**Supplementary Table 1** Specific primers used for qPCR and qRT-PCR.

|  |  |
| --- | --- |
| **Gene name** | **Primer sequences (5’ to 3’)** |
| *Actin-7**qPCR* | Forward:TCATTGGAATGGAAGCTGCTGGCATTReverse:CGACCTTAATCTTCATGCTGCTTGGA |
| *Cutinase**qPCR* | Forward:AAGAACCAGATCAAGGGCGTCGTGReverse:GCGTCCGCAATGTCGCAGTAGA |
| *Fra a 5**qRT-PCR* | Forward:AGATTGCACCTCAGGCAGTAAAReverse:GTGGTACTTGCTGGTGGTCTT |
| *Fra a 1**qRT-PCR* | Forward:GAAGGTGATGGAGGAGTTGGAAReverse:CTCCCTCGGATGCAATCAAC |
| *Fra a 1.02**qRT-PCR* | Forward:ACTTATGAAACCGAGTTTACATCTGTReverse:TTAACTGCTTGTGGAGCAATCTTT |
| *CHP1**qRT-PCR* | Forward:CACCGTCCTTTCTTCCATTTReverse:ACTTCTCATCCCAGGCACTC |
| *GAPDH1**qRT-PCR* | Forward:TCCATCACTGCCACCCAGAAGACTGReverse:AGCAGGCAGAACCTTTCCGACAG |

**Supplementary Table 2** Allergenicity prediction analyses of strawberry Bet v 1 homologous proteins in Allergen Online Database.

|  |  |  |
| --- | --- | --- |
| **Abbreviated** **protein name** | **80mer Identity (%)** | **Full fasta Identity (%)** |
| **Full alignment** | **Best hit** |
| Fra a 1.01 | 91.80 | 93.80 | 93.80 |
| Fra a 1.02 | 90.60 | 92.50 | 90.60 |
| Fra a 1.03 | 100 | 100 | 100 |
| Fra a 1.04 | 100 | 100 | 100 |
| Fra a 1.05 | 100 | 100 | 100 |
| Fra c 1.01 | 84.30 | 88.78 | 84.30 |
| Fra v 1.01 | 100 | 100 | 100 |
| Fra v 1.02 | 43.90 | 57.52 | 45.70 |
| Fra v 1.03 | 52.20 | 58.70 | 54.00 |
| Fra v 1.04 | 50.60 | 62.50 | 52.50 |
| Fra v 1.05 | 49.40 | 63.79 | 50.90 |
| Fra v 1.06 | 83.10 | 90.00 | 86.90 |
| Fra v 1.07 | 88.10 | 92.50 | 88.10 |
| Fra v 1.08 | 100 | 100 | 100 |
| Fra v 1.09 | 79.40 | 82.50 | 79.40 |
| Fra v 1.10 | 91.90 | 93.80 | 91.90 |
| Fra v 1.11 | 84.90 | 88.78 | 84.90 |
| Fra v 1.12 | 87.50 | 91.20 | 87.50 |
| Fra v 1.13 | 96.30 | 98.80 | 96.30 |

A criterion of >70% identity was set in our analyses.

**Supplementary Table 3** Linear epitope prediction of strawberry Bet v 1 homologous proteins in IEDB Database.

|  |  |  |
| --- | --- | --- |
| **Abbreviated protein name** | **Epitopes numbers** | **Blast Identity (>%)** |
| Fra a 1.01 | 28 | 70 |
| Fra a 1.02 | 27 | 80 |
| Fra a 1.03 | 25 | 80 |
| Fra a 1.04 | 12 | 90 |
| Fra a 1.05 | 20 | 90 |
| Fra c 1.01 | 36 | 80 |
| Fra v 1.01 | 20 | 90 |
| Fra v 1.02 | 3 | 70 |
| Fra v 1.03 | 6 | 80 |
| Fra v 1.04 | 6 | 70 |
| Fra v 1.05 | 11 | 80 |
| Fra v 1.06 | 15 | 90 |
| Fra v 1.07 | 43 | 80 |
| Fra v 1.08 | 25 | 80 |
| Fra v 1.09 | 19 | 90 |
| Fra v 1.10 | 20 | 90 |
| Fra v 1.11 | 33 | 80 |
| Fra v 1.12 | 21 | 80 |
| Fra v 1.13 | 12 | 90 |

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**Supplementary Fig. 1 Comparative transcriptional level of *Fra a 1.05*, *Fra a 1.01* and *Fra a 1.02* genes in strawberry fruits.** The mRNA level of *Fra a 1.05* was about 100 fold higher compared with those of *Fra a 1.01* and *Fra a 1.02* genes. Although the relative comparison of gene transcriptional levels in one tissue may be not accurate considering the amplification efficiencies of RT primers, we still could conclude that *Fra a 1.05*geneis the most abundant one from the striking trend. Data were shown as mean±standard deviation derived from three biological and three technical replicates.

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**Supplementary Fig. 2 The susceptibility of Benihoppe, SY, YW and HW4 leaf tissues to *C. fructicola*.** Four varieties were sprayed with the same concentration of *C. fructicola* conidia. Pictures were taken at 5 dpi for two cultivars and 8 dpi for two diploids. Anthracnose symptoms of Benihoppe and SY appeared 2 days earlier than those of HW4 and YW.