|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample type** | **Sample** | **Subspecies** | **Amino acid sequence of the hypervariable region** | **Total coverage\*** | **Abundance in the**  **sample** | **NCBI accession number** |
| worker bee | Cw1\_SA2, Jap\_SA12 | *ligustica* | IISSLSNKTIHNNNNYKYNYNNNYNNNNNYNNYNNTNYKKLYYNINYI | 4 577 (972+3 605) | 12.4%, 1.5% | MK241931.1 identity to the most homologous existing sequence: 88% |
| honey | Ves\_SA4 | *carnica* | IISSLSNKTIHDNNNYKYNYNNNNNNYKNYNNYKKLYYNINYI | 1 448 | 0.6% | MK241934.1 identity to the most homologous existing sequence: 98% |
| honey | Ves\_SA5 | *carnica* | IISSLSNNYNYSNYNNYNNYNKNYNNYKKLYYNINYI | 1 317 | 0.5% | MK241935.1 identity to the most homologous existing sequence: 97% |
| honey | Ves\_SA6, Gru\_SA4 | *carnica / caucasica* | IISSLSNKTIHNNNNYKYNYNNNNNYKNYNNYKKLYYNINYI | 2 090 (1 035+1 055) | 0.4%, 0,4% | MK241936.1 identity to the most homologous existing sequence: 98% |
| honey | Ves\_SA7, Chi\_SA3, Gru\_SA3 | *carnica / caucasica* | IISSLSNKTIHNNNNYKYNYNNNNNYYKNYNNYKKLYYNINYI | 3 482 (1 027+1 383+1 072) | 0.4%, 0.7%, 0.4% | MK241937.1 identity to the most homologous existing sequence: 98% |
| honey | SzG\_SA4 | *carnica* | IISSLSNKTIHNNNNYKYNYNNNNYNNNNYKKLQYYNINYI | 22 572 | 3.5% | MK241933.1 identity to the most homologous existing sequence: 93% |
| honey | Jap\_SA14 | *ligustica* | IISSLSNKTIHNNNNYNNNNYNNYNNNYNNNNYNNYKKLYYNINYI | 1 345 | 0.5% | MK241932.1 identity to the most homologous existing sequence: 96% |

**Table 3.** New alleles reported in the present study

\* Coverage includes only the two most abundant sequences, that were considered to be relevant