## SUPPLEMENTARY MATERIALS

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## SUPPLEMENTARY TABLES

Table S1. Genetic diversity indexes

| Pop | MLG | H | G | lambda | E. 5 | Hexp | Ia | rbarD |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| BE | 10 | 2.3 | 10 | 0.9 | 1 | 0.123 | 1.568 | 0.0832 |
| GE | 9 | 2.16 | 8.33 | 0.88 | 0.952 | 0.111 | 1.057 | 0.0713 |
| LI | 10 | 2.3 | 10 | 0.9 | 1 | 0.247 | 2.019 | 0.0654 |
| PO | 12 | 2.48 | 12 | 0.917 | 1 | 0.233 | 1.958 | 0.068 |
| TU | 5 | 1.61 | 5 | 0.8 | 1 | 0.203 | 4.41 | 0.1764 |
| ER | 9 | 2.16 | 8.33 | 0.88 | 0.952 | 0.249 | 4.004 | 0.134 |
| SM | 4 | 1.39 | 4 | 0.75 | 1 | 0.195 | 0.265 | 0.0126 |
| LA | 6 | 1.79 | 6 | 0.833 | 1 | 0.155 | 0.272 | 0.0151 |
| IS | 8 | 2.08 | 8 | 0.875 | 1 | 0.142 | 1.745 | 0.1027 |
| Total | 73 | 4.28 | 71.2 | 0.986 | 0.985 | 0.332 | 2.261 | 0.0411 |

Pop Population name.
MLG Number of multilocus genotypes (MLG) observed.
H Shannon-Wiener Index of MLG diversity (Shannon, 1948).
G Stoddart and Taylor's Index of MLG diversity (Stoddart \& Taylor, 1988).
lambda Simpson's Index (Simpson, 1949).
E. 5 Evenness, E5 (Pielou, 1975; Ludwig \& Reynolds, 1988; Grünwald et al., 2003).

Hexp Nei's unbiased gene diversity (Nei, 1978).
Ia The index of association, IA (Brown, Feldman \& Nevo, 1980; Smith et al., 1993).
rbarD The standardized index of association, $\mathrm{r}^{-} \mathrm{d}[@]$.

## References

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Table S2. Morphological overlap: Pairwise $\beta$ total (Carvahlo \& Cardoso, 2020; Mammola \& Cardoso, 2020) values among the morphospaces of the nine populations

|  | BE | ER | GE | IS | LA | LI | PO | SM | TU |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| BE | 0.00 | 0.89 | 0.92 | 0.88 | 0.68 | 0.96 | 0.98 | 0.81 | 1.00 |
| ER | 0.89 | 0.00 | 0.99 | 0.98 | 0.94 | 0.99 | 0.89 | 0.97 | 0.87 |
| GE | 0.93 | 0.98 | 0.00 | 0.57 | 0.84 | 0.61 | 0.99 | 0.70 | 1.00 |
| IS | 0.88 | 0.98 | 0.57 | 0.00 | 0.75 | 0.69 | 0.99 | 0.62 | 1.00 |
| LA | 0.67 | 0.94 | 0.84 | 0.75 | 0.00 | 0.90 | 0.99 | 0.59 | 1.00 |
| LI | 0.95 | 0.99 | 0.61 | 0.69 | 0.90 | 0.00 | 0.99 | 0.81 | 1.00 |
| PO | 0.98 | 0.89 | 0.99 | 0.99 | 0.99 | 0.99 | 0.00 | 0.99 | 0.97 |
| SM | 0.80 | 0.96 | 0.69 | 0.62 | 0.59 | 0.81 | 0.99 | 0.00 | 1.00 |
| TU | 1.00 | 0.87 | 1.00 | 1.00 | 1.00 | 1.00 | 0.97 | 1.00 | 0.00 |

Table S3. Morphological distance: Pairwise distances between centroids among the morphospaces of the nine populations.

|  | BE | ER | GE | IS | LA | LI | PO | SM | TU |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| BE | 0.0 | 3.60 | 1.92 | 2.28 | 3.12 | 0.95 | 7.55 | 2.64 | 6.25 |
| ER | 3.60 | 0.00 | 3.93 | 3.65 | 3.71 | 3.74 | 4.88 | 3.20 | 3.49 |
| GE | 1.92 | 3.93 | 0.00 | 0.67 | 1.47 | 0.98 | 7.83 | 1.35 | 6.25 |
| IS | 2.28 | 3.65 | 0.67 | 0.00 | 0.99 | 1.42 | 7.72 | 0.72 | 5.88 |
| LA | 3.12 | 3.71 | 1.47 | 0.99 | 0.00 | 2.29 | 7.45 | 0.82 | 5.50 |
| LI | 0.95 | 3.74 | 0.98 | 1.42 | 2.29 | 0.00 | 7.74 | 1.92 | 6.25 |
| PO | 7.55 | 4.88 | 7.83 | 7.72 | 7.45 | 7.74 | 0.00 | 7.36 | 5.00 |
| SM | 2.64 | 3.20 | 1.35 | 0.72 | 0.82 | 1.92 | 7.36 | 0.00 | 5.29 |
| TU | 6.25 | 3.49 | 6.25 | 5.88 | 5.50 | 6.25 | 5.00 | 5.29 | 0.00 |

Table S4. GenAlex formatted matrix used for fingerprinting analysis (csv format)

66,75,9,10,10,10,12,5,10,4,6,8,
,,,BE,GE,LI,PO,TU,ER,SM,LA,IS,
Ind,Pop,11_1,11_2,11_3,11_4,11_5,11_6,11_7,11_8,11_9,11_10,11_11,11_12,11_13,11_14,11_15,11_16,11_17,11_18,11_19,11_2 $0,11 \_21,11 \_22,11 \_23,11 \_24,11 \_25,12 \_1,12 \_2,12 \_3,12 \_4,12 \_5,12 \_6,12 \_7,12 \_8,12 \_9,12 \_10,12 \_11,12 \_12,14 \_01,14 \_02,14 \_03,14 \_04$ ,14_05,14_06,14_07,14_08,14_09,14_10,14_11,14_12,14_13,14_14,14_15,14_16,14_17,14_18,14_19,14_20,14_21,15_1,15_2,15_3, 15_4,15_5,15_6,15_7,15_8

BE01,BE, $0,0,1,0,1,0,0,1,0,1,1,1,1,1,1,1,1,0,1,0,0,1,0,1,1,0,0,0,0,0,0,1,0,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,0,0,0,0,0,0,1,0,0,0,1,1,0,0,1,0,1,1$ BE02,BE, $0,0,0,1,1,1,0,1,0,1,1,1,1,0,1,1,1,0,1,0,0,1,0,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,0,1,0,0,1,0,1,1,0,0,1,1,0,0,1,1,1,1$ BE03,BE, 1,0,0,1,0,1,0,1,0,1,1,1,1,0,1,1,1,0,1,0,0,1,0,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,0,1,0,0,1,0,1,1,0,0,1,1,0,0,1,0,1,1 BE04,BE, $0,0,1,0,1,1,0,1,0,1,1,1,1,0,1,1,1,0,1,0,1,1,0,1,1,1,1,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,1,1,0,1,1,1,1,0,0,1,0,1,1,0,0,1,1,0,0,1,0,1,1$ BE05,BE,0,0,0,1,0,1,0,1,0,1,1,1,1,1,1,1,1,0,1,0,0,1,1,1,1,0,1,0,0,1,1,1,1,0,0,0,0,1,1,1,0,1,0,0,1,1,1,1,0,1,0,0,1,1,1,1,0,0,1,1,0,0,1,1,1,1 BE06,BE,0,0,1,0,1,0,0,1,0,1,1,1,1,1,1,1,1,0,1,0,0,1,1,1,1,0,1,0,0,1,1,1,1,0,0,0,0,1,1,1,0,1,0,0,1,1,1,1,0,1,0,0,1,1,1,1,0,0,1,1,0,0,1,0,1,1 BE07,BE,0,0,0,1,1,1,0,1,0,1,1,1,1,0,1,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,0,1,1,0,0,1,1,0,0,1,0,1,1 BE08,BE,1,0,1,0,0,1,0,1,0,1,1,1,1,1,1,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,0,1,1,0,0,1,1,0,0,1,1,1,1 BE09,BE, $0,0,0,1,0,1,0,1,0,1,1,1,1,0,1,1,1,0,1,0,0,1,0,1,1,1,1,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,1,1,0,0,1,0,1,1,0,0,1,1,0,0,1,1,1,1$ BE10,BE,0,0,0,1,0,1,0,1,0,1,1,1,1,0,1,1,1,0,1,0,0,1,0,1,1,0,1,0,0,1,0,1,1,0,0,0,0,1,1,1,0,1,0,0,1,0,1,1,0,1,0,0,1,0,1,1,0,0,1,1,0,0,1,1,1,1 GE01,GE, $0,1,0,0,0,1,0,0,1,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,1,0,0,0,0,0,0,0,0,0,1,1$ GE02,GE,0,1,0,0,0,1,0,0,1,0,0,0,0,1,0,1,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,0,0,0,0,0,0,1,1,1 GE03,GE,0,1,0,0,0,1,0,0,1,0,0,0,0,1,0,1,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,0,1,1 GE04,GE,0,1,0,0,0,1,0,0,1,0,0,0,0,1,0,0,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,1,0,0,0,1,1,1,1,1 GE05,GE, $0,1,0,0,0,1,0,0,1,0,0,0,1,1,0,0,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,0,0,0,0,1,1,0,1,1$ GE06,GE, $0,1,0,0,0,1,0,0,1,0,0,0,1,1,0,1,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,0,1,1$ GE07,GE, $0,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,0,1,1$ GE08,GE, $0,0,0,0,0,1,0,0,1,0,0,0,0,1,0,1,0,1,0,0,0,0,0,0,0,1,0,1,0,1,0,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,1,0,1,0,1,0,1,0,0,0,1,0,0,0,0,0,1,1$ GE09,GE,0,0,0,0,0,1,0,0,1,0,0,0,0,1,0,1,0,1,0,0,0,0,0,0,0,0,1,1,0,1,0,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,1,1,0,1,0,1,0,0,0,0,0,0,0,0,0,1,1 GE10,GE, $0,0,0,0,0,1,0,0,1,0,0,0,0,1,0,1,0,1,0,0,0,0,0,0,0,0,1,1,0,1,0,1,0,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,1,1,0,1,0,1,0,0,0,0,0,0,0,0,0,1,1$ LI01,LI,0,0,0,0,0,0,1,0,0,1,0,0,0,1,1,1,0,0,1,0,0,0,1,0,1,0,0,1,0,1,0,1,0,0,0,0,0,1,1,0,0,1,0,0,0,1,0,1,0,0,1,0,1,0,1,0,0,0,0,0,0,0,1,1,1,1 LIO2,LI,0,0,0,0,0,0,1,0,1,1,0,0,0,1,1,1,0,0,1,1,0,0,1,0,1,1,0,0,0,1,0,1,0,0,0,0,0,1,1,0,0,1,1,0,0,1,0,1,1,0,0,0,1,0,1,0,0,0,1,0,0,0,0,1,1,1 LI03,LI, $0,0,0,0,0,0,1,0,0,0,0,0,0,1,1,1,1,0,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,0,0,0,1,1,1,0,0,0,0,0,0,0,0,1,1,1,0,1,0,1,0,0,0,1,0,0,0,0,1,1,1$ LI04,LI,0,0,0,0,0,0,1,0,1,0,0,0,0,1,1,1,0,0,1,0,1,0,1,0,1,0,0,0,0,1,0,1,1,0,0,0,0,1,1,0,0,1,0,1,0,1,0,1,0,0,0,0,1,0,1,1,0,0,1,0,0,1,0,1,1,1

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Table S5. Primers details

| Primer name | Amplified region | Annealing <br> temperature | Fragment size | Reference |
| :--- | :--- | :--- | :--- | :--- |
| ITS-u1 I ITS-u2 | ITS2 (mitochondrial) | $55^{\circ} \mathrm{C}$ | 450 bp | Cheng et al. 2016 |
| ucp-e I ucp-f/trnF-r | trnL exon2 (plastidial) | $55^{\circ} \mathrm{C}$ | 430 bp | Taberlet et al. 1991 |
| psbB-B61 F I psbB-B66 R | psbB (plastidial) | $45^{\circ} \mathrm{C}$ | 1084 bp | Graham and Olmstead 2000 |
| psbC-f I psbC-r | psbC (plastidial) | $62^{\circ} \mathrm{C}$ | 865 bp | Demesure et al. 1995 |
| SCOT11 | N.A. | $55^{\circ} \mathrm{C}$ | N.A. | Collard and Mackill 2009 |
| SCOT12 | N.A. | $55^{\circ} \mathrm{C}$ | N.A. | Collard and Mackill 2009 |
| SCOT14 | N.A. | $55^{\circ} \mathrm{C}$ | N.A. | Collard and Mackill 2009 |
| SCOT15 | N.A. | $55^{\circ} \mathrm{C}$ | N.A. | Collard and Mackill 2009 |
| SCOT16 | N.A. | Collard and Mackill 2009 |  |  |

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## SUPPLEMENTARY FIGURES

Figure S1. Genotype Accumulation Curve: A plateau has been reached, then the number of loci is enough to discriminate individuals. Each locus was randomly samples 1000 times to create the distribution.


Figure S2. ITS based phylogeny of Tephroseris genus considering all the populations: Each label (where available) include the following information: population code, GenBank accession number, species name and ribotype. Labels are colored by geographic origin: T.E.-App = Tosco-Emilian Appennine; Lig.-App = Ligurian Appennine: W-Alps = Western Alps; EAlps = Eastern Alps; Pannonia = Pannonia geographic region; W-Carp. = Western Carpathians; others = geographic regions far from the study area such as Spain or Turkey. The phylogenetic tree edited int iTOL. The full availability of this figure is available at the link http://itol.embl.de/shared/MartinoAdamo.


Figure S3. Collinearity among predictors: Predictors used for modelling the species distribution; from top left to bottom right: altitude, isothermality, organic soil content at 15 cm depth, average annual precipitations, soil pH at a depth 15 cm , precipitation seasonality, solar radiation, mean annual temperature, annual and daily temperature range, water vapour pressure, wind speed. For each predictor, histograms showing the distribution of extracted values are displayed on the diagonal. Bivariate scatter plots are displayed below the diagonal and the Pearson $r$ correlations above the diagonal (threshold for collinearity set at $|r|>0.7$ ).


Figure S4. Contribution of variables to principal components (PCs): first ten most important variables, used to measure leaves morphology, are reported in order of relative contribution to PC1 (top graph) and PC2 (bottom graph).

Contribution of variables to PC1


Contribution of variables to PC2


