Data Article

Species composition and plant traits of south Atlantic European coastal dunes and other comparative data

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A R T I C L E   I N F O

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A B S T R A C T

The data reported in this article relates to the research article entitled “Changes in plant diversity patterns along dune zonation in south Atlantic European coasts” (Torca et al., 2019) [1]. Data about traits of species from coastal dunes, a synoptic table and PERMANOVA comparisons are given. The information detailed in the methodology section can be used as a guide to perform analyses on taxonomic, functional and phylogenetic diversity.

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Specifications table

| Subject area                  | Biology
|------------------------------|--------------------------------------------------|
| More specific subject area   | Botany, floristic studies
| Type of data                 | Tables, excel file, word file
| How data was acquired        | Field measures and databases. Visual identification and cover estimation of plant species.
| Data format                  | Raw and analyzed

Abbreviations: CWM, community weighted mean; MPD, mean pairwise distance; MNTD, mean nearest taxon distance; NRI, net relatedness index; NTI, nearest taxon index

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Experimental factors  
Collected plant species were pressed before identification or measurement in the laboratory.

Experimental features  
10 m × 10 m temporary plots in coastal dunes, where plant species composition and cover was estimated. 12 sites. A total of 244 plots.

Data source location  
Coasts of north Spain and south west France

Data accessibility  
Data are included in this article.

Related research article  
M. Torca, J.A. Campos, M. Herrera; 2019
Changes in plant diversity patterns along dune zonation in south Atlantic European coasts. (http://dx.doi.org/10.1016/j.ecss.2018.11.016) [1]

Value of the data

- The presented data allows keeping track of the coastal dune species composition in the southwestern part of Atlantic Europe.
- The raw data of traits allows the performance of further analyses for functional diversity in coastal dunes.
- The methodology section summarizes common indices for taxonomic, functional and phylogenetic diversity and can be used as a guide.

1. Data

Raw data of ten traits for 110 species from coastal dunes of southwest Atlantic Europe is provided in Table S1 of the Supplementary material. Information for traits from Table S1 was extracted from the following online databases of traits and floras:

- Biolflor [2].
- Claves ilustradas de la flora del País Vasco y territorios limítrofes [3].
- Flora Iberica [4].
- Kew Garden [5].
- LEDA [6].
- Seed Dispersal [7].
- Try [8].

Table 1
PERMANOVA results for community assemblage at scales of plot, location and sector for each dune habitat. df = degrees of freedom, MS = mean squares, ns = no significant. VC = Variance Component. * p < 0.05, ** p < 0.01, *** p < 0.001.

| Habitat | df | MS       | Pseudo-F | VC   |
|---------|----|----------|----------|------|
|         |    |          |          |      |
| Embryo  |    |          |          |      |
| Sector = Se | 3  | 5901.8   | 0.960    | ns   | 0.0 |
| Local = Lo(Se) | 8  | 6128.9   | 3.910    | ***  | 562.9 |
| Plot = Pl(Lo(Se)) | 36 | 1565.7   | 2.230    | ***  | 431.7 |
| Residual | 48 | 702.2    |          |      | 702.2 |
| Total   | 95 |          |          |      |      |
| Mobile  |    |          |          |      |
| Sector = Se | 3  | 12,958.0 | 2.230    | **   | 297.9 |
| Local = Lo(Se) | 8  | 5808.9   | 3.791    | ***  | 534.6 |
| Plot = Pl(Lo(Se)) | 36 | 1532.3   | 2.069    | ***  | 395.8 |
| Residual | 48 | 740.7    |          |      | 740.7 |
| Total   | 95 |          |          |      |      |
| Fixed   |    |          |          |      |
| Sector = Se | 3  | 42,095.0 | 3.690    | ***  | 1279.1 |
| Local = Lo(Se) | 8  | 11,396.0 | 6.240    | ***  | 1196.1 |
| Plot = Pl(Lo(Se)) | 36 | 1827.1   | 3.380    | ***  | 643.7 |
| Residual | 48 | 539.8    |          |      | 539.8 |
| Total   | 95 |          |          |      |      |
### Table 2

PERMANOVA results for Taxonomic Diversity (Shannon Index and Species richness), Phylogenetic Diversity (NRI and NTI) and Functional Diversity (RaoQ and CWM). df = degrees of freedom, MS = mean squares, ns = no significant. VC = Variance Component. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

| Taxonomic Diversity | df | Shannon | Pseudo-F | VC | Richness | MS | Pseudo-F | VC |
|---------------------|----|---------|----------|----|----------|----|----------|----|
| **Embryo**          |    |         |          |    |          |    |          |    |
| Sector = Se         | 3  | 0.252   | 0.169    | ns | 0.000    | 12.372 | 0.486    | ns |
| Location = Lo(Se)   | 8  | 1.49    | 5.150    | ***| 0.100    | 25.469 | 3.818    | ** |
| Plot = Pl(Lo(Se))   | 36 | 0.290   | 16.078   | ns | 0.055    | 6.670  | 1.699    | *  |
| Residual            | 48 | 0.180   | 0.180    |    | 0.180    | 3.927  | 3.927    |    |
| Total               | 95 |         |          |    |          |       |          |    |
| **Mobile**          |    |         |          |    |          |    |          |    |
| Sector = Se         | 3  | 1.301   | 2.100    | ns | 0.028    | 21.361 | 0.616    | ns |
| Location = Lo(Se)   | 8  | 0.619   | 2.469    | *  | 0.046    | 34.688 | 4.078    | ** |
| Plot = Pl(Lo(Se))   | 36 | 0.251   | 1.641    | ns | 0.049    | 8.507  | 2.490    | ** |
| Residual            | 48 | 0.153   | 0.153    |    | 0.153    | 3.417  | 3.417    |    |
| Total               | 95 |         |          |    |          |       |          |    |
| **Fixed**           |    |         |          |    |          |    |          |    |
| Sector = Se         | 3  | 1.254   | 4.102    | ns | 0.038    | 99.038 | 2.820    | ns |
| Location = Lo(Se)   | 8  | 0.306   | 0.988    | ns | 0.000    | 35.115 | 3.518    | ** |
| Plot = Pl(Lo(Se))   | 36 | 0.309   | 2.818    | ***| 0.027    | 9.983  | 2.183    | ** |
| Residual            | 48 | 0.110   | 0.184    |    | 0.184    | 4.573  | 4.573    |    |
| Total               | 95 |         |          |    |          |       |          |    |

| Phylogenetic Diversity | df | NRI | Pseudo-F | VC | NTI | Pseudo-F | VC |
|------------------------|----|-----|----------|----|-----|----------|----|
| **Embryo**             |    |     |          |    |     |          |    |
| Sector = Se            | 3  | 0.540| 0.901    | ns | 0.000| 2.532   | 1.255| ns |
| Location = Lo(Se)      | 8  | 0.599| 1.911    | ns | 0.034| 2.018   | 3.590| ** |
| Plot = Pl(Lo(Se))      | 36 | 0.313| 2.776    | **| 0.100| 0.562   | 2.520| ** |
| Residual               | 48 | 0.113| 0.113    |    | 0.113| 0.223   | 0.223|    |
| Total                  | 95 |       |          |    |     |          |     |    |
| **Mobile**             |    |     |          |    |     |          |    |
| Sector = Se            | 3  | 0.180| 0.443    | ns | 0.000| 0.985   | 0.656| ns |
| Location = Lo(Se)      | 8  | 0.406| 2.056    | ns | 0.018| 1.501   | 1.645| ns |
| Plot = Pl(Lo(Se))      | 36 | 0.198| 1.246    | ns | 0.020| 0.912   | 1.847| *  |
| Residual               | 48 | 0.159| 0.159    |    | 0.159| 0.494   | 0.494|    |
| Total                  | 95 |       |          |    |     |          |     |    |
| **Fixed**              |    |     |          |    |     |          |    |
| Sector = Se            | 3  | 2.506| 2.413    | ns | 0.061| 0.527   | 0.473| ns |
| Location = Lo(Se)      | 8  | 1.038| 1.456    | ns | 0.041| 1.113   | 1.313| ns |
| Plot = Pl(Lo(Se))      | 36 | 0.713| 2.892    | **| 0.233| 0.848   | 2.184| ** |
| Residual               | 48 | 0.247| 0.247    |    | 0.247| 0.388   | 0.388|    |
| Total                  | 95 |       |          |    |     |          |     |    |

| Functional Diversity  | df | RaoQ | Pseudo-F | VC | CWM | Pseudo-F | VC |
|-----------------------|----|------|----------|----|-----|----------|----|
| **Embryo**            |    |      |          |    |     |          |    |
| Sector = Se           | 3  | 0.008| 0.060    | ns | 0.000| 874.5   | 0.675| ns |
| Location = Lo(Se)     | 8  | 0.133| 5.387    | ***| 0.009| 1295.1  | 4.909| *** |
| Plot = Pl(Lo(Se))     | 36 | 0.025| 1.703    | *  | 0.005| 263.8   | 2.771| *** |
| Residual              | 48 | 0.014| 0.014    |    | 0.014| 95.2    | 95.2 |    |
| Total                 | 95 |       |          |    |     |          |     |    |
| **Mobile**            |    |      |          |    |     |          |    |
| Sector = Se           | 3  | 0.101| 2.289    | ns | 0.002| 2674.4  | 0.687| ns |
| Location = Lo(Se)     | 8  | 0.044| 2.428    | *  | 0.003| 3891.8  | 4.946| *** |
| Plot = Pl(Lo(Se))     | 36 | 0.018| 1.360    | ns | 0.002| 786.9   | 1.142| ns |
| Residual              | 48 | 0.013| 0.013    |    | 0.013| 689.2   | 689.2|    |
| Total                 | 95 |       |          |    |     |          |     |    |
| **Fixed**             |    |      |          |    |     |          |    |
| Sector = Se           | 3  | 0.033| 1.381    | ns | 0.000| 11932.0 | 2.511| ns |
| Location = Lo(Se)     | 8  | 0.024| 1.393    | ns | 0.001| 4752.6  | 6.232| *** |
| Plot = Pl(Lo(Se))     | 36 | 0.017| 2.858    | ***| 0.006| 762.5   | 0.990| ns |
| Residual              | 48 | 0.006| 0.006    |    | 0.006| 770.1   | 766.9|    |
Table S2 of the Supplementary material provides a synoptic representation of the IndVal values. Finally, in Tables 1 and 2 a PERMANOVA analysis of species composition, taxonomic, functional and phylogenetic diversity is reported.

2. Experimental design, materials and methods

2.1. Study area

The research was conducted along the Atlantic coasts of north Spain and southwest of France. The Cantabrian coast lies in E-W direction with a dominant north face [9]. Galicia and Cantabria show high sedimentary deposition, while in Asturias cliffs are abundant [10]. In Galicia and Cantabria estuaries open and there sand dune fields occur in numerous localities [9]. In the south of France cliffs are less common and a continuous dune field is present. Along the western areas temperate hyper-oceanic submediterranean conditions predominate, while in the eastern areas a temperate oceanic bioclimate is dominant [11]. Climatic characterization of the studied locations is shown in Table 3.

2.2. Diversity indices

For taxonomic diversity Shannon index was calculated

\[ H = - \sum_{i=1}^{n} p_i \ln p_i \]

where \( p_i \) is the relative abundance of species i.

For phylogenetic diversity, NRI (Net Relatedness Index) and NTI (Nearest Taxon Index) were calculated:

\[ NRI = -1 \left( \frac{MPD_{obs} - MPD_{rand}}{sd\ MPD_{rand}} \right) \]
\[ NTI = -1 \left( \frac{MNTD_{obs} - MNTD_{rand}}{sd\ MNTD_{rand}} \right) \]

where MPD stands for Mean Pairwise Distance both observed (obs) and random (rand). The difference between the observed and random value is divided by the standard deviation of the random distribution. NTI is the same except that the MNTD (Mean Nearest Taxon Distance) is applied. Both NRI and NTI can be calculated using species presence-absence data but, in this study, weighed abundance was measured.

Regarding the phylogenetic tree used for distances, the reference tree selected was Phylomatic tree R20120829 for plants. As one species, Cynodon dactylon was not included, it was manually added. Then, polytomies were randomly resolved, as trees containing polytomies have less resolution and statistical power [13]. Finally, branch length was estimated using BLADJ (Branch Length Adjustment).

Table 3

| Station         | Sector | Long   | Lat     | Ele  | T    | Pp   | lc   | los1 | los2 | los3 | los4 | It   | Im1  |
|-----------------|--------|--------|---------|------|------|------|------|------|------|------|------|------|------|
| Noia            | GP     | 8°53’W | 42°47’N | 104  | 13.8 | 1833 | 11.4 | 1.24 | 1.88 | 2.42 | 3.34 | 334  | 4.71 |
| Padrón          | GP     | 8°38’W | 42°44’N | 58   | 14.8 | 1692 | 11.8 | 1.24 | 1.88 | 2.42 | 3.34 | 334  | 4.71 |
| La Coruña       | GA     | 8°22’W | 43°23’N | 57   | 13.7 | 963  | 8.6  | 1.83 | 2.08 | 2.14 | 2.52 | 332  | 3.69 |
| Porto do Baqueiro | GA    | 7°41’W | 43°47’N | 80   | 13.1 | 2080 | 8.6  | 2.36 | 3.08 | 4.21 | 5.66 | 317  | 2.41 |
| Comillas        | CB     | 3°17’W | 43°23’N | 24   | 13.5 | 1242 | 10.1 | 2.49 | 3.99 | 4.06 | 4.52 | 309  | 2.32 |
| Oriñón          | CB     | 3°19’W | 43°24’N | 63   | 13.9 | 1400 | 10.7 | 2.87 | 3.30 | 3.94 | 4.39 | 320  | 1.99 |
| Hondarribia     | AL     | 1°47’W | 43°21’N | 8    | 14.1 | 1720 | 12   | 4.34 | 5.08 | 5.16 | 5.9  | 310  | 1.35 |
| Bordeaux        | AL     | 0°42’W | 44°49’N | 49   | 12.8 | 1539 | 15.3 | 2.38 | 2.43 | 2.27 | 2.99 | 234  | 2.49 |
and an age file according to Wikström et al. [14] in Phylocom [15]. Having few dated nodes, the resulting phylogenetic distance can be considered as a marked improvement over using only the number of intervening nodes as phylogenetic distance [16].

For functional diversity, CWM (Community Weighted Mean) was used. It is a metric of functional composition and it was proposed by Garnier et al. [17] to calculate the average of trait values weighted by the relative abundances of each species [18]. It is a good indicator of the expected functional value of a trait in a random community sample [19], and can also be used to understand how environmental gradients select trait composition at local communities [20].

\[
\text{CWM} = - \sum_{i=1}^{S} p_i x_i
\]

where \( p_i \) is the relative abundance of species \( i (i = 1, 2, ..., S) \), and \( x_i \) is the trait value for species \( i \).

Another functional index used was RaoQ based on Rao [21] quadratic diversity and proposed by Pavoine and Dolédec [22] and Leps et al. [23]. RaoQ is considered the expected dissimilarity between two individuals of a given species assemblage selected at random with replacement [18].

\[
Q = - \sum_{i=1}^{S} d_{ij} p_i p_j
\]

where \( d_{ij} \) is the dissimilarity (i.e., not necessarily a metric distance) between species \( i \) and \( j \) and \( p_i \) and \( p_j \) the relative abundance of species \( i \) and \( j \) respectively. CWM and RaoQ are complementary as CWM quantifies the weighted mean of a given functional trait within a given species assemblage, while the RaoQ is a measure of trait dispersion or divergence sensu Villéger et al. [24] (see [18]).

2.3. Sampling and data analysis

Plant community composition was assessed by visual identification and cover estimation of species in the plots. Details are provided in [1]. Permutational multivariate analyses of variance (PERMANOVA) [25] was performed using PERMANOVA+ for Primer software [26]. Synoptic table based on IndVal values was filled with the multipatt function of the indicspecies [27] package of R [28].

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Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.12.005.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.12.005.
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