**Table S1:** Proteins of *Xanthomonas citri* subsp. *citri* 306 strain sharing the Peptidase M23 Domain according to an *in-silico* search using the IMG ‘find function’ tool (img.jgi.doe.gov).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Locus Tag** | **IMG Gene ID** | **Original Gene Product Name** | **Signal Peptide** | **Amino acid Residue** | **Length bp** | **Pfam ID** |
| XAC0024 | 637293275 | hypothetical protein | Yes | 411 | 1236 | pfam01551 Peptidase\_M23 |
| XAC0466 | 637293717 | lytic enzyme | No | 584 | 1755 | pfam01551 Peptidase\_M23 |
| XAC0787 | 637294037 | peptidase | No | 313 | 942 | pfam01551 Peptidase\_M23 |
| XAC1728 | 637294977 | lipoprotein | Yes | 259 | 780 | pfam01551 Peptidase\_M23 |
| XAC2361 | 637295610 | peptidase | Yes | 280 | 843 | pfam01551 Peptidase\_M23 |
| XAC2928 | 637296177 | peptidase | No | 205 | 618 | pfam01551 Peptidase\_M23 |
| XAC3041 | 637296290 | hypothetical protein | Yes | 297 | 894 | pfam01551 Peptidase\_M23 |
| XAC3368 | 637296617 | hypothetical protein | No | 239 | 720 | pfam01551 Peptidase\_M23 |
| XAC3898 | 637297147 | hypothetical protein | No | 472 | 1419 | pfam01551 Peptidase\_M23 |

**Table S2:** Primers used in this study.

|  |  |
| --- | --- |
| **Primer Name** | **Sequence (5’ → 3’)** |
| A(F) | CAGAGCCAGCGCGAGACCGAG |
| B(R) | ACGGTGGTGCAGCGGTGCATTGCGGCCCAC |
| C(F) | GCACCGCTGCACCACCGTGACTGCAGTGGC |
| D(R) | TCAGCGGCGTTGCAGCCAGCT |
| 0024\_500\_IF\_F | AGATCCATGGCACTCGAGCGCCACTGATCTGGC |
| 0024\_500\_IF\_R | GCTCACCATCTCGAGGTCGTCGATCGGCGCGATCA |
| 0024\_IF\_F | AGATCCATGGCACTCGAGATGTGGCTGGCGGTG |
| 0024\_IF\_R | GCTCACCATCTCGAGGCGGCGTTGCAGCCAGCTCGA |
| M13/pUC F-20 | GTAAAACGACGGCCAGT |
| M13/pUC R-48 | AGCGGATAACAATTTCACACAGGA |
| pGCD1-F | CACACTTTGCTATGCCATAGC |
| XAC0024\_mcherry-F | GTCTCGAGATGTGGCTGGCGGTGGGCGTG |

F: forward primer, R: reverse primer.

Underlined bases: sequences that enable the double-joint of fragments A-B and C-B by PCR

**Table S3:** *Xanthomonas* speciesused for the phylogenetic reconstruction based on the XAC0024 nucleotide sequence of *X. citri*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Species name** | **amino acid residues** | **GenBank accession no.** | **Genome position** | **% of identity** |
| *Xanthomonas arboricola* pv. *juglandis* CPBF 427 | 422 | LR824643.1 | 24462..25695 | 89% |
| *Xanthomonas arboricola* pv. *pruni* strain 15-088 | 405 | CP044334.1 | 2764090..2765323 | 89% |
| *Xanthomonas* *axonopodis* pv. *commiphoreae* strain LMG26789 | 411 | CP031059.1 | 25792..27027 | 96% |
| *Xanthomonas axonopodis* pv. *vasculorum* strain NCPPB 796 | 411 | CP053649.1 | 25983..27218 | 96% |
| *Xanthomonas campestris* pv. *badrii* strain NEB122 | 425 | CP051651.1 | 4480484..4481713 | 88% |
| *Xanthomonas campestris* pv. *campestris* str. ATCC 33913 | 405 | AE008922.1 | 25781..27013 | 85% |
| *Xanthomonas campestris* pv. *musacearum* NCPPB 4379 | 411 | CP034655.1 | 24291..25526 | 93% |
| *Xanthomonas campestris* pv. *raphani* strain MAFF106181 | 429 | CP058243.1 | 25980..27212 | 85% |
| *Xanthomonas campestris* pv. *vesicatoria* str. 85-10 | 411 | CP017190.1 | 3549491..3550726 | 96% |
| *Xanthomonas citri* pv. *glycines* strain EB08 | 411 | CP026334.1 | 25875..27110 | 99% |
| *Xanthomonas citri* pv. *malvacearum* strain MS14003 | 411 | CP023159.1 | 25878..27113 | 99% |
| *Xanthomonas citri* pv. *phaseoli* var. *fuscans* strain CFBP6991 | 411 | CP021015.1 | 2719200..2720435 | 98% |
| *Xanthomonas citri* pv. *punicae* strain LMG 859 | 411 | CP030178.1 | 928824..930059 | 99% |
| *Xanthomonas citri* pv. *vignicola* strain CFBP7113 | 411 | CP022270.1 | 27974..29206 | 98% |
| *Xanthomonas cucurbitae* strain ATCC 23378 | 420 | CP033326.1 | 23211..24440 | 87% |
| *Xanthomonas euvesicatoria* strain LMG930 | 411 | CP018467.1 | 4550833..4552068 | 96% |
| *Xanthomonas fragariae* strain PD885 | 439 | LT853882.1 | 28773..30007 | 87% |
| *Xanthomonas fuscans* subsp. *aurantifolii* strain FDC 1561 | 411 | CP011250.1 | 26157..27389 | 98% |
| *Xanthomonas gardneri* strain CFBP 8129 | 413 | LR828253.1 | 23961..25200 | 88% |
| *Xanthomonas hortorum* pv. *gardneri* strain ICMP 7383 | 440 | CP018731.1 | 90415..91654 | 88% |
| *Xanthomonas hortorum* pv. *gardneri* strain JS749-3 | 440 | CP018728.1 | 544060..545299 | 88% |
| *Xanthomonas hyacinthi* strain CFBP 1156 | 407 | CP043476.1 | 1562009..1563187 | 75% |
| *Xanthomonas oryzae* pv. *oryzicola* strain CFBP7342 | 432 | CP007221.1 | 34791..36026 | 93% |
| *Xanthomonas oryzae* strain NCPPB 4346 | 411 | CP036253.1 | 25678..26913 | 93% |
| *Xanthomonas perforans* 91-118 | 405 | CP019725.1 | 2777398..2778633 | 96% |
| *Xanthomonas perforans* strain LH3 | 411 | CP018475.1 | 3366136..3367371 | 96% |
| *Xanthomonas translucens* pv. *cerealis* strain 01 | 409 | CP038228.1 | 4306080..4307258 | 75% |
| *Xanthomonas translucens* pv. *translucens* DSM 18974 | 437 | LT604072.1 | 471751..472929 | 74% |
| *Xanthomonas vasicola* pv. *vasculorum* strain Xv1601 | 411 | CP025272.1 | 24271..25506 | 93% |
| *Xanthomonas vesicatoria* ATCC 35937 strain LMG911 | 405 | CP018725.1 | 2926304..2927535 | 90% |