Table S1

Results of the similarity percentage procedure (SIMPER; Clarke 1993) analysis on species composition between-group for two selected location (Marche Region and Lazio Region). We reported how much plant species contributed (Species contribution %) to differentiate the two forest communities, and the average cover of each species for both locations. Only significance species are reported.

| Taxon	Species contribution (%)	Average Lazio cover (%)	Average Marche cover (%)	Pvalue
Adenostyles australis	0.302	0.048158	0	0.035
Arabis turrita	0.6092	0.080263	0.003226	0.001
Aremonia agrimonoides	1.2302	0.010526	0.154839	0.032
Cephalanthera damasonium	0.6583	0.053158	0.045161	0.031
Coronilla emerus	0.3981	0.092105	0	0.021
Cotoneaster nebrodensis	0.1694	0.031842	0	0.035
Epipactis microphylla	0.2366	0	0.022581	0.049
Euphorbia amygdaloides	1.1805	0.029211	0.167742	0.02
Hepatica nobilis	1.917	0.397368	0.074194	0.031
Hieracium sylvaticum	0.4898	0.110789	0	0.002
Lilium martagon	0.7637	0.131842	0.009677	0.023
Lonicera xylosteum	0.1781	0.034474	0	0.007
Luzula sylvatica	8.6807	2.437368	0.022581	0.038
Orthilia secunda	0.2347	0.045	0	0.046
Polygonatum multiflorum	0.1218	0.024211	0	0.024
Polypodium vulgare	0.115	0.021579	0	0.041
Rosa arvensis	0.351	0.048158	0.006452	0.014
Rubus caesius	0.4726	0.060526	0	0.025
Solidago virgaurea	2.8182	0.571053	0.016129	0.017

References

Clarke K.R. Non-parametric multivariate analysis of changes in community structure. Aust J Ecol **1993**, 18: 1 17-143.

Table S2. Comparison between functional diversity and standardized functional diversity. In detail, the response of the functional diversity of lateral spread (LS), persistence of clonal growth organ (PCGO) and number of clonal offsprings (NCO) to the considered structural features. We reported the significance and the coefficient of predictor resulted from multiple regression models, both for functional diversity without approach of permutation model (FD) and with permutation model (SES-FD). Model permutation has been carried out with shuffling traits values across species pool (Botta-Dukát & Czúcz 2016).

	Trait	DBH	Sh_{DBH}	H	Sh_H	Em.d.	Sub.d.	Dom.d.	Tot.d.
FD	LS	-	-	**0.013***	-	-	-	-	-
	PCGO	-	-	**0.02***	-	-	-	-	-
	NCO	**-0.033****	-0.02 n.s.	-	-	-	-	-	-
SES-FD	LS	-	-	**0.29****	-	-	0.16 n.s.	-	-
	PCGO	-	-	**0.34****	-	**-**	0.04 n.s.	0.14 n.s.	-
	NCO	**-0.31****	-0.21 n.s.	-	-	-	-	-	-

DBH= mean diameter of standards; H= mean height of standards; Sh_{DBH} = diversity of the diameters of standards; Sh_H= diversity of the height of standards; Em.d. = emergent density layer; Sub.d.= subordinate density layer; Dom.d.= dominant density; Tot.d.= total density layer. $^{***}P$ = 0.001; $^{**}P$< 0.01; $^{*}P$< 0.05; n.s. not significant. Significant results are represented in bold.

Figure S1 Relationship between standardized effect size of functional diversity of clonal traits: a) lateral spread; b) persistent of clonal growth organ; c) number of clonal offsprings with standards structural features. Positive SES-FD values (>0) indicates trait divergence, while negative SES-FD values indicates traits convergence.
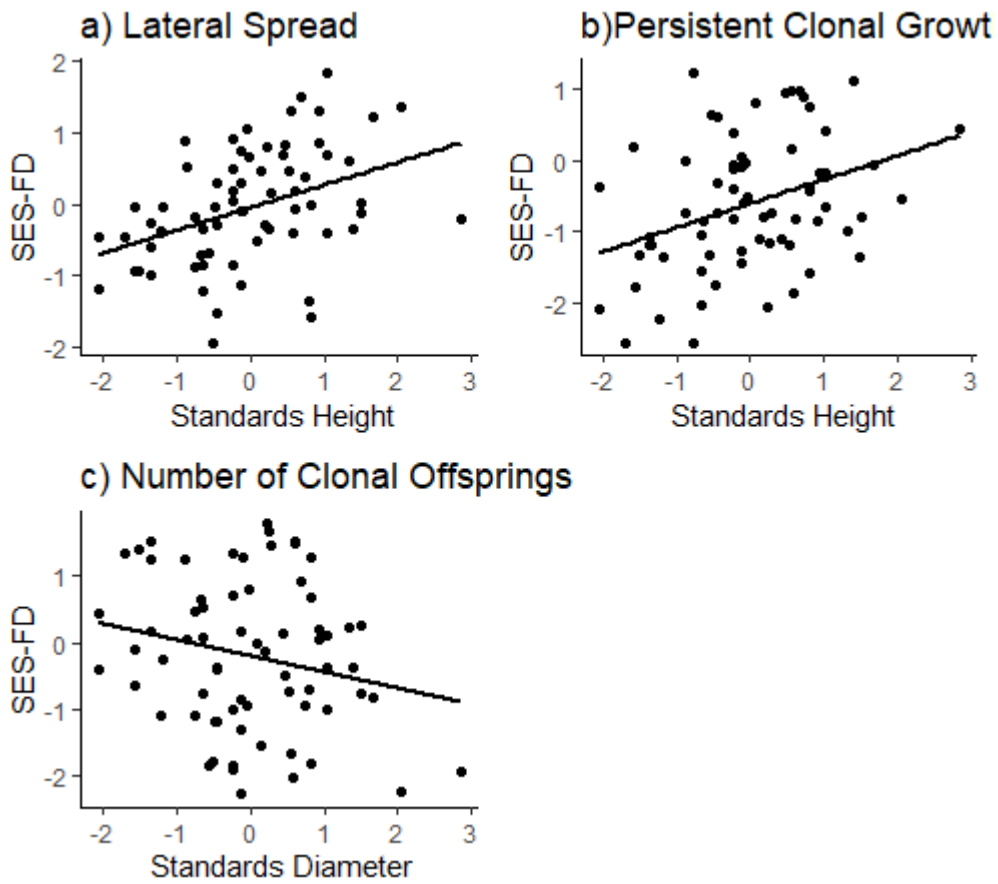
References
Botta-Dukát Z.; Czúcz B. Testing the ability of functional diversity indices to detect trait convergence and divergence using individual-based simulation. *Methods Ecol Evol* **2016**, *7* (1), 114-126.

Table S3 Results of the Pearson's correlation test between the mean height (H) and the mean diameter (DBH) of the standard with the total canopy cover of the stand. We reported the values of the correlation coefficient and the significance results in bold. $^{***}P = 0.001$; $^{**}P < 0.01$; $^{*}P < 0.05$; n.s. not significant. We ran correlation tests using the *cor.test* function (stats package).

Standard's structural parameter	Canopy cover	pvalue
H	$0.16^{n.s.}$	0.18
DBH	**0.40^{***}**	<0.001