

Appendix 6. Summary information of the AFLP data generated in the studied *Viola* populations.

Taxon	Pop.	N _{ind} / N _{gen}	N _{fragm} ± SD	%poly	D _{Nei}	Private	Dia- gnostic	Rare	DW1
<i>V. pyrenaica</i>	271	7/5	77 ± 1	2.72	0.0111	1	0	2	7.47
	272	7/2	76 ± 0	0.54	<i>0.0013</i>	0	0	0	3.98
	275	6/4	77 ± 1	2.72	<i>0.0088</i>	1	0	2	8.83
<i>V.*</i> ‘Spain’ – blue	165	6/2	114 ± 0	0.54	<i>0.0015</i>	0	2	5	21.34
<i>V.*</i> ‘Spain’ – white	170	5/1	111 ± 0	0	<i>0</i>	0	1	4	10.18
<i>V.* suavis</i> – blue	211	5/3	114 ± 1	5.98	0.0261	0	0	0	<i>4.06</i>
	4	4/2	112 ± 1	1.09	<i>0.0048</i>	1	0	1	<i>4.16</i>
	206	5/4	117 ± 2	3.8	0.0165	0	0	1	<i>4.72</i>
<i>V.* suavis</i> – white	181	5/5	114 ± 1	2.72	<i>0.0087</i>	0	3	4	18.89
	207	5/1	110 ± 0	0	<i>0</i>	0	0	0	<i>4.36</i>
	147	4/2	113 ± 3	3.26	0.0163	4	0	6	12.1
<i>V.*</i> ‘Trieste’	246	7/2	111 ± 1	1.09	<i>0.0027</i>	0	0	0	5.11
	247	7/2	111 ± 1	1.09	<i>0.0053</i>	0	0	0	5.23
<i>V.* adriatica</i>	249	7/7	113 ± 3	13.59	0.0492	2	0	1	7.43
	251	7/7	112 ± 3	11.41	0.039	0	0	0	5.06
	253	6/6	112 ± 1	5.43	0.0211	1	0	0	5.05
<i>V.* adriatica</i>	255	7/7	115 ± 3	9.78	0.039	0	0	4	9.27
	258	7/6	114 ± 5	13.59	0.0466	2	0	5	10.34
	259	7/7	113 ± 3	15.22	0.051	3	0	4	10.55
	260	7/7	113 ± 2	8.7	0.0319	0	0	0	5.47
	262	7/7	113 ± 2	15.22	0.0497	3	0	6	13.91
	244	7/7	114 ± 2	9.78	0.0328	2	0	3	7.98
	243	6/6	116 ± 4	13.59	0.0519	2	0	5	10.07
	263	7/5	112 ± 1	5.98	0.0209	0	0	0	5.19
	228	7/6	118 ± 1	8.15	<i>0.0271</i>	1	0	1	8.24
	268	6/1	112 ± 0	0	<i>0</i>	0	0	1	5.95
	267	4/1	112 ± 0	0	<i>0</i>	0	0	1	<i>3.58</i>
	235	7/6	112 ± 1	4.35	0.016	0	0	2	6.63
<i>V.* austrodalmatica</i>	242	7/5	114 ± 1	4.89	0.0182	0	0	3	8.58
	241	6/6	113 ± 1	5.43	0.0242	1	0	2	7.71
	238	7/6	113 ± 1	5.98	0.0231	0	2	3	19.72

The columns show: taxon name (* = *suavis* subsp.); population codes (Pop.; see Supplementary data 1); number of analysed individuals (N_{ind})/number of AFLP multilocus genotypes (N_{gen}) per population; number of AFLP fragments (N_{fragm} ± standard deviation [SD]) per individual; percentage of markers exhibiting intrapopulation polymorphism (%poly); Nei’s gene diversity (D_{Nei}) per population (high values are in bold, intermediate values in normal type, and low values in italics); number of private (exclusive) fragments (Private); number of private fixed (diagnostic) fragments (Diagnostic); number of rare (present in <10% of the investigated individuals) markers (Rare); frequency-down-weighted marker values – “rarity index 1” (DW1) (high values are in bold, intermediate values in normal type, and low values in italics). Island populations are in frames.