**Table S1**. Name species and code of five *Salvia* species used in this research

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Name species | code | number | Name species | code | number |
| *S.cereal* | cere12 | 28 | *S.virgata* | v41 | 1 |
| *S.cereal* | cere41 | 29 | *S.virgata* | v42 | 2 |
| *S.cereal* | cere42 | 30 | *S.virgata* | v43 | 3 |
| *S.cereal* | cere43 | 31 | *S.virgata* | v44 | 4 |
| *S.cereal* | cere44 | 32 | *S.virgata* | v45 | 5 |
| *S.cereal* | cere45 | 33 | *S.virgata* | v46 | 6 |
| *S.cereal* | cere46 | 34 | *S.virgata* | v47 | 7 |
| *S.cereal* | cere47 | 35 | *S.virgata* | v48 | 8 |
| *S.cereal* | cere48 | 36 | *S.virgata* | v49 | 9 |
| *S.sclarea* | scl22 | 37 | *S.virgata* | v40 | 10 |
| *S.sclarea* | scl23 | 38 | *S.virgata* | v51 | 11 |
| *S.sclarea* | scl24 | 39 | *S.virgata* | v52 | 12 |
| *S.officinalis* | of41 | 40 | *S.nemorosa* | nem41 | 13 |
| *S.officinalis* | of42 | 41 | *S.nemorosa* | nem44 | 14 |
| *S.officinalis* | of43 | 42 | *S.nemorosa* | nem46 | 15 |
| *S.officinalis* | of44 | 43 | *S.nemorosa* | nem49 | 16 |
| *S.officinalis* | of45 | 44 | *S.nemorosa* | nem51 | 17 |
| *S.officinalis* | of46 | 45 | *S.nemorosa* | nem53 | 18 |
| *S.officinalis* | of47 | 46 | *S.nemorosa* | nem54 | 19 |
| *S.officinalis* | of52 | 47 | *S.nemorosa* | nem55 | 20 |
| *S.officinalis* | of11 | 48 | *S.nemorosa* | nem56 | 21 |
| *S.officinalis* | of12 | 49 | *S.nemorosa* | nem57 | 22 |
| *S.officinalis* | of13 | 50 | *S.nemorosa* | nem58 | 23 |
| *S.officinalis* | of14 | 51 | *S.nemorosa* | nem59 | 24 |
| *S.officinalis* | of15 | 52 | *S.nemorosa* | nem61 | 25 |
| *S.officinalis* | of17 | 53 | *S.nemorosa* | nem62 | 26 |
| *S.officinalis* | of18 | 54 | *S.cereal* | cere11 | 27 |

**Table S2.** Polymorphism number and rate for 14 SRAP PCs used to amplify 54 genomic DNA templates from five *Salvia* species

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Primercombination | Number oftotalfragments | Number ofpolymorphicfragments | Percentage ofpolymorphicfragments | PICvalue |
| Me6 - Em6 | 31 | 27 | 87 | 0.3938 |
| Me8 - Em1 | 21 | 20 | 95 | 0.2878 |
| Me8 - Em6 | 23 | 23 | 100 | 0.3012 |
| Me3-Em18 | 14 | 14 | 100 | 0.2810 |
| Me3-Em17 | 18 | 18 | 100 | 0.2627 |
| Me4 - Em6 | 28 | 28 | 100 | 0.3845 |
| Me6-Em17 | 20 | 19 | 95 | 0.3747 |
| Me1 - Em5 | 11 | 11 | 100 | 0.2197 |
| Me3 - Em2 | 15 | 15 | 100 | 0.3434 |
| Me8-Em17 | 30 | 30 | 100 | 0.3255 |
| Me2 - Em4 | 7 | 7 | 100 | 0.2010 |
| Me3 - Em6 | 11 | 11 | 100 | 0.2154 |
| Me3 - Em1 | 16 | 15 | 94 | 0.2198 |
| Me4-Em17 | 20 | 17 | 85 | 0.2196 |
| **Total** | **265** | **255** |  |  |
| **Mean** | **18.92** | **18.21** | **96** | **0.308** |

**Table S3.** Measures of genetic distance among different *Salvia* species based on coancestry coefficients obtained from the pairwise *Fst* distance matrices produced by POPGENE 1.32 software

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Species name | *S. virgata* | *S. nemorosa* | *S. cereal* | *S. sclarea* | *S. officinalis* |
| *S. virgata* | \*\*\* |  |  |  |  |
| *S. nemorosa* | 0.1263 | \*\*\* |  |  |  |
| *S. cereal* | 0.3171 | 0.3527 | \*\*\* |  |  |
| *S. sclarea* | 0.5424 | 0.5648 | 0.5378 | \*\*\* |  |
| *S. officinalis* | 0.1579 | 0.2319 | 0.3390 | 0.5564 | \*\*\* |

**Fig. S1**. Sampling location sites of five *Salvia* species, *S.virgata*, *S. nemorosa*, *S. officinalis*, *S. sclarea* and *S. cereal* from different geographical regions of Iran used in study.