3' 5'- CGGAATAGGTAATGGCCTTC -3' | 62 | 530 ^b | <i>TaqI</i> |
| Rex-1 | Codominant | REX-F REX-R | 5'- TCGGAGCCTTGGTCTGAATT -3' 5'- GCCAGAGATGATTCGTGAGA -3' | 58 | 750 ^b | <i>TaqI</i> |
| C8B | Dominant | C8B-F C8B-R | 5'- TACCCACGCCCCATCAATG -3' 5'- TGCAAGAGGGTGAATATTGAGTGC -3' | 58 | 360 ^c 360, 400 | SCAR |
| <i>Aps-1</i> | Codominant | APS-F1 APS-R1 | 5'- GGATTTTCGTGTTCTTGGTG -3' 5'- GCCCAGTCAGCAAGAAAAC -3' | 58 | 1600 ^b | <i>TaqI</i> |
| Mint-1 | Codominant | Mint-do Mint-up | 5'- TTCTCTAGCTAAACTTCAGCC -3' 5'- TTTTCGTTTTTCCATGATTCTAC -3' | 57 | 1,235, 713, 556 ^c 1,372, 844, 786, 752 | SCAR |

^aPCR annealing temperature. ^bA single fragment of the same size was amplified from both accessions prior to restriction. ^cProduct(s) on the top lane is from LA392 and on the bottom lane is from LA2157.

Supplemental Table II. Genetic analysis of F₃ progeny

Segregation of F₃ progenies of *S. arcanum* LA2157 x LA392 for root-knot nematode heat-stable resistance at 32°C. Class designation is from Table I.

| F ₂ family | Number of plants | | Chi Square ^a | P ^a |
|-----------------------|------------------|---|-------------------------|----------------|
| | R | S | | |
| Class 4 | | | | |
| E43 | 9 | 4 | 0.230 | 0.63 |
| M15 | 14 | 4 | 0.074 | 0.78 |
| G7 | 10 | 4 | 0.095 | 0.75 |
| P36 | 11 | 3 | 0.095 | 0.75 |
| R36 | 9 | 3 | 0 | 1 |
| G58 | 11 | 3 | 0.095 | 0.75 |
| Class 5 | | | | |
| I13 | 13 | 4 | 0.019 | 0.88 |
| B26 | 15 | 4 | 0.158 | 0.69 |
| G26 | 13 | 4 | 0.019 | 0.88 |
| E40 | 12 | 4 | 0 | 1 |
| I62 | 16 | 5 | 0.016 | 0.90 |
| B14 | 12 | 4 | 0 | 1 |
| E2 | 11 | 3 | 0.095 | 0.76 |
| A6 | 11 | 3 | 0.095 | 0.76 |
| Class 8 | | | | |
| R35 | 10 | 3 | 0.025 | 0.87 |
| R26 | 18 | 5 | 0.130 | 0.72 |
| E42 | 16 | 6 | 0.06 | 0.80 |
| D52 | 16 | 4 | 0.267 | 0.60 |
| A56 | 9 | 3 | 0 | 1 |
| Class 10 | | | | |
| E27 | 11 | 4 | 0.022 | 0.88 |

^aBased on 3R:1S expected ratio. ^bBased on df=1.

Supplemental Table III. Segregation of *Mi-9* phenotype, *Mi-1* homologues, and linked markers in parents and key recombinants

Parental, F₂ and F₃ plants were genotyped using PCR and AFLP markers. Class designation is from Table II. Genotype designation (1) homozygous resistant locus, (2) homozygous susceptible, (3) heterozygous, (1/3) resistant allele is dominant, and (2/3) susceptible allele is dominant. *Mi-1* homologues were amplified using *Mi-1* intron 1 (Mint) flanking primers. Plants were also evaluated for nematode resistance (R) or susceptibility (S) to root knot nematodes strain VW4 at 32°C.

| Plant | Generation | Phenotype | Mint | Markers | | | | | | |
|--------|------------------------|-----------|--------------------------------------|---------|-------------|-------|--------|-------|----------------|--------------|
| | | | | CT119 | <i>Cf-2</i> | Rex-1 | C264.1 | C32.1 | C8B | <i>Aps-1</i> |
| LA2157 | Parent | R | RH1, RH2, RH3, RH4, | 1 | 1 | 1 | 1/3 | 1 | 1/3 | 1 |
| LA392 | Parent | S | SH1, SH2, SH3 | 2 | 2 | 2 | 2 | 2/3 | 2 | 2 |
| E42 | F ₂ class 8 | R | RH1, RH2, RH3, RH4, SH1, SH2, SH3 | 3 | 3 | 3 | 1/3 | 2/3 | 1 ^a | 1 |
| E42-A4 | F ₃ | S | SH1, SH2, SH3 | 2 | 2 | 2 | 2 | 2/3 | 1/3 | 1 |
| R26 | F ₂ class 8 | R | RH1, RH2, RH3, RH4, SH1, SH2, SH3 | 3 | 3 | 3 | 1/3 | 2/3 | 1/3 | 1 |
| R26-D6 | F ₃ | S | SH1, SH2, SH3 | 2 | 2 | 2 | 2 | 2/3 | 1 ^a | 1 |
| D52 | F ₂ class 8 | R | RH1, RH2, RH3, RH4, SH1, SH2, SH3 | 3 | 3 | 3 | 1/3 | 2/3 | 1/3 | 1 |
| D52-B5 | F ₃ | S | SH1, SH2, SH3 | 2 | 2 | 2 | 2 | 2/3 | 1 ^a | 1 |
| R35 | F ₂ class 8 | R | RH1, RH2, RH3, RH4, SH1, SH2, SH3 | 3 | 3 | 3 | 1/3 | 2/3 | 1/3 | 1 |
| R35-B1 | F ₃ | S | SH1, SH2, SH3 | 2 | 2 | 2 | 2 | 2/3 | 1 ^a | 1 |
| A56 | F ₂ class 8 | R | RH1, RH2, RH3, RH4, SH1, SH2 | 3 | 3 | 3 | 1/3 | 2/3 | 1 ^a | 1 |

| | | | | | | | | | | |
|--------|-------------------------|---|--------------------------------------|---|---|---|-----|-----|----------------|---|
| A56-E3 | F ₃ | R | RH1, RH2, RH3, SH1, SH2 | 2 | 2 | 2 | 2 | 2/3 | 1/3 | 1 |
| A42 | F ₂ class 9 | R | RH1, RH2, RH3, SH1, SH2, SH3 | 2 | 2 | 2 | 2 | 2/3 | 3 ^a | 3 |
| A42-D2 | F ₃ | R | RH1, RH2, RH3, SH1, SH2 | 2 | 2 | 2 | 2 | 1 | 1/3 | 1 |
| E27 | F ₂ class 10 | R | RH1, RH2, RH3, RH4, SH3 | 1 | 1 | 1 | 1/3 | 2/3 | 3 ^a | 3 |
| E27-H3 | F ₃ | S | RH4, SH3 | 1 | 1 | 1 | 2 | 2/3 | 2 | 2 |
| I47 | F ₂ class 11 | R | RH1, RH2, RH3, RH4, SH1, SH2, SH3 | 2 | 2 | 3 | 1/3 | 2/3 | 1/3 | 3 |
| M59 | F ₂ class 12 | S | RH4, SH1, SH2, SH3 | 3 | 3 | 2 | 2 | 2/3 | 2 | 2 |
| M59-F4 | F ₃ | S | RH4, SH3 | 1 | 1 | 2 | 2 | 2/3 | 2 | 2 |
| U4 | F ₂ class 12 | S | SH1, SH2, SH3 | 3 | 3 | 2 | 2 | 2/3 | 2 | 2 |
| 188 | F ₂ class 14 | R | RH1, RH2, RH3, RH4, SH1, SH2, SH3 | 2 | 3 | 3 | 1/3 | 2/3 | 3 ^a | 3 |
| 188-D2 | F ₃ | R | RH1, RH2, RH3, RH4, SH1, SH2 | 2 | 1 | 1 | 1/3 | 1 | 1/3 | 1 |

^aAllele designation is based on F₃ progeny genotyping.
