|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene / gene family | Pfam domain | From ref. | Highest AI in MiV1 | MiV1 accession | Highest AI in G.ros | G. ros accessions | Function | Process |
| GH5\_2 Cellulases | PF00150 Cellulase (glycosyl hydrolase family 5) | 1,2,3,4,5,6,7 | 39.14 | Minc12674 (+22 other) | 198.94 | GROS\_g11949  (+10 other) | Cellulose degradation | Plant Cell Wall Degradation |
| GH30 xylanase | PF02055  Glycosyl hydrolase family 30 TIM-barrel domain | 7,8 | 259.49 | Minc11164 (+5 other) | - | - | Xylan degradation | Plant Cell Wall Degradation |
| GH28 Polygalacturonase | PF00295  Glyco\_hydro\_28 | 7,9 | 351.60 | Minc18543b (+3 other) | - | - | Pectin decorations degradation | Plant Cell Wall Degradation |
| Expansin-like proteins | PF03330  Rare lipoprotein A (RlpA)-like double-psi beta-barrel | 7,10,11,12 | 86.11 | Minc07960 (+7 other) | 29.93 | GROS\_g11727  (+6 other) | Softening of non-covalent bonds | Plant Cell Wall Degradation |
| GH43 candidate Arabinanase | PF04616  Glyco\_hydro\_43 | 7\* | 69.07 | Minc10639 (+1 other) | - | - | Pectin decorations degradation | Plant Cell Wall Degradation |
| GH53 candidate Arabinogalactan endo-1,4-beta-galactosidase | PF07745  Glycosyl hydrolase family 53 | 13\* | - | Specific to Globodera (so far) | 349.30 | GROS\_g08150 | Pectinose / arabinogalactan degradation | Plant Cell Wall Degradation |
| PL3 Pecate Lyase | PF03211  Pectate lyase | 7,14,15,16 | 137.46 | Minc05972 (+30 other) | 137.06 | GROS\_g04366  (+2 other) | Pectin degradation | Plant Cell Wall Degradation |
| GH32 invertase | PF00251  Glycosyl hydrolases family 32 N-terminal domain | 17 | 154.42 | Minc09960 | 241.26 | GROS\_g08674  (+10 other) | Degradation of sucrose in glucose + fructose | Nutrient processing |
| Chorismate Mutase | PF01817  Chorismate mutase type II | [18][19][20] | 15.02 | Minc07025 | 42.36 | GROS\_g08190  (+1 other) | Conversion of Chorismate into SA | Plant defense manipulation |
| Candidate Isochorismatase | PF00857  Isochorismatase family | [21]\* | 91.41 | Minc14448 | 66.08 | GROS\_g01640 | Conversion of Chorismate into SA | Plant defense manipulation |
| Candidate Cyanate Lyases | PF02560  Cyanate lyase C-terminal domain | [22] [23]\* | 9.90 | Minc06015 (+1 other) | 11.51 | GROS\_g09531 |  | Detoxification |
| VB1 thiD | PF08543  Phosphomethylpyrimidine kinase | [24]\* | - | There are proteins containing a PF08543 domain but none with an AI>0 | 154.50 | GROS\_g07352 | Vitamin B1 biosynthesis | Nutrient processing |
| VB1 thiE | PF02581  Thiamine monophosphate synthase/TENI | [24]\* | - | Specific to globodera (so far?) | 163.99 | GROS\_g07353 | Vitamin B1 biosynthesis | Nutrient processing |
| VB1 thi4 | PF01946  Thi4 family | [24]\* | - | - | 108.07 | GROS\_g10855 | Vitamin B1 biosynthesis | Nutrient processing |
| VB1 thiM | PF02110  Hydroxyethylthiazole kinase family | [24]\* | - | - | 46.05 | GROS\_g07354 | Vitamin B1 salvage | Nutrient processing |
| VB1 tenA | PF03070  TENA/THI-4/PQQC family | [24]\* | - | - | 108.33 | GROS\_g05327  GROS\_g07355 | Vitamin B1 salvage | Nutrient processing |
| VB5 panC | PF02569  Pantoate-beta-alanine ligase | [24]\* | 16.52 | Minc14603 | 183.11 | GROS\_g05752 | Vitamin B5 biosynthesis | Nutrient processing |
| VB6 SNO | PF01174  SNO glutamine amidotransferase family | [25] | - | - | - | GROS\_g08955Ŧ | Vitamin B6 biosynthesi | Nutrient processing |
| VB6 SOR-SNZ | PF01680  SOR/SNZ family | [25] | - | - | 12.72 | GROS\_g08956 | Vitamin B6 biosynthesis | Nutrient processing |
| NodL - like | PF12464  Maltose acetyltransferase  +  PF00132  Bacterial transferase hexapeptide (six repeats) | [26,27]\* | Not in MiV1 |  | 13.12 | GROS\_g11033 | Candidate acetyltransferase | Feeding site induction |
| Candidate GSI Glutamine Synthase | PF00120  Glutamine synthetase, catalytic domain | [27][28]\* | 35.59 | Minc08077 (+3 other) | 29.24 | GROS\_g02362 | Nitrogen assimilation | Nutrient processing |
| Candidate L-threonine aldolase | PF01212  Beta-eliminating lyase | [27][28]\* | Not in MiV1 | Minc3s06087g39310  Minc3s03983g35231  Minc3s09176g42992 | 164.69 | GROS\_g10423  GROS\_g10421  GROS\_g10422 | ?? | ?? |
| Candidate Phosphorybosyl transferase | PF00156  Phosphoribosyl transferase domain | [27][28]\* | 202.63 | Minc16723 | 198.13 | GROS\_g06735  GROS\_g04632 | ?? | ?? |

\* no functional characterization so far

Ŧ protein with an annotation problem in the genome, only the N-terminal part corresponds to SNO

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