

Table S1.

Measures of population diversity and differentiation in *Centaurea aspera* and *C. seridis* using a large SNP set. STRUCTURE analysis was used for establishing $k = 4$ genetic populations.

Population	H_S	H_T	n	G'_{ST}	F_{ST}		
					F_{ST}	5% - 95% confidence interval	p -value
<i>C. aspera</i> cluster 1 (2n)	0.144		22.047				
<i>C. aspera</i> cluster 2 (2n)	0.088		6.286				
<i>C. aspera</i> spp. <i>gentilii</i> (4n)	0.109		9.966				
<i>C. seridis</i> (4n)	0.231	0.291	14.491	0.461	0.271	0.242 0.295	0
<i>C. x subdecurrens</i> (3n)	0.300		5.794				
<i>C. x subdecurrens</i> nothosp. <i>paucispina</i> (4n)	0.288		4.389				

H_S : average population heterozygosity, H_T : Total population heterozygosity, n : number of alleles observed in each population, G'_{ST} : genetic population differentiation G'_{ST} weighted by the number of alleles observed in each population, F_{ST} : Fixation index, values along with confidence intervals (5% and 95%) and p -values between populations following 100 bootstrappings across loci.