DATA PAPER

Geographic variation of tree height of three pine species (*Pinus nigra* Arn., *P. pinaster* Aiton, and *P. pinea* L.) gathered from common gardens in Europe and North-Africa

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Abstract

· *Key message* This datapaper collects individual georeferenced tree height data from *Pinus nigra* Arn., *P. pinaster* Aiton, and *P. pinea* L. planted in common gardens in France, Germany, Morocco, and Spain. The data can be used to assess genetic variation and phenotypic plasticity with further applications in biogeography and forest management. The three datasets are available at https://doi.org/10.5281/zenodo.3250704 (Vizcaíno-Palomar et al. 2018a), https://doi.org/10.5281/zenodo.3250698 (Vizcaíno-Palomar et al. 2018b), and https://doi.org/10.5281/zenodo.3250707 (Vizcaíno-Palomar et al. 2018c), and the associated metadata are available at https://metadata-afs.nancy.inra.fr/geonetwork/srv/eng/catalog.search#/metadata/644682d3-78c6-4fcc-af26-b1a928be7b1b, https://metadata-afs.nancy.inra.fr/geonetwork/srv/eng/catalog.search#/metadata/535b8ad0-9315-4d78-80bd-d0f6cbb9d0ce and https://metadata-afs.nancy.inra.fr/geonetwork/srv/eng/catalog.search#/metadata/4cc0d2f0-00a9-42c8-aa34-fbbc647e3eb9 for *P. nigra*, *P. pinaster* and *P. pinea*, respectively.

1 Background

Understanding how tree species and populations will perform under future climatic conditions has become essential for sustainable forest management. Plastic responses and genetic variation are two of the processes that can generate phenotypic variation within species, and thus help populations to cope with climate change (Bolnick

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et al. 2011; Alberto et al. 2013; Benito Garzón et al. 2019). In forest trees, genetic diversity is generally involved in long-term adaptive responses while plasticity entails shorter responses to acclimatize (Franks and Hoffmann 2012; Chevin et al. 2013).

Pines are keystone species in many Mediterranean and European ecosystems and are often used for ecological restoration and in multi-purpose plantations. Their evolutionary history, ecology, and the ecosystem services they provide are well-known (Tapias et al. 2004; Ruiz-Benito et al. 2012; Fady 2012). However, understanding their fine-scale local adaptation patterns and how phenotypes and genotypes are associated remain a scientific challenge.

Rather recently, common garden experiments established with the aim of selecting the best forest reproductive material and to provide resources for breeding programs have been rediscovered and now reanalyzed as climate change experimental designs, see for example, Rehfeldt et al. (2002), Benito Garzón et al. (2011), O'Neill and Nigh (2011), Benito Garzón and Fernández-Manjarrés (2015) and Vizcaíno-Palomar et al. (2016). Common gardens provide highly valuable information for disentangling the genetic component of phenotypic trait variability, for detecting evidence of local adaptation and phenotypic plasticity. Because of this legitimate renewed interest, great efforts are currently made to digitize, harmonize, and compile datasets obtained from common gardens beyond the national scale (e.g., Robson et al. 2018).

2 Methods

In this datapaper, we gather individual and georeferenced phenotypic variation data of tree height from three pine species of high importance for Mediterranean and European forestry and habitat management: *Pinus nigra* Arn., *P. pinaster* Aiton, and *P. pinea* L. Tree height data have been generated in common gardens distributed across the species ranges where different genetic units have been grown. The genetic units included in these datasets are wild type resources whose names are those of the locality where they were collected from. In some cases, they correspond to identified seed stands and are listed in country databases as forest reproductive material. When appropriate, they can be found in the European Union FOREMATIS information system http://ec.europa.eu/forematis/.

Specifically, we compiled data from 15 *P. nigra* common gardens located in France, Germany, and Spain and planted between years 1968 and 2009. The experimental design varies depending on the common garden, from a randomized complete block design (RCB) to a randomized incomplete block design, RIB, see Table 1. Likewise, the number of blocks varies from 1 to 70, and in the case of the German common gardens, blocks have been called X, Y, and Z. The total number of genetic units (here provenances) tested varies from 2 to 48 (Table 1). In *P. pinaster*, the data were compiled from 14 common gardens located in France, Morocco, and Spain, planted between 1966 and 1992 (Table 1). In this specific species, the data have been compiled from both provenance and progeny tests. Specifically, Pavillon and Malgaches are provenances tests, while Saint Alban, Le Bray, and La Mole are progeny-provenance tests. The experimental design depends on the common garden, being RCB or RIB; the number of blocks varies from 4 to 127 and the number of genetic units from 10 to 467. For the data collected from the progeny tests, we only gathered the data derived from crosses between parents from the same geographic origin. Finally, in *P. pinea*, the data were compiled from 9 common gardens located in France and Spain, and planted between 1993 and 1997 (Table 1). The experimental design was RIB with 43 to 171 blocks, except in one site with 15 RCB. The number of tested genetic units (here provenances) tested varies from 26 to 38.

Tree height data were measured on site with a telescopic ruler with a centimeter precision, see https://urgi.versailles.inra.fr/ephesis/ephesis/ontologyportal.do and specify CO_357:1000037 in the search button (Steinbach et al. 2013), and depending on the common garden, tree height was recorded at different tree ages. These data were always collected block by block to minimize temporal variance.

The raw data collected in the common gardens were compiled into three datasets, one for each species. The same process to generate a clean and ready dataset was repeated for each one of them. Firstly, as tree height measurements were taken in different years, we created a new variable called "Age" by subtracting the Year when the measurement was taken to the Year when the common garden was installed. This variable measures the number of years an individual tree has been growing in the common garden. Secondly, we created a code for each tree measured in a common garden. This code allows us for tracking each individual tree height over years and it is useful to assess individual tree variation. Thirdly, the geographic origin of the different genetic units (either originated in provenance tests or in progeny tests) and common gardens were georeferenced. Finally, we filtered and cleaned the dataset by eliminating negative and/or missing tree height values.

The final dimensions of each dataset were of 194,642 individual tree height data measurements for *P. nigra* with 15 common gardens and 78 different provenances, 123,801 individual tree height data measurements for *P. pinaster* with 14 common gardens and 182 different

Table 1 Summary information of the common gardens of each pine species. The number of genetic units makes reference to the original number established in the common garden, i.e., not accounting for catastrophic events which could have depleted one or some of the genetic units

Species	Country	Common garden	Year of plantation	Exp. design	Number of blocks	Number of trees per unit plot	Number of genetic units per block	Total number of genetic units
P. nigra	France	Cestas	1974	RIB	7	6	7	15
P. nigra	France	Levens	1968	RIB	36	56	6	8
P. nigra	France	Pomet	1973	RIB	70	16	5	15
P. nigra	France	Verdun	1968 and 1971	RIB	36	36	5	13
P. nigra	Germany	Bad Windsheim	2009	RCB	3	50	10	10
P. nigra	Germany	Eglsee	2009	–	1	50	2	2
P. nigra	Germany	Geibenstetten	2009	RCB	3	50	39	39
P. nigra	Germany	Gickelhausen	2009	RCB	3	50	21	21
P. nigra	Germany	Vilseck	2009	RCB	3	50	48	48
P. nigra	Spain	Herrera	1996	RCB	7	8	9	9
P. nigra	Spain	La Granja	1996	RCB	12	4	19	19
P. nigra	Spain	Rebolleda	1996	RIB	10	4	17[2]	17
P. nigra	Spain	Rucandio	1996	RIB	7	8	7-10	11
P. nigra	Spain	Sancedo[1]	1996 and 1997	RCB	7-10-10	8-4-4	10-16-14	10-16-14
P. nigra	Spain	Trespaderne[3]	1996	RCB	15-9	4	16-13	16-13
P. pinaster	France	Alban	1981	RIB	127	4	15	163[4]
P. pinaster	France	Bray	1971	RIB	28	3-100	14-83	408[5]
P. pinaster	France	Malgaches	1972	RCB	4	33-63	10	10
P. pinaster	France	Mole	1982	RIB	34	4	20	67[6]
P. pinaster	France	Pavillon	1970	RIB	80	13	4	16
P. pinaster	Morocco	Ain Rami	1992	RCB	6	10	43	43
P. pinaster	Morocco	BV13	1992	RCB	6	36	33	33
P. pinaster	Morocco	Ouid Lille	1992	RCB	8	10	42	42
P. pinaster	Spain	Acebo	1966	RCB	4	16	52	52
P. pinaster	Spain	Cabañero	1967	RCB	4	16	52	52
P. pinaster	Spain	Espinoso	1967	RCB	4	16	50	50
P. pinaster	Spain	Miravete	1966	RCB	4	16	52	52
P. pinaster	Spain	Negrillas	1967	RCB	4	16	51	51
P. pinaster	Spain	Riofrío	1967	RCB	4	16	53	53
P. pinea	France	Baume	1993	RIB	64	3	10	26
P. pinea	France	Gaillarde	1995	RIB	59	3	-	37
P. pinea	France	Laquina	1995	RIB	66	3	10	37
P. pinea	France	Loupian	1994	RIB	80	3	9	26
P. pinea	France	Treps	1994	RIB	171	3	-	38
P. pinea	Spain	Cucalón	1995	RIB	68	3	12	34
P. pinea	Spain	Quintos	1996	RIB	43.5[7]	3	12 (b44: 6)	29
P. pinea	Spain	Tordesillas	1996	RIB	51	3	12	34
P. pinea	Spain	Trespaderne	1997	RCB	15	3	29	29

Exp. design means the type of experimental design, can be RCB or RCB. See below the meaning

RCB and RIC mean randomized complete block design and incomplete block design, respectively

[1] The experimental design of the common garden of Sancedo is composed of three separated plots though they belong to the same trial

[2] Block number 10 includes 13 provenances

[3] The experimental design of the common garden of Trespaderne is composed of two separated plots though they belong to the same trial

[4] This is a progeny and provenance test. It has a total of 163 genetic units: 154 hybrid progenies from 10 provenances, plus 9 true provenances

[5] This is a progeny and provenance test. It has a total of 408 genetic units: 365 progenies from 34 populations from Landes and Corsica, plus 43 provenances from Landes and Corsica

[6] This is a progeny and provenance test. It has a total of 467 genetic units: 25 true provenances plus 42 hybrid progenies from 10 provenances

[7] Due to a lack of seedlings, in the last block, the 44th, only 6 provenances were planted instead of 12

genetic units, and 56,624 individual tree height measurements for *P. pinea* with 9 common gardens and 55 different provenances. Figure 1 shows for each pine species the genetic units tested and the sites where the common gardens were established. We used the R version 3.2.3 (2015-12-10) run in linux-gnu operating system for data
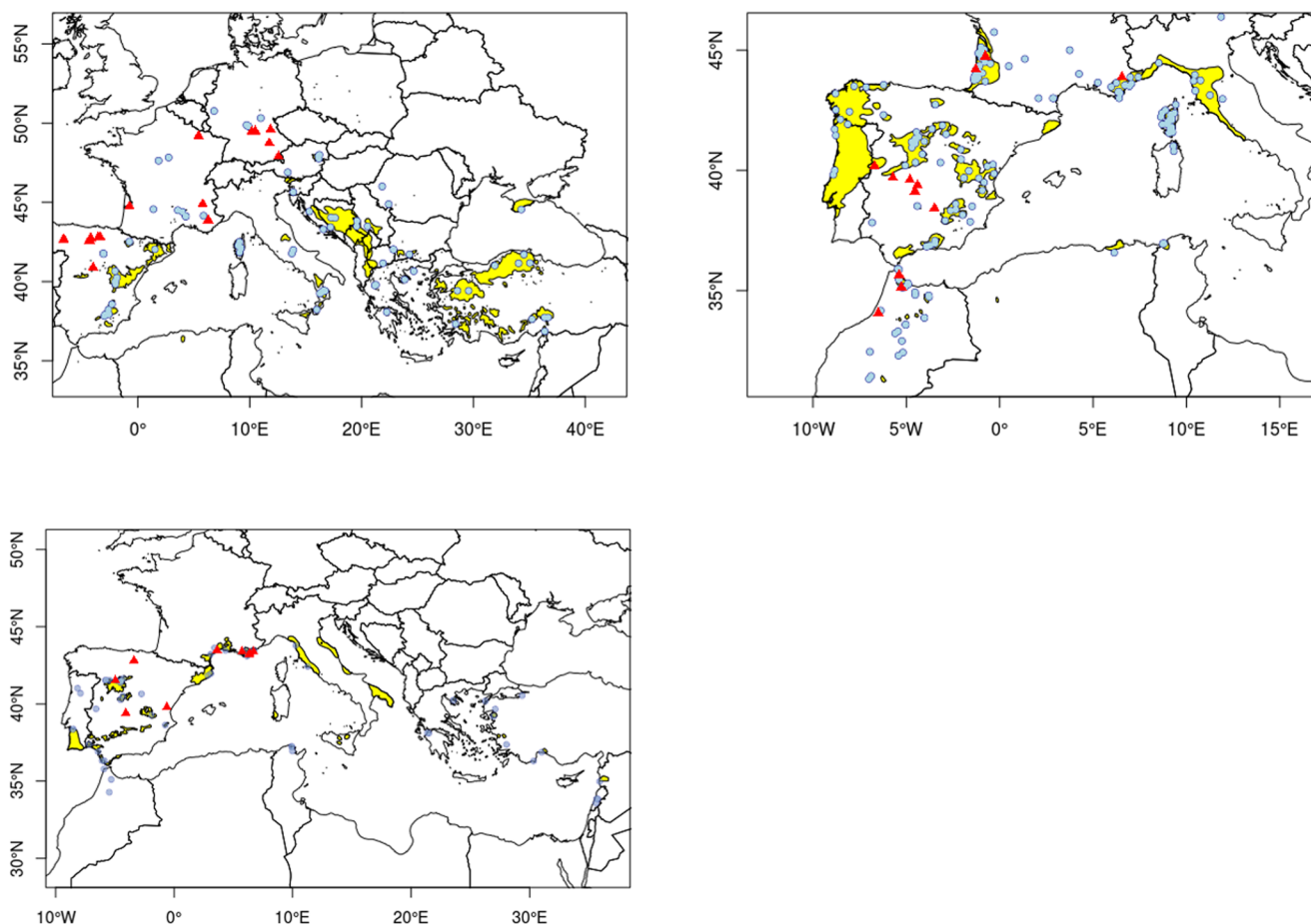
Fig. 1 The three networks of common gardens are represented in a separate map. Red triangles represent common gardens, light-blue circles represent genetic units, and yellow areas represent the natural distribution of the species according to EUFORGEN source (http://www.euforgen.org/). Top left *Pinus nigra*, top right *Pinus pinaster*, bottom left *Pinus pinea*

and file quality check and compilation. We employed basic functions, e.g., merge, rbind, spTransform, to build the datasets.

3 Access to data and metadata description

The three datasets are available on ZENODO, please always refer to the latest version, at https://doi.org/10.5281/zenodo.3250704 (Vizcaíno-Palomar et al. 2018a), https://doi.org/10.5281/zenodo.3250698 (Vizcaíno-Palomar et al. 2018b), and https://doi.org/10.5281/zenodo.3250707 (Vizcaíno-Palomar et al. 2018c) for *P. nigra*, *P. pinaster*, and *P. pinea*, respectively.

The data records are described in the metadata description files.

The associated metadata are available at https://metadata-afs.nancy.inra.fr/geonetwork/srv/eng/catalog.search#/metadata/644682d3-78c6-4fcc-af26-b1a928be7b1b, https://metadata-afs.nancy.inra.fr/geonetwork/srv/eng/catalog.search#/metadata/535b8ad0-9315-4d78-80bd-d0f6cbb9d0ce

and https://metadata-afs.nancy.inra.fr/geonetwork/srv/eng/catalog.search#/metadata/4cc0d2f0-00a9-42c8-aa34-fbbc647e3eb9 for *P. nigra*, *P. pinaster* and *P. pinea*, respectively.

4 Technical validation

Data acquisition in the field followed strict, high-quality standards, such as block-by-block measurement paths to minimize environmental and temporal variance, and the use of prefilled data loggers (when it was possible) to match previous measurements with the current status of each tree. Back-to-the-lab, quality checks such as computing minimum and maximum values, visualizing data distribution histograms, and checking differences between current and previous values were systematically used and aberrant values were removed. Part of these data have already been used successfully in previous studies (Alía et al. 1995; Harfouche et al. 1995; Climent et al. 2008; Šeho et al. 2010; Mutke et al. 2010, 2013; Benito Garzón et al. 2011; Huber and Šeho 2016; Vizcaíno-Palomar et al. 2016).

5 Reuse potential and limits

The reuse of the data presented here is simple. The data files are encoded in UTF-8; hence, potential users just need to load the data and indicate this encode. For example, R users just need to add encoding = "UTF-8" in the function used for reading the file. If users open the file in Excel, they need to indicate the source of the data which is the UTF-8. Once the data is loaded, it is ready to be analyzed; users do not need to combine or merge any other files. Users will find that each row contains individual tree height data, defined by a set of variables (a total of 19) such as the name and the geographical position of the common garden —either provenance or progeny test— (Site_name, Long_S, Lat_S) and the name of the genetic unit and the geographical position (Prov_name, Long_P, Lat_P), year of plantation, age, etc. For further information, users can check the metadata description files. Differences among genetic units and sites should be only interpreted in the environmental context of the test sites from where the data were gathered.

Datapapers gathering common gardens (such as provenance tests) are starting to appear due to their relevance to help assess the ability of forests to deal with climate change, see for example, the recent datapaper on European beech common garden networks (Robson et al. 2018). Here, we present for the first time a datapaper collecting tree height from an extensive network of common gardens within and across countries and for three Mediterranean pine species covering European and African distribution ranges. Actually, these are powerful datasets enhancing to assess plastic responses in large climatic gradients, which is of high relevance within the climate change context; for further analysis on modeling, species ranges based on their phenotypic variation and applications for forest management as for example assisted migration programs.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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