

Appendix

Appendix A. Full Diagnostic Statistics for Quantitative Traits

A total of 26 quantitative traits, plus the derived metric Curvature per Length, were examined at the image-level median scale for the six focal Solanaceae species. *Shapiro–Wilk* tests indicated that most traits deviated from normality. *Kruskal–Wallis* tests showed that many traits exhibited interspecific differences, but the focal path–curvature traits did not all show the same degree of stand-alone support.

Only mean curvature ($W = 0.996868$, $p = 0.982696$) and Sum upper curvature traits ($W = 0.984390$, $p = 0.061016$) were not significant in the *Shapiro–Wilk* test at $\alpha = 0.05$. For the derived metric Curvature per Length, *Shapiro–Wilk* yielded $W = 0.774405$ and $p = 1.16 \times 10^{-14}$, indicating strong deviation from normality. In *Kruskal–Wallis* testing, the non-significant traits were ellipse angle, max curvature, skeleton ratio, mean curvature, and tortuosity, whereas Curvature per Length showed significant interspecific differentiation ($H = 27.825834$, $p = 3.94 \times 10^{-5}$).

Table S1. Full Shapiro–Wilk Test Results for All Quantitative Traits.

Trait	n	W	p	BH _q	Non-normal after BH
Contraction Ratio	163	0.426383	1.15158e-22	2.25107e-21	True
Max Upper Curvature Traits	165	0.444147	1.73159e-22	2.25107e-21	True
Ellipse Major Axis	144	0.380365	4.04666e-22	2.71949e-21	True
Max Lower Curvature Traits	165	0.465806	4.18384e-22	2.71949e-21	True
Max Curvature	165	0.618622	5.34856e-19	2.78125e-18	True
Area	165	0.713614	1.48e-16	6.41333e-16	True
Straight Length	165	0.719953	2.25621e-16	8.38022e-16	True
Length	165	0.738042	7.8175e-16	2.54069e-15	True
Bounding Box Aspect Ratio	165	0.763691	5.08725e-15	1.46965e-14	True
Ellipse Minor Axis	144	0.799312	9.05117e-13	2.3533e-12	True
Mean Lower Curvature Traits	165	0.834068	2.0817e-12	4.92038e-12	True
Skeleton Ratio	165	0.863365	4.32242e-11	9.36525e-11	True
Perimeter	165	0.865966	5.77452e-11	1.1549e-10	True
Skeleton Length	165	0.869114	8.24062e-11	1.5304e-10	True
Mean Upper Curvature Traits	165	0.870768	9.95588e-11	1.72569e-10	True
Ellipse Angle	144	0.878625	1.70239e-09	2.76638e-09	True
Sum of Curvature	165	0.923615	1.20842e-07	1.84817e-07	True
Tortuosity	165	0.931681	4.55897e-07	6.58518e-07	True
Width (Max)	165	0.950814	1.58314e-05	2.1664e-05	True
Number of Endpoints	165	0.952467	2.22033e-05	2.88643e-05	True
Width (Base)	165	0.956236	4.90938e-05	6.07828e-05	True
Width (Tip)	165	0.968088	0.000747947	0.00083938	True
Sum Lower Curvature Traits	165	0.975350	0.00483803	0.00546907	True
Number of Branchpoints	165	0.983310	0.0446896	0.0484137	True
Sum Upper Curvature Traits	165	0.984390	0.0610165	0.0634572	False
Mean Curvature	165	0.996868	0.982696	0.982696	False

Table S2. Full Kruskal–Wallis Test Results for All Quantitative Traits.

Trait	H	df	p	BH q	Different after BH
Area	98.5977	5	1.04364e-19	2.71346e-18	True
Skeleton Length	85.182	5	6.8945e-17	8.96285e-16	True
Max Lower Curvature Traits	68.7461	5	1.86839e-13	1.61927e-12	True
Number of Branchpoints	66.4331	5	5.65052e-13	3.67284e-12	True
Max Upper Curvature Traits	65.4991	5	8.8301e-13	4.59165e-12	True
Width (Max)	58.2556	5	2.78586e-11	1.2072e-10	True
Mean Upper Curvature Traits	56.952	5	5.1735e-11	1.92158e-10	True
Perimeter	56.6658	5	5.92605e-11	1.92597e-10	True
Width (Tip)	53.4662	5	2.69795e-10	7.79409e-10	True
Sum Upper Curvature Traits	47.6494	5	4.18811e-09	1.08891e-08	True
Mean Lower Curvature Traits	45.7367	5	1.02751e-08	2.42866e-08	True
Width (Base)	42.6302	5	4.39096e-08	9.51375e-08	True
Length	39.9889	5	1.5011e-07	3.0022e-07	True
Straight Length	39.583	5	1.81231e-07	3.36572e-07	True
Ellipse Major Axis	33.6717	5	2.76755e-06	4.79709e-06	True
Sum Lower Curvature Traits	29.143	5	2.17369e-05	3.53225e-05	True
Ellipse Minor Axis	27.7171	5	4.13393e-05	6.32248e-05	True
Sum of Curvature	20.4024	5	0.00105003	0.00144544	True
Contraction Ratio	20.3887	5	0.00105628	0.00144544	True
Number of Endpoints	13.9499	5	0.0159309	0.0207101	True
Bounding Box Aspect Ratio	12.1213	5	0.0331627	0.0410585	True
Ellipse Angle	9.09721	5	0.105249	0.124385	False
Max Curvature	8.89905	5	0.113159	0.127919	False
Skeleton Ratio	6.41096	5	0.268259	0.289523	False
Mean Curvature	6.29695	5	0.278388	0.289523	False
Tortuosity	4.49213	5	0.480937	0.480937	False

Appendix B. Supporting Analyses for Trait Selection and Exclusion Logic

Trait prioritization was supported using internal analyses of size dominance, redundancy, and exploratory distance-based behavior. Size-axis analysis showed that several excluded descriptors were strongly associated with a common size dimension, whereas Tortuosity and Mean Curvature were nearly independent of that axis and Curvature per Length showed reduced size dependence after normalization by length.

The strongest positive correlations with the size axis were observed for area ($\rho = 0.884$), skeleton length ($\rho = 0.848$), width(max) ($\rho = 0.843$), width(tip) ($\rho = 0.766$), and length ($\rho = 0.714$). Strong redundancy was also concentrated among size-oriented descriptors. The highest pairwise correlations were length vs. straight length ($\rho = 0.997$), perimeter vs. ellipse major axis ($\rho = 0.969$), area vs. skeleton length ($\rho = 0.966$), perimeter vs. ellipse minor axis ($\rho = 0.939$), and ellipse major axis vs. ellipse minor axis ($\rho = 0.893$).

Exploratory single-trait exact Mantel tests showed that the focal traits did not all act as individually dominant markers: tortuosity yielded Spearman $r_M = 0.654$ ($p = 0.078$), mean curvature yielded $r_M = 0.439$ ($p = 0.054$), and curvature per length yielded $r_M = 0.571$ ($p = 0.069$). In contrast, the focal path–curvature block yielded the strongest Spearman exact Mantel correspondence among the main candidate blocks examined ($r_M = 0.775$, $p = 0.044$), whereas all 26 traits ($r_M = -0.029$, $p = 0.467$) and size core traits ($r_M = -0.046$, $p = 0.535$) did not show meaningful correspondence.

Table S3. Trait Correlations With the Size Axis.

Trait	Spearman ρ with size PC1	p-value
Area	0.884	1.18e-48
Skeleton Length	0.848	4.67e-41
Width (Max)	0.843	4.04e-40
Width(Tip)	0.766	4.98e-29
Length	0.714	9.7e-24
Straight Length	0.708	3.54e-23
Width(Base)	0.672	2.74e-20
Ellipse Major Axis	0.672	2.84e-20
Perimeter	0.668	6.31e-20
Ellipse Minor Axis	0.651	1.09e-18
Number of Branchpoints	0.465	4.26e-09
Max Lower Curvature Traits	0.416	2.13e-07
Contraction Ratio	0.331	5.11e-05
Max Upper Curvature Traits	0.326	6.65e-05
Sum Lower Curvature Traits	0.323	7.69e-05
Sum Upper Curvature Traits	0.306	0.000191
Sum of Curvature	0.282	0.000623
Max Curvature	0.244	0.00314
Bounding Box Aspect Ratio	0.084	0.316
Number of Endpoints	0.074	0.378
Tortuosity	-0.072	0.391
Ellipse Angle	-0.073	0.382
Mean Curvature	-0.076	0.366
Skeleton Ratio	-0.178	0.0326
Mean Lower Curvature Traits	-0.180	0.0307
Mean Upper Curvature Traits	-0.237	0.00423
Curvature per Length	-0.549	1.03e-12

Table S4. Strongly Redundant Trait Pairs Based on Spearman Correlation ($|\rho| \geq 0.80$).

Trait 1	Trait 2	Spearman ρ
Length	Straight Length	0.997
Perimeter	Ellipse Major Axis	0.969
Area	Skeleton Length	0.966
Perimeter	Ellipse Minor Axis	0.939
Ellipse Major Axis	Ellipse Minor	0.893
Width(Tip)	Width(Max)	0.881
Tortuosity	Mean Curvature	0.872
Width(Base)	Width(max)	0.872
Perimeter	Contraction Ratio	0.843

Table S5. Exploratory Single-Trait Exact Mantel Results.

Trait	Spearman r M	Spearman p	Pearson r M	Pearson p
Tortuosity	0.654	0.078	0.986	0.060
Mean Curvature	0.439	0.054	0.244	0.239
Curvature per Length	0.571	0.069	0.703	0.033
Skeleton Ratio	-0.257	0.629	-0.286	0.699
Ellipse Angle	0.771	0.022	0.742	0.065
Area	0.043	0.444	-0.058	0.367
Length	0.014	0.464	-0.272	0.636
Bounding Box Aspect Ratio	0.111	0.303	-0.092	0.229
Contraction Ratio	0.139	0.287	-0.171	0.279

Table S6. Exploratory Trait-Block Exact Mantel Results.

Trait block	n traits	Spearman r M	Spearman p	Pearson r M	Pearson p
Focal Path Curvature	3	0.775	0.044	0.865	0.046
Curvature Only	2	0.696	0.053	0.725	0.036
Path Only	2	0.704	0.065	0.883	0.031
Focal Plus Contraction	4	0.661	0.086	0.316	0.197
All	26	-0.029	0.467	-0.092	0.429
Size Extended	10	-0.004	0.500	-0.187	0.535
Size Core	3	-0.046	0.535	-0.089	0.544
Branch Counts	2	-0.182	0.619	-0.307	0.890

Appendix C. Supplementary Ordination and Topology Checks

Although the main text focuses on matrix-level correspondence rather than morphology-based topology, supplementary ordination and hierarchical clustering analyses were retained for completeness. The raw image-level PCA is provided as an additional descriptive view of morphospace, whereas Ward clustering and bootstrap resampling were used only as supplementary topology checks.

Bootstrap resampling of the Ward dendrogram (10,000 replicates) indicated that internal branching support was generally low. The highest support among the original clades was 43.50% for the five-species cluster excluding *B. suaveolens*, whereas the pairing of *C. annuum* var. *grossum* and *S. nigrum* was recovered in 36.24% of replicates. These results support cautious interpretation of morphology-based topology.

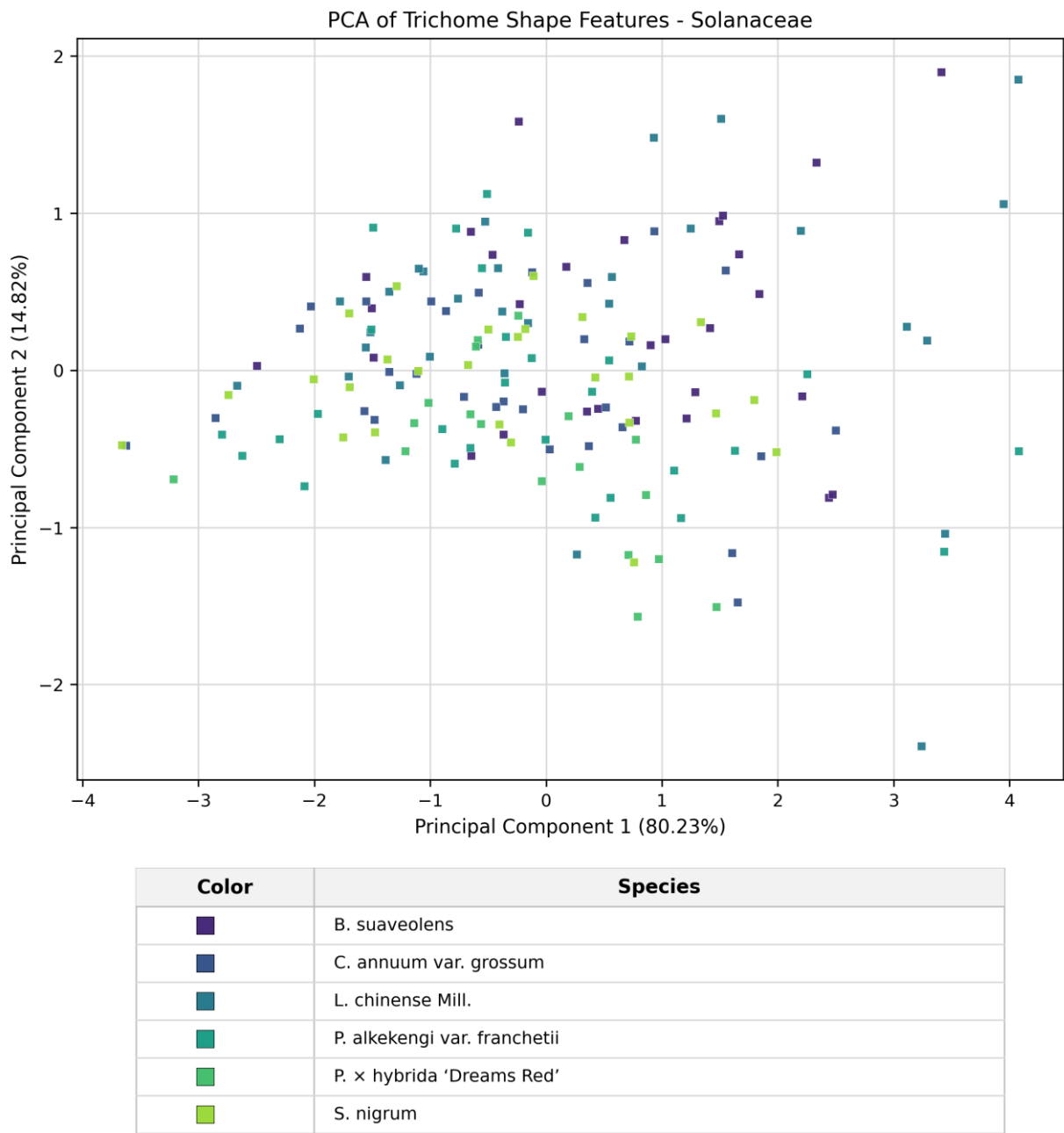


Figure S2. Raw image-level PCA visualization of the focal path–curvature trait block.

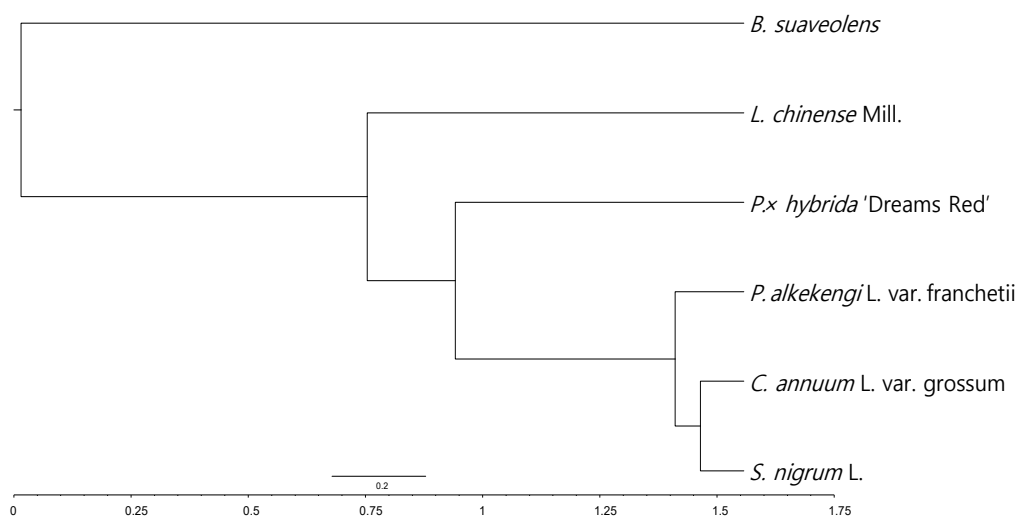


Figure S3. Ward hierarchical clustering dendrogram based on focal trichome traits.

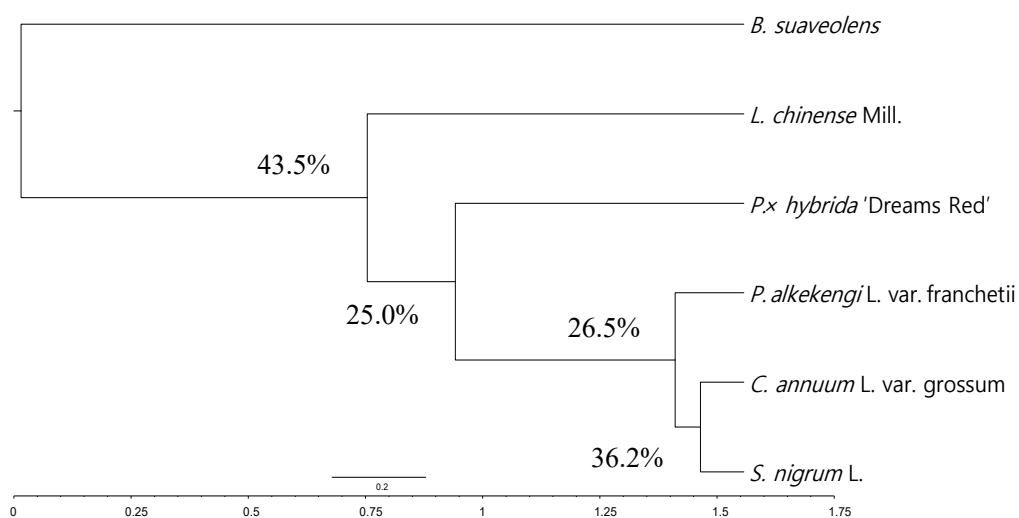


Figure S4. Bootstrap summary for Ward hierarchical clustering (10,000 replicates).

Table S7. Bootstrap Support Values for the Original Ward Clades.

Original clade	No. of taxa	Bootstrap support (%)
C. annum var. <i>grossum</i> S. <i>nigrum</i>	2	36.24
C. annum var. <i>grossum</i> P. <i>alkekengi</i> var. <i>franchetii</i> S. <i>nigrum</i>	3	26.48
C. annum var. <i>grossum</i> P. <i>alkekengi</i> var. <i>franchetii</i> P. × hybrida ‘Dreams Red’ S. <i>nigrum</i>	4	24.98
C. annum var. <i>grossum</i> L. <i>chinense</i> Mill. P. <i>alkekengi</i> var. <i>franchetii</i> P. × hybrida ‘Dreams Red’ S. <i>nigrum</i>	5	43.50

Table S8. Most Frequently Recovered Clades in Ward Bootstrap Resampling.

Recovered clade	No. of taxa	Bootstrap support (%)
C. annum var. <i>grossum</i> L. <i>chinense</i> Mill. P. <i>alkekengi</i> var. <i>franchetii</i> P. × hybrida ‘Dreams Red’ S. <i>nigrum</i>	5	43.50
C. annum var. <i>grossum</i> S. <i>nigrum</i>	2	36.24
C. annum var. <i>grossum</i> P. <i>alkekengi</i> var. <i>franchetii</i> S. <i>nigrum</i>	3	26.48
C. annum var. <i>grossum</i> L. <i>chinense</i> Mill. P. <i>alkekengi</i> var. <i>franchetii</i> S. <i>nigrum</i>	4	25.29
C. annum var. <i>grossum</i> P. <i>alkekengi</i> var. <i>franchetii</i> P. × hybrida ‘Dreams Red’ S. <i>nigrum</i>	4	24.98
C. annum var. <i>grossum</i> P. <i>alkekengi</i> var. <i>franchetii</i>	2	24.44
B. <i>suaveolens</i> L. <i>chinense</i> Mill.	2	23.00
P. <i>alkekengi</i> var. <i>franchetii</i> S. <i>nigrum</i>	2	19.94
L. <i>chinense</i> Mill. P. <i>alkekengi</i> var. <i>franchetii</i>	2	15.35
P. <i>alkekengi</i> var. <i>franchetii</i> P. × hybrida ‘Dreams Red’	2	12.99
L. <i>chinense</i> Mill. S. <i>nigrum</i>	2	11.94
C. annum var. <i>grossum</i> P. × hybrida ‘Dreams Red’ S. <i>nigrum</i>	3	11.80
C. annum var. <i>grossum</i> L. <i>chinense</i> Mill. S. <i>nigrum</i>	3	10.69
C. annum var. <i>grossum</i> P. × hybrida ‘Dreams Red’	2	10.20
C. annum var. <i>grossum</i> L. <i>chinense</i> Mill.	2	9.05

Table S9. Most Frequently Recovered Bootstrap Topologies.

Rank	Frequency (%)	Topology summary
1	3.68	{B. <i>suaveolens</i> , L. <i>chinense</i> Mill.} {C. annum var. <i>grossum</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
2	3.15	{C. annum var. <i>grossum</i> , S. <i>nigrum</i> } {P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’} {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
3	3.02	{C. annum var. <i>grossum</i> , S. <i>nigrum</i> } {L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> } {C. annum var. <i>grossum</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
4	3.00	{C. annum var. <i>grossum</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
5	2.67	{B. <i>suaveolens</i> , L. <i>chinense</i> Mill.} {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
6	2.65	{B. <i>suaveolens</i> , L. <i>chinense</i> Mill.} {P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
7	2.47	{C. annum var. <i>grossum</i> , S. <i>nigrum</i> } {L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
8	2.45	{B. <i>suaveolens</i> , L. <i>chinense</i> Mill.} {C. annum var. <i>grossum</i> , S. <i>nigrum</i> } {P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’} {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
9	2.31	{P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }
10	1.92	{C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> } {C. annum var. <i>grossum</i> , P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , S. <i>nigrum</i> } {C. annum var. <i>grossum</i> , L. <i>chinense</i> Mill., P. <i>alkekengi</i> var. <i>franchetii</i> , P. × hybrida ‘Dreams Red’, S. <i>nigrum</i> }

Appendix D. Extended Sensitivity Analyses

At the image-level median scale, PERMANOVA performed on the focal trait block yielded $F = 2.718$, $p = 0.009$, and $R^2 = 0.0787$. PERMDISP was also significant ($F = 2.329$, $p = 0.045$), indicating that among-group dispersion contributed to the observed multivariate separation.

Auxiliary matrix comparisons showed no significant correspondence between morphology and habitat, between molecular phylogeny and habitat, between morphology and histochemical staining, or between molecular phylogeny and histochemical staining. These results indicate that the focal morphology–molecular correspondence was not recapitulated by the available habitat or histochemical matrices.

Table S10. PERMANOVA and PERMDISP Summary for the Focal Trait Block.

Statistic	Value
PERMANOVA F	2.7182
PERMANOVA p	0.0090
PERMANOVA R^2	0.0787
PERMDISP F	2.3295
PERMDISP p	0.0452

Table S11. Group Mean Distances to Centroid in PERMDISP.

Species	Mean distance to centroid
<i>B. suaveolens</i>	1.3568
<i>C. annuum</i> var. <i>groszum</i>	1.2904
<i>L. chinense</i> Mill.	1.8388
<i>P. × hybrida</i> ‘Dreams Red’	1.1548
<i>P. alkekengi</i> var. <i>franchetii</i>	1.5126
<i>S. nigrum</i>	1.2511

Table S12. Auxiliary Matrix Correlation Summary.

Comparison	Pearson r	Pearson p	Spearman r M	Spearman p
morph vs molecular	0.865	0.046	0.775	0.044
morph vs environment (Jaccard)	0.310	0.483	0.374	0.317
molecular vs environment (Jaccard)	0.006	0.817	-0.052	0.933
morph vs stain (Jaccard)	-0.261	0.611	-0.401	0.304
molecular vs stain (Jaccard)	-0.528	0.071	-0.456	0.228