**Electronic Appendix 1.** – List of the 16 traits used to differentiate the various clonal growth forms used in this study. Each trait was coded as a binary variable (zero vs. one). For each vegetation type (having a different number of species and plots) the relative abundance of each trait as weighted by total species cover in a vegetation type is reported. The relative abundance of each trait was compared to that expected by chance (based on randomizing species cover within each vegetation type). Results of observed vs. expected relative abundance are reported for each trait and vegetation type (e.g. ↑ = more even than expected by chance, which implies a % closer to 50%; ↓ = less even). Vegetation types identified by the TWINSPAN analyses were: vegetation on screes, alpine meadows, shrubby vegetation, steppes, subnival vegetation, animal resting places, salt marshes and vegetation near to water bodies. GCO=clonal growth organ.

| TRAITS | Screes (20 plots x 66 sp.) % | Obs vs. Exp | Meadow (54 plots x 143 sp.) % | Obs vs. Exp | Shrubs (48 plos x 117 sp) % | Obs vs. Exp | Steppe (83 plos x 157 sp) % | Obs vs. Exp | Subnival (52 plos x 144 sp) % | Obs vs. Exp | Resting places (9 plos x 42 sp) % | Obs vs. Exp | Salt (92 plos x 149 sp) % | Obs vs. Exp | Water bodies (11 plos x 71 sp) % | Obs vs. Exp |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| perennial main root, no adventitious roots, none clonal growth | 45.2 | ↑ | 45.1 | ns | 43.5 | ↓ | 39.4 | ↓ | 37.3 | ↓ | 27.3 | ns | 35.6 | ↓ | 27.5 | ↓ |
| perennial primary shoot | 19.4 | ↓ | 17.6 | ns | 15.4 | ns | 13.1 | ↓ | 16.2 | ns | 15.5 | ns | 13.39 | ns | 8.9 | ns |
| shoots herbaceous | 100 | ns | 88.5 | ↑ | 98.5 | ns | 96.1 | ns | 92.6 | ns | 97.2 | ns | 98.5 | ns | 97.3 | ns |
| extensive lateral spread | 30.7 | ↑ | 34.4 | ↑ | 33.1 | ns | 39.8 | ↑ | 41.3 | ↑ | 48.1 | ↑ | 38.7 | ↑ | 28 | ns |
| small lateral spread | 49.9 | ns | 47.9 | ns | 51.4 | ns | 46.9 | ns | 42.2 | ↓ | 36.4 | ns | 47.9 | ns | 63 | ns |
| cushion | 2.1 | ns | 0.8 | ns | 2.2 | ns | 2.6 | ns | 1.1 | ns | 0 | ns | 2.24 | ns | 0 | ns |
| adventitious buds on roots | 5.4 | ns | 3.6 | ns | 2.7 | ns | 3.1 | ns | 7.9 | ns | 0.2 | ns | 1.07 | ns | 0.5 | ns |
| integrator | 50.7 | ↓ | 49.1 | ns | 45.6 | ↓ | 42.3 | ↓ | 46.2 | ↓ | 27.7 | ↓ | 37.33 | ↓ | 28.1 | ↓ |
| slow splitter | 46.3 | ↑ | 50.4 | ns | 51.5 | ↑ | 49.7 | ↑ | 51.5 | ns | 55.1 | ns | 54.8 | ↑ | 67.7 | ↓ |
| CGO photosynthetising | 2.9 | ns | 0.46 | ns | 2.9 | ns | 7.9 | ↑ | 2.2 | ↑ | 17.1 | ↑ | 7.84 | ns | 4.1 | ↑ |
| CGO has storage function | 46.3 | ↑ | 50.4 | ns | 51.6 | ↑ | 49.7 | ↑ | 51.4 | ↑ | 55.4 | ns | 54.8 | ↑ | 67.3 | ↓ |
| clonal offspring resemble seedling | 0.2 | ns | 0 | ns | 0.29 | ns | 1.8 | ns | 0 | ns | 3.6 | ns | 1.3 | ns | 0 | ns |
| CGO provides anchorage | 55.1 | ↓ | 64.6 | ↓ | 64.1 | ↓ | 60.5 | ↑ | 67.9 | ↓ | 58.2 | ns | 62.2 | ↓ | 74.1 | ↓ |
| high potential multiplication rate | 30.2 | ns | 16.8 | ↑ | 31.9 | ↑ | 29.3 | ↑ | 26.4 | ↑ | 34.9 | ns | 32.9 | ↑ | 36.4 | ↑ |
| more CGOs combined in one species | 2.9 | ns | 0.5 | ns | 2.8 | ns | 7.9 | ↑ | 2.2 | ns | 17.1 | ↑ | 7.5 | ns | 4.11 | ↑ |
| deep bud bank | 27.9 | ↑ | 35.9 | ↑ | 31.4 | ↑ | 35.3 | ns | 39.4 | ↑ | 34.5 | ns | 32.9 | ↑ | 28.1 | ns |

**Electronic Appendix 2**. – Centred and standardized PCA of the different environmental factors considered in this study. Abbreviations are: soil.moist=Soil moisture; stabil=soil stability.