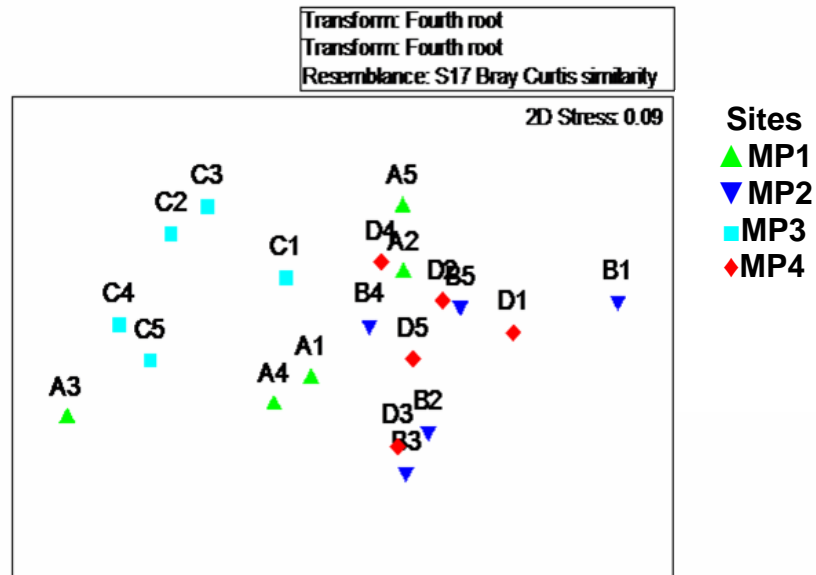


Supplementary information

S1: Non metric multidimensional scaling (MDS) plot obtained from the analysis on morphological data of *Noccaea caerulescens* populations of the four different sub-sites measured in year 2009 (leaf number, leaf length, leaf width, height of stalk).



S2: PERMANOVA test for the simultaneous response of morphological traits (leaf number, leaf length, leaf width, height of stalk) of *Noccaea caerulescens* to sub-sites in the year 2009.

Groups	t	P(perm)	Unique perms
MP1,MP2	1.9643	0.050	126
MP1,MP3	1.5358	0.118	126
MP1,MP6	1.8664	0.050	126
MP2,MP3	3.9673	0.009	126
MP2,MP4	0.7717	0.727	126
MP3,MP4	4.2411	0.005	125

Non significant differences were found between MP1/MP3 and MP2/MP4 (*P<0.05)

S3: MALDI-TOF/MS identification of proteins from *Noccaea caerulescens* shoots of plants from the different Monte Prinzera sub-sites.

Protein name^a	MP1^b	MP2^b	MP3^b	MP4^b
Metallothionein-like protein 4C	3.60±0.11 a	4.95±0.34 b	2.40±0.08 c	2.50±0.08 c
ABC transporter G family member 27	0.15±0.06 a	3.93±0.05 b	0.15±0.06 a	0.28±0.10 a
Pectinesterase/pectinesterase inhibitor	3.55±0.05 a	3.21±0.2 a	3.46±0.10 a	0.33±0.04 b
Putative defensin-like protein 40	7.18±0.10 a	6.37±0.57 a	5.85±0.37 a	0.20±0.08 b
Putative defensin-like protein 235	9.20±0.47 a	3.08±0.32 b	1.53±0.10 c	2.53±0.10 d
Antifungal protein (Fragment)	5.33±0.10 a	3.88±0.54 a	1.68±0.33 b	0.18±0.09 c
Defensin-like protein 74	5.15±0.06 a	3.03±0.13 b	1.63±0.05 c	0.15±0.06 d
Disease resistance protein RPM1	1.40±0.26 a	1.30±0.24 a	1.35±0.29 a	0.28±0.10 b
Acyl-coenzyme A oxidase, peroxisomal	0.53±0.10 a	2.33±0.43 b	2.70±0.29 ab	0.48±0.33 c
NAD(P)H-quinone oxidoreductase subunit I, chloroplastic	2.30±0.16 a	2.80±0.08 a	1.60±0.36 b	1.58±0.22 b
NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, cytoplasm	0.75±0.06 ab	1.00±0.00 a	0.55±0.06 b	0.15±0.06 c
Oxygen-evolving enhancer protein 1, chloroplastic	3.45±0.19 a	4.43±0.45 b	1.63±0.10 c	1.65±0.13 c
NAD(P)H-quinone oxidoreductase subunit J, chloroplastic	5.78±0.13 a	6.55±0.44 a	2.05±0.31 b	0.50±0.14 c

Probable complex I intermediate-associated protein 30 , mitochondrion	0.20±0.08 ac	4.93±0.15 b	0.35±0.06 a	0.18±0.05 c
Probable thylakoidal processing peptidase 2	6.70±0.08 a	8.55±5.70 b	5.55±0.10 c	5.30±0.22 c
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin	11.58±2.11 a	3.80±0.57 b	0.63±0.17 c	0.13±0.05 d
Glycine-rich protein 2	3.38±0.51 a	3.00±0.14 a	3.33±0.43 a	0.38±0.10 b
Zinc finger protein CONSTANS-LIKE 9	2.35±0.37 a	8.42±0.22 b	0.88±0.05 c	2.50±0.22 a
Heat stress transcription factor B-1	24.35±0.13 a	75.50±3.38 b	54.98±6.77 c	65.10±5.85 bc
Serine/threonine-protein phosphatase PP1	7.60±0.61 a	5.33±0.19 ab	4.13±0.41 b	0.15±0.6 c
Serine/threonine-protein kinase SRK2H	15.73±0.10 a	74.40±6.56 b	44.53±3.97 c	0.15±0.06 d
F-box protein DOR	2.18±0.10 ab	2.65±0.39 a	2.15±0.10 b	1.58±0.17 c
Uncharacterized 2.5 kDa protein in tRNA-Arg-tRNA-Asn intergenic region	4.28±0.21 a	4.25±0.33 b	3.28±0.22 c	2.45±0.13 d

^a Putative protein identification of the closest match in the SWISS PROT database

^b Amount of protein estimated by the DeltaVue software by Absorbance at 214 nm. ANOVAs after log transformation and Tukey's Post Hoc tests were performed on data. Intensity values with similar letters are not significantly different (P<0.01)