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Quercus suber L. and *Quercus ilex* L. in Spain. Updating the Provenance Regions Maps and Calculating Conservation Indicators for their Genetic Resources.

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RESUMEN

Las regiones de procedencia de las especies forestales, es un sistema utilizado en España y en otros países que proporciona orientación para la selección y comercialización de materiales forestales de reproducción (MFR), donde se tienen en cuenta tanto las diferencias ambientales como la variabilidad genética de las poblaciones arbóreas. Además, en el sentido de la conservación de los recursos genéticos de FRM, existen estrategias importantes para la manipulación y preservación de la capacidad de adaptación de las especies y poblaciones, como son los materiales de base (MB) y las unidades de conservación genética (UCG). El objetivo de esta investigación fue analizar y actualizar la información de los mapas de procedencia de *Quercus suber* L. y *Quercus ilex* L. en España, utilizando la información del más reciente Mapa Forestal Español (MFE50) como fuente sobre la distribución de estas especies en el país. Se investigó, además, los MB identificados, seleccionados y las UCG de ambas especies, para realizar una comparación con el MFE50 y las RP. Finalmente, el objetivo central de este trabajo se enmarcó en la incorporación de la información de origen de los rodales forestales desde el mapa RP al MFE50, mediante la creación de un nuevo atributo en la base de datos. Como resultado, se encontró que el mapa de RP fue considerablemente diferente en comparación con el MFE50, presentando un incremento en el área total de la distribución de especies en el país. Se evidenció que muchas áreas del MFE50 no están presentes en el mapa de PR y su ubicación no es exacta en municipios englobados por el Sistema de RP, por lo anterior, se recomienda incorporar y actualizar. El 35% de los MB y las UCG para las dos especies no corresponden a masas forestales en el MFE50, lo que supone la necesidad de una comprobación de campo de cara a la ubicación de estos rodales que tienen una importancia ecológica significativa. Fue posible concluir que los datos disponibles en las fuentes oficiales no son precisos a todas las escalas y deben ser revisados para proporcionar datos e información apropiados respecto a los RP, los MB y las UCG.

Palabras clave: Región de Procedencia, Mapa Forestal Español, actualización, Material de Base, Unidades de Conservación Genética.

ABSTRACT

The Region of Provenance of forest trees is a system used in Spain and in many other countries in order to provide guidance for the selection and commercialization of reproductive forest materials (FRM), taking into account the environmental differences and genetic variability of trees populations. In addition, in the sense of the conservation of the genetic resources and selection of FRM, Basic Materials (BM) and Genetic Conservation Units (GCU) are also important strategies to manipulate and preserve the adaptive capacity of tree species and populations. This work aimed to analyse and updated the information of the RP maps of *Quercus suber* L. and *Quercus ilex* L. in Spain using the most updated Spanish Forest Map (MFE50) as the most recent source of information on the forest distribution in the country. Moreover, it aimed to investigate the information regarding the Source-identified BMs, Selected BMs and GCUs of the two species in comparison with the MFE50 and the RP maps. The final objective of this work was the incorporation of the information of the origin of the forest stands from RP map to the MFE50, by the creation of a new field in its table of attributes. As a result of this study, it was found that the RP map for the two species is considerably different from the most updated MFE, presenting in general an increment in the total area of the species distribution around the regions. Also, many forest areas that are present in the MFE50 are not present in the RP map and are located in municipalities that are currently not englobed

by this system, therefore should be incorporated and updated. Many important problems were found when analysing the maps. Furthermore, when analysing the MBs and GCUs for the two species, the location of more than thirty percent of them did not correspond to any forest stands in the MFE50 map, what supposes the necessity of a field verification on face to the location of these stands that have a seminal ecological value. It was possible to conclude that the data available in the official sources are not accurate at all scales and should be revised to provide appropriate data and information regarding RPs, MBs and UCGs.

Key words: Region of Provenance, Spanish Forest Map, update, Basic Material, Genetic Conservation Unit.

1. INTRODUCTION

1.1. Region of provenance of forest trees

Commonly, tree species that present a wide distribution range hold great levels of standing genetic diversity (Alberto et al. 2013). The Mediterranean region represents a biodiversity hotspot, where tree species are characterised by high genetic diversity within and between populations (Fady-Welterlen 2005). Many of the tree species that are present in the Mediterranean basin are genetically diverse in terms of its latitudinal and longitudinal distribution (Atkinson, Rokas, and Stone 2007). It is also to be considered that in this region the high variability respect to microclimates, geography and abiotic factors can lead to a speciation through local adaptation (Fady and Conord 2010).

When it comes to forest management practices that takes into account intra-specific variability, there is a demand for guidance on the selection of appropriated forest reproductive material and the region these materials can be deployed from their natural environment (Bower, Clair, and Erickson 2014). The genetic differences between populations characteristics, especially those related to grow, adaptation and yield, are highly important for the commercialization of reproductive forest materials (FRM). In this sense, a regionalization is established for the FRM market (European Directive 95/105) According to previous studies that analysed the adaptive capacity of tree species and populations, it was found that this characteristic is best understandable when taking into account its genetic variability and the phenotypic plasticity (Chevin, Lande, and Mace 2010; Fady et al. 2016). Although there is a lack of data on genetic variation for many native plant species, the use of a system of Regions of Provenances (or Seed Zones) is the primary guideline for seed movement and, within these geographically delimited regions, seeds of a plant species can be transferred and planted with low risk of maladaptation (Bower, Clair, and Erickson 2014).

Regions of Provenances (RP) are defined as ecologically homogeneous areas in the distribution of a species and, therefore, meant to group populations that are genetically similar and prone to be locally adapted, differing in their productivity and consequently in their impact on local economies, serving as a perfect guideline to help forest management as they serve as appropriate management units.

It is well known that species ecotypic variation exists, and the adoption of an RP system helps to secure that plant materials are adapted to the local habitat, a key aspect to consider when making a restoration or revegetation planning (Johnson et al. 2004). Furthermore, it also helps to maintain the populations' capacity to adapt and respond to changes in the environment by preserving their integrity of natural genetic structure (Bower, Clair, and Erickson 2014). For these reasons, especially under a changing environment, the importance of forest genetic diversity is broadly recognised and should not be ignored when developing guidelines and indicators for forest management (Fady et al. 2016).

In Spain, the Regions of Provenance were defined for those species that a certification system is applicable in order to commercialize their reproductive material. The Spanish law follows the EU and OCDE scheme regarding the regulation of plant material commercialization and regions of provenance, defining it as being a zone or a group of them, delimited for a species or subspecies, that are under homogenous ecological conditions, in which seed sources or stands present similar genetic or phenotypic characteristics, taking into account limits for altitude when appropriate (RD289/2003 Art. 2.f.).

Two methods have been used in order to establish regions of provenance for forest tree species in Spain. The first one, which is known as the "agglomerative method" has been applied to the 18 main species in which a deeper knowledge regarding their distribution and variation patterns was available, generating therefore different limits for each species and regions, and conforming each region every forest stand in which the

specie is present . On the other hand, the defined as "divisive method" was based on the division of the complete territory in a limited number of regions (57 regions of provenances) ecologically uniform. This regionalisation has been applied to 39 species or genera, and the delineation were adjusted to the administrative limits (Regiones de procedencia n.d.).

1.2.   The species and their Regions of Provenance

Quercus suber L. cork oak as common name ("Alcornoque" in Spanish), is a widely distributed tree species in the occidental Mediterranean region. In Spain, its distribution is predominant in the southwest of the country and it ranges from Cádiz to Salamanca and, to a lesser extent, in the province of Girona, in the northeast of the country (Heredia and Gil 2006). According to the same authors, the species only started to gain more commercial value and attention in the XX century, when it started to be replanted after centuries of overexploitation for firewood and charcoal production. It is currently most cultivated for its thick and characteristic bark that can be extracted for the production of cork used as raw material for many industrial purposes. In the Iberian Peninsula, more than 90% of cork stands are located in private lands, making it difficult to create and to develop strategies and plans to improve its conservation status, as it depends on the forest owner's goodwill to allow the progress of the forest (Martín Albertos, Díaz-Fernández, and de Miguel 1998).

The delineation of the Regions of Provenances for cork oak in Spain consist on nine regions of wide use and seventeen Provenances of Restricted Area (Diaz Fernández et al, 1995, Martín et al, 1998, Alia et al, 2009), taking into account the ecological variation and geographical differentiation (Figure 1). The Provenances of Restricted Area are represented by letters and were created for the small forest that are present outside the main area of distribution of the species. Moreover, these regions correspond to the small regions with low economic interest for the commercial seed production but with a high ecological value

By using a variety of molecular markers, it was possible to identify groups with different genetic structures in the Iberian Peninsula. The utilization of molecular markers allows the reconstruction of the evolutionary history of the species, through the identification of demographic and historical processes of the different populations. In general terms, the neutral diversity markers are intended to provide the differences between central populations (southwest and central "dehesas" of the Iberian Peninsula) and marginal populations (cork oak stands of the east of the peninsula) (Heredia and Gil 2006).
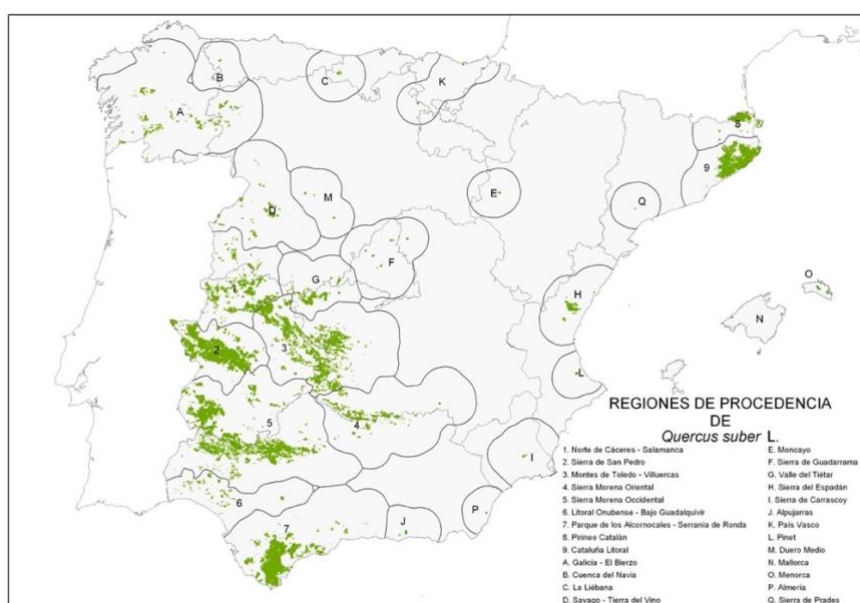

Figure 1: Regions of Provenance of *Quercus suber* L. in Spain (Alía et al. 2009).

Quercus ilex L., holm oak or holly oak as common name ("encina" in Spanish), is the Mediterranean species that have been mostly used since the Ancient World mainly for firewood charcoal and animal feeding. Its importance has been higher for the population than cork oak, and in this sense has been favored. The consequence is the historical fragmentation and reduction of the area occupied by the cork oak (Heredia and Gil 2006). Holm oak distribution area extends to all the countries in the Mediterranean Basin and in Spain it appears in all the provinces, except the Canary Islands. It is considered the most characteristic species of the Mediterranean forests due to its wide distribution range in many different lithologic and climatic environments. This implies that it can appear as a dominant or secondary species in the majority of the peninsular territory, except in extremely dry environments with low soil fertility (Ramírez-Valiente et al. 2018). The climatic conditions and its uses have determined the characteristics of the forest of this species. In the littoral it presents in dense forest stands and inland it appears as open forests, frequently in the form of savannah-type ecosystem, known as "dehesas" in Spanish. (Alía et al. 2009).

For the delineation of the Regions of Provenances for holm oak it has been considered the climatic similarity and the geographic contiguity that can be seen in Figure 2. There are seventeen regions of wide use and eleven Provenances of Restricted Area for this species (Jiménez et al, 1996, Martín et al, 1998, Alía et al. 2009).
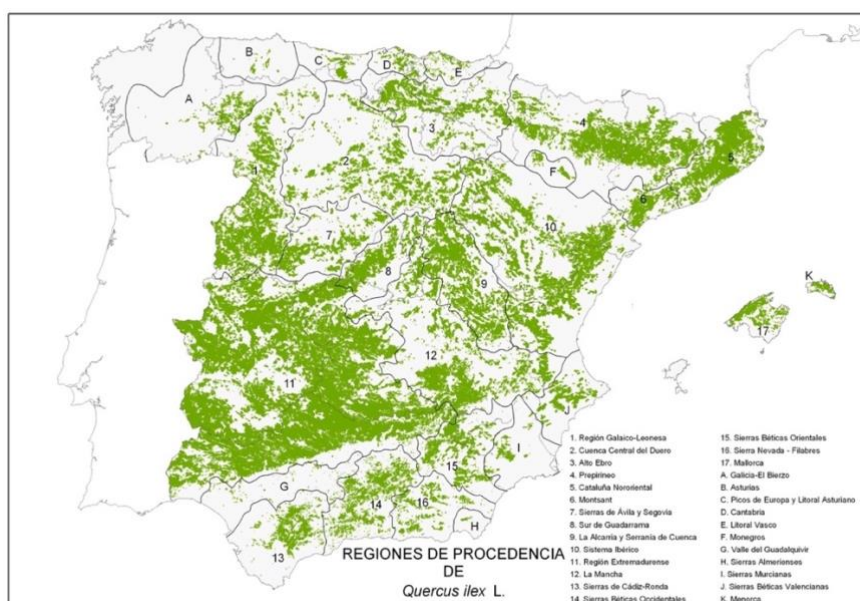

Figure 2: Regions of Provenance of *Quercus ilex* L. in Spain (Alía et al. 2009).

1.3. Conservation Indicators of the Genetic Resources

The Basic Material (BM) are specific forest stands that are used in order to collect reproductive materials (seeds and plants). They are comprised of populations, plantations and clones from which the forest reproductive material is obtained to be used in reforestation (INIA 2009). The types of BM currently approved in Spain are seed sources, selected stands, seed orchards, family progenitors, clones and clone mixture. The four types of reproductive materials for many species in the country; source-identified, selected, qualified and controlled, can be collected from BM that are listed in the National Catalogue of Basic Material. The use of this system provides to stakeholders a guarantee of the origin and quality of the forest reproductive material and an information of their characteristics, facilitating at the time of choosing from which source to collect the material from and which is the most appropriated. Each of the approved BM is ecologically and phenotypically characterized in the National Catalogue and all the information

corresponding to the different admission, selection and characterization forms, and the location maps of the different units of the Catalogue are found in paper files and in the Silvadat database, developed for the management of the Catalogue (REGISTRO Y CATÁLOGO NACIONAL DE MATERIALES DE BASE n.d.).

The creation of a National Registry of Genetic Conservation Units is included in the Spanish Strategy for the Conservation and Sustainable Use of Forest Genetic Resources (MIMAM, 2006) as basic elements of in-situ and ex-situ conservation strategies. In general, the selection criteria for the Genetic Conservation Units (GCU) follows certain basic principles such as: to cover the entire area of distribution of the species targeted by the network, to ensure the natural origin of the populations subject to conservation, to restrict the management regarding the possibility of using reproductive materials not coming from the population, to give preference to the selection of units in the State lands to ensure the viability of conservation, and if possible, include a mention of the unit in the forest management plan (García del Barrio et al, 2018). The National Network of in situ conservation must cover all the spatial genetic variation of the species, as well as the most frequent alleles of each population. Therefore, it is necessary to consider the sampling of populations for each species and the size of the sample within each population. In the first case, the regions of origin of the species must be the starting point for the choice of the desired number (goal) of populations to be conserved. This number must be agreed upon by the National Committee for the Improvement and Conservation of Genetic Resources at the proposal of the National Plan for the Conservation of Genetic Resources. As a basic criterion, it is proposed to take as a reference the number of RPs of the species and prioritize the identification of genetic conservation units that include several species. Finally, it is proposed to act under the concept of MBPS to build this network (INIA 2009).

2. OBJECTIVES

The aim of this study is, through the analysis and comparison of the current maps of the regions of provenances and the latest update Spanish Forest Map (MFE) provided by the Ministry of Agriculture, Fisheries and Food (MAPAMA), to analyse the changes that the current RP's map of Spain might have suffered and to provide a new and updated Spanish Forest Map (MFE50), with information on the origins of stands and the RP for two different tree species: *Quercus ilex* and *Quercus suber*. Furthermore, to calculate for the given species indicators for the development of programmes of conservation and use of the forest genetic resources.

Our specific objectives are:

1) Compare the forest stands in the two maps (Regions of Provenance and Spanish Forest Map) and test their equivalences
2) Assign to the maps a field corresponding to the origin of the stands that will be associated to the new updates of the Spanish Forest Map and the Forest Inventory.
3) Analyse the number of Basic Materials and Conservation Units for the two species in each one of their Regions of Provenances and confirm their location in a given forest stand in the MFE50.

3. MATERIAL AND METHODS

3.1. Data acquisition and preparation

The analysed area comprises the whole Peninsular Spain and the Balearic Islands. The digital maps of the Regions of Provenance for, *Quercus suber* (cork oak) and *Quercus ilex* (holm oak) were provided al INIA-CIFOR. These maps are composed by several layers that included information about the species distribution and origin. For this work,

two layers from the RP's map has been used; one that contains the information of the limits of the several RPs for each species (RP_diss) (see ANNEX 1 and ANNEX 2), which matches with the limits of the municipalities, and a second one that is composed by polygons that corresponds to the forest stands in which the presence of the species is dominant (RP_aut) (ANNEXES 3 and 4). After the collection of the maps and selection of the layers, an operation to change the coordinate reference system (CRS) was needed in order to set all the maps in the same and current used CRS in the territory of Spain, which is EPSG:25830 - ETRS89 / UTM zone 30N. The original CRS of these maps was ED50, used at the time these maps were prepared, and if not changed before it can cause a displacement of the polygons and errors in the analysis. Afterwards, by unifying these two layers, we were able to generate the maps of the limits of Regions of Provenances with information on the forest area and its distribution in which *Q. suber* and *Q. ilex* are present.

The second step of this work consisted first on the collection of the most updated Spanish Forest Map (MFE50) produced in 2015 and provided by the Ministry of Agriculture, Fisheries and Food. This map contains information on the ecology and structure of the thousands of forests stands around Spain. Regarding the tree forest species, up to three different species are contemplated, each one with its state of development. In order to extract the material that corresponded to the two tree species considered in this work from the MFE50, it was used the information represented on the table of attributes in the field SPX to infer about the presence of each species in each area. These fields correspond to the presence of a maximum of three species (SP1, SP2 and SP3) in which their presence is indicated by the code of the species in one of their fields. The specie we are going to work with are represented by the code "45" for *Q. ilex* and "46" for *Q. suber*. This step enabled us to produce two different maps (ANNEXES 5 and 6), each one of them corresponding to the most updated forest map for each one of the species.

In order to compare the changes in the forest area, its new distribution range and update the maps, we unified the maps produced in the first step - the unification of the current maps of the limits of the region of provenances and its forest distribution, provided by CIFOR-INIA – with the maps produced in the second step – the maps extracted from the most updated Spanish Forest Map for each species.

Two conservation indicators of the genetic resources were analysed in this work: the Genetic Conservation Units (GCU), proposed by the National Plan for the Conservation of Forest Genetic Resources, and two types of Basic Materials: source-identified and selected. The data required for this analysis was also acquired from CIFOR-INIA and was composed of three map layers for each species, each one of the layers with information on one of the indicators. These map layers were all composed of a several points, each one of them representing the location in which a GCU or a BM is located. The analysis was made in order to examine the number of GCU and BM present in each of the Regions of Provenances and to verify if their locations was analogue with a forest stand that is currently present in the area. In order to so, it was used the last map layer produced in the previous steps by the unification of the most updated MFE and the RP's maps as an input layer. To create the overlay layer, we had first to execute a buffer operation in order to transform the points from the indicator layers into circular polygons. This step was necessary as to proceed with a unification of the layers both of them had to present the same type of vector. The buffer operation created a circular polygon of fifty meters radius around each of the points, making it possible for it to be used as the overlay layer for its union with the input layer. As a result, it was generated a map containing information on the location of the GCUs and the BMs and in which region of provenance they were located as well as if it coincides with any forest stand in the most updated MFE (ANNEXES 7 and 8).

3.2. Data analysis

The analysis was conducted by exporting the final table of attributes of the final maps to the software R, where we calculated the current area, locations and statistics of the maps as well as the changes in area. With R we also created a new table of attributes with new fields that was later incorporated to the MFE and can be used in the upcoming National Forest Inventories. The scrips used in order to run the analysis can be seen in ANNEX 9 AND ANNEX 10

We firstly calculated the total area of the original maps (MFE50 and RP_aut) as well as the area of the forest area in each of the regions of provenances. This was made by grouping the polygons of the MFE50 that overlapped with the RP_diss map in the same region of provenance and summing up their areas. Some of these polygons felt outside a region of provenance, which made us create a category "NO", that corresponds to "no region of provenance assigned", making it possible to infer about the area of the MFE50 that is currently outside a RP.

Afterwards, by comparing the two maps, we firstly identified the vectors of the MFE50 that were not overlapping with the current species distribution of the region of provenance's map (RP_aut). As a result, we could obtain two classes of polygons – noRP and RP – which corresponds to polygons with no overlapping and polygons with overlapping respectively. Similarly, by analysing the overlapping and the previous and current areas of the vectors we identified the polygons which had its area reduced (RP_aut $_{(red)}$) and the ones that completed disappeared (RP_aut$_{(des)}$) after the union operation. Thus, with the identification of these vectors it was possible to calculate the total area of the RP_aut that have been lost or gained in comparison with to the most updated MFE50 for each species in each region of provenance.

Furthermore, in order to investigate about the area of dominance of the species we identified the polygons in which the species were dominant in the final combined map. The area where the species is dominant was assigned by inspecting the field "FIRST_DOMI" in the RP_aut map, which the code "D" represents that the species is dominant, and the field "SP1" in the MFE map, which the code "46" represented the presence of the species as the most important in the area.

As a result, we could calculate the total area, the number of polygons and area of the initial and final maps and the different categories of polygons created (MFE$_{(noRP)}$, RP_aut $_{(red)}$ and RP_aut$_{(des)}$) and compare this statistics with the to the ones where the species is dominant in the two original maps.

In addition, it was inspected the number of polygons that disappeared and reduced (RP_aut $_{(red)}$ and RP_aut$_{(des)}$) considering the cartographic source from where the information was acquired and also the dominance of the species, in order to evaluate if there was any relationship between mismatching and cartographic source and dominance.

Finally, by importing the table of attributes from the unions of the final map with BMs and GCU to R, we were able to calculate the number of Genetic Conservation Units and Basic Materials in each of the regions of provenances as well as the ones that did not match with any forest stand of the MFE50. The scrip to this last step can be found in ANNEX 3.

3.3. MFE map updating

The final part of this work consisted in the update of the MFE map by the creation of new field in its table of attributes that corresponds to the origin of the forest stands. That is to say, if the tree species in the forest is from an autochthonous or a non-autochthonous (or unknown) origin. This information would then be part of the MFE and can be used whenever its needed and updated in the future forest inventories.

As a result of the combination of the maps of the RP and the MFE, it was generated a final map with a larger number of polygons as this operation split the polygons where they do not perfectly overlap but maintain the information of both maps in overlapping areas. This step aimed to re-extract and re-unify the polygons of the MFE from the unified map although maintaining the information regarding the origin of the species that is present in the RP map. This step was done simultaneously with the other data analysis and the details of this operation can be found in the script present in ANNEX 1 and 2 in the "Fase 3: Actualización de Mapas". After the elaboration of the new table of attributes using R and the corresponding script, the last step was to incorporate this new table to the MFE map using Qgis. The new table of attributes that was incorporated to the MFE50 contained three fields: "id", "area" and "origen". The "id" of the new table created corresponded to the field "idFF2015" of the MFE50 original map table of attributes and using a join operation we could unify this two tables and inspect errors with the "area" field. A scheme chart showing the steps of the MFE50 updating is showed in Figure 3.
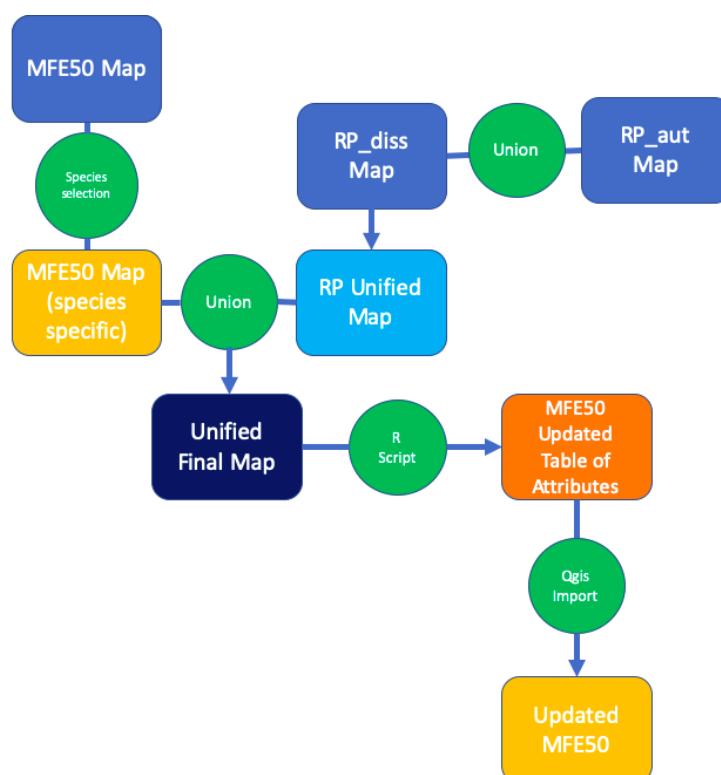

Figure 3: Scheme chart of the process of the MFE50 updating

4. RESULTS

4.1. *Quercus suber*

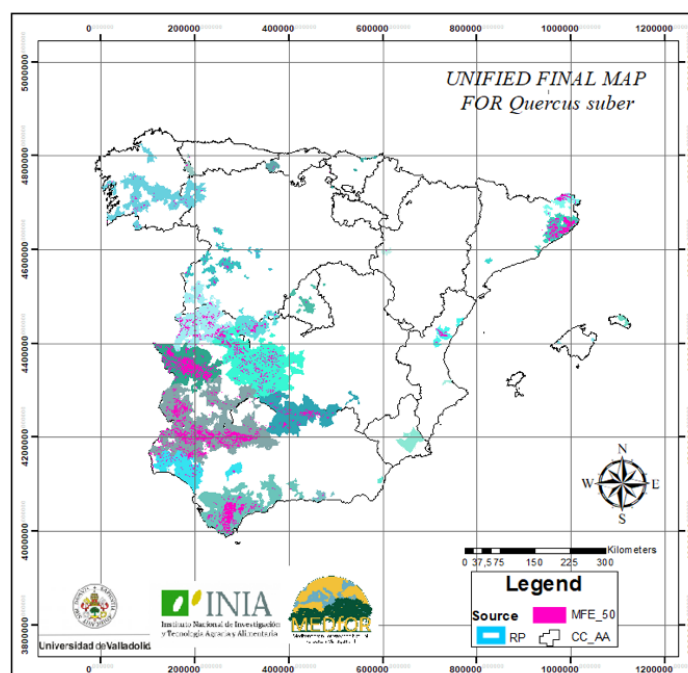Figure 4 shows the final combined map for *Q. suber* from where we imparted the analysis.

Figure 4: Unified final map for *Q. suber*.

The analysis of the forested area by regions of provenances for *Q. suber* shows how the forested area of this species is distributed in each of them (Figure 5). The forested area of cork oak was taken from the most updated MFE and it is important to point out that restricted area regions "I", "N", "O" and "P", corresponding respectively to Sierra de Carrascoy, Mallorca, Menorca and Almeria, do not have correspondence in the MFE that could justify the maintenance of the provenance regions early delimited. This may be due to the reduced extension of *Q. suber* patches that could have not been detected at MFE scale. This is a seminal evidence that highlights the need to periodically contrast the different forest cartographic sources available. On the other hand, in terms of its original forest area and total area of the region, Sierra Morena Ocidental (RP 5), and Sierra de San Pedro, represented by (RP 2), are the ones with the largest forested area, both of them together representing almost 40% of the total area inhabited by the species.
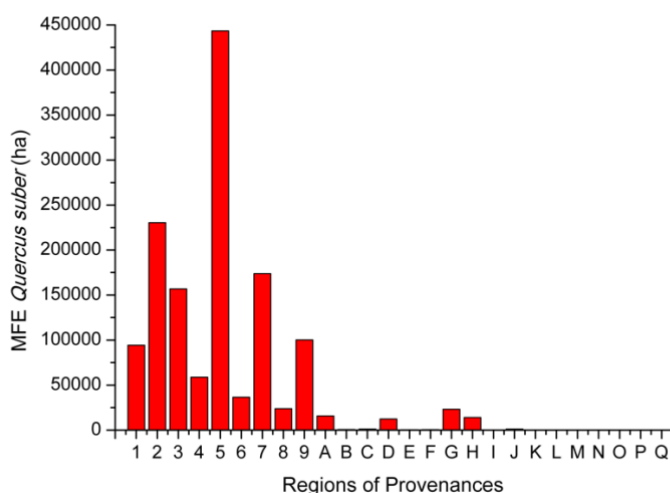

Figure 5: Total area forested with *Q. suber* by Provenance Region based on MFE data

Table 1 shows the changes in area after the unification of the RP maps and the most updated MFE map. An important circumstance to be considered after the unification is the already commented disappearance of several restricted area provenance regions by "losing" completely its forested area. In the case of region "O", "P" and "Q", their initial

forest area was null and they did not have any increment in the forest area after the unification with the most updated MFE, meaning these regions still do not present forest areas in which *Q. suber* appears as one of the three main species. Furthermore, regions of Sierra de Carrascoy and Sierra de Prades, represented by the letters "I" and "Q" respectively, do not present in the MFE any forest area where the species was present, meaning although they presented forests in the RP's map, the most updated MFE do not show any forest area in neither of these regions. Another region that had the cork oak woodland drastically changed when comparing the two maps is the region of Pinet, represented by "L", decreasing its area by almost 90% from the RP map to the MFE50 map. In opposite, regions of Litoral Onubense – Bajo Guadalquivir and Cuenca de Navia, represented respectively by (RP6) and "B", showed the most increment in forest area, increasing their areas by 3,2 and 2,4 times when compared with their area in the RP map. Finally, there are some *Q. suber* forest area that have not been assigned yet to any provenance region, most of them detected in the latest update of the MFE.

Table 1: Total reduced or gained area after the unifications of the regions of provenances with the most updated MFE for *Q. suber*.

Region of Provenance	RP_aut Surface Area (ha)	Updated MFE Surface Area (ha)	Area Gained or Lost (ha)	Fraction of the Total (%)
1	82150	94350	12200	14,85
2	220873	230296	9424	4,27
3	165731	156782	-8949	-5,40
4	29184	58872	29688	101,73
5	243779	443436	199657	81,90
6	8704	36586	27882	320,33
7	144268	173913	29646	20,55
8	24104	23804	-300	-1,25
9	109294	100304	-8990	-8,23
A	21389	15763	-5627	-26,31
B	180	616	436	242,08
C	1140	1164	024	2,15
D	12769	12377	-392	-3,07
E	450	450	000	0,00
F	638	494	-144	-22,55
G	23495	23220	-276	-1,17
H	14374	13989	-385	-2,68
I	1006	0	-1006	-100,00
J	617	1137	520	84,18
K	25	15	-10	-38,63
L	357	38	-319	-89,40
M	140	140	0	0
N	0	0	0	0
O	0	0	0	0
P	0	0	0	0
Q	219	0	-219	-100,00
No Region Assigned	173	22643	22470	-
Total	**1105058**	**1410391**	**305332**	

The total area and the area where the species is dominant in the initial MFE50 (MFE(i)) and on the updated region of provenance's map are the same (Table 2). This result was expected, and it shows that there were almost no errors when running the data analysis as the updated map should be the same as the most updated MFE. When unifying the different maps, polygons tend to split where vectors overlap and, as a result, it produces an updated map with a significant higher number of polygons when compared to the initial maps. The number of polygons that felt outside any region of provenance (noRP) and the area their represent are relatively low compared to the total number of polygons and total area of the updated region of provenance map, representing 0,73% and 1,19 % of the totals respectively. The disappeared number of polygons are also relatively low, 1,64% of the total, and their respective area accounts for 1,32% of the original area from the updated map. The polygons that have been reduced represent a more significant amount of the total, being them 10,90% of the total number of polygons and 18,28% of the total area. The area where the species is dominant decreased in about 9 percent when comparing the updated map and the original RP map. Its respective area that felt outside any RP was 19,19 percent of the total NoRP area, and its area inside the disappeared and reduced polygons were proportional to its total area, being 38,82 and 30,64% of the total forested area of *Q. suber*.

Table 2: Total number of polygons, total surface area and surface area where the species is dominant in the initial maps, the updated maps and the three categories of areas created for *Q. suber*.

Maps / Categories	N˚ of polygons	Fraction of Total (%)	Total Surface Area (ha)	Fraction of Total (%)	Surface of Dominance (ha)	Fraction of Total (%)
MFE(i)	26741		1410391		536373	38,03
RP_aut(i)	8337		1093695		515188	47,11
MFE(upd)	48723		1410391		536373	38,03
MFE(noRP)	357	0,73	16826	1,19	3228	19,19
RP_aut(des)	799	1,64	18578	1,32	7213	38,82
RP_aut(red)	5311	10,90	257809	18,28	78998	30,64

(i) = initial map – before union, (upd) = updated map – after union, (noRP) = forest surface outside the RP_diss map, (des) = disappeared area, (red) = reduced area

Table 3 shows the study of the number of polygons that had their areas reduced or that completely disappeared after the union of the maps, firstly according to the source of the data and secondly according to the dominance of cork oak in the area. It shows that the majority of the disappeared polygons corresponds to polygons from the cartographic source of the National Forest Inventory (IFN). A total of 14,88% of the polygons from this source completely disappeared after the unification of the maps. In terms of total number of disappeared polygons, the cartographic source that had the highest amount was AND25, produced by the autonomous community of Andalucía. Similarly, this same cartographic source showed the highest number of polygons that reduced its size after the unification: a total of 21,7% of their polygons. Vectors from the IFN also showed a high number of reduced polygons, having a total of 19,8% of their polygons diminishing in size. On the other hand, when considering the dominance of the species, the results were more homogeneous. The number of polygons in which the species was dominant and non-dominant that disappeared counted for only 2,90% and 1,88% of the total number of polygons. The polygons in which the species was dominant and non-dominant that completely disappeared counted for 16,78% and 15,9% of the total respectively.

Table 3: Total number of polygons according to each cartographic source and dominance of *Q. suber* and its corresponding number of disappeared and reduced polygons.

Cartographic Source / Dominance	N˚ of Polygons	RP$_{(des)}$	(%)	RP$_{(red)}$	Fraction of Total (%)
AND25	11171	514	4,60	2423	21,7
IFN	121	18	14,88	24	19,8
MFE50	20868	240	1,15	2810	13,5
MFRT	374	26	6,95	54	14,4
Others	1	1	100,00	0	0,0
Dominant	18302	531	2,90	3045	16,6
Non-dominant	14233	268	1,88	2266	15,9

AND25 = Andalucía25 , IFN = Forest National Inventory, MFE50 = most updated Spanish Forest Map, MFRT = Ruiz de la Torre forest map

Table 4 presents the results of the analysis of the Conservation Indicators of the Genetic Resources for cork oak. Firstly, it is important to point out that the regions "I", "N", "O" and "P", where there is no forested area detected, do not present any Identified or Selected BMs as well as conservation units for *Q. suber*. The number of Identified Base Materials is higher in the region RP 3 and RP 7, that correspond respectively to Montes de Toledo – Villuercas and Parque de los Alcornocales – Serranía de Ronda. These two regions collectively include a total of sixty-three out of the one-hundred-and-seventy-seven Identified BM, and five of them are outside any RP. A total of seventy-five Identified BM felt outside of any forest area, the majority of them in the region RP 3. This mismatch may be due to an imprecise location of the BM source.

Region RP 7 also presents a high number of Selected Base Materials, only behind Sierra Morena Ocidental region, represented by the RP 5. None of the regions represented by letters comprise a Selected BM. Sixteen of this selected BMs felt outside any forested area, the majority of them in the regions RP 2 and RP 5.

The number of conservation units in each RP was very homogeneous distributed amongst them and no RP have more than one GCU. Besides the regions that lack in forest area, region B also does not possess any GCU, and seven out of the twenty-one GCU felt outside forest areas.

Table 4: Number of Base Materials and Genetic Conservation Units according to each RP for *Q. suber*.

Region of Provenance	N° of Source-Identified BM	N° of Source-Identifies BM$_{(noMFE)}$	N° of Selected BM	N° of Selected BM$_{(noMFE)}$	N° of GCU	N° of GCU$_{(noMFE)}$
1	11	3	7	1	1	NE
2	4	2	24	5	1	NE
3	33	20	8	1	1	NE
4	7	6	2	NE	1	1
5	14	7	36	6	1	NE
6	1	1	2	1	1	1
7	30	6	33	2	1	NE
8	3	NE	3	NE	1	NE
9	12	NE	3	NE	1	NE
A	6	3	NE	NE	1	1
B	1	1	NE	NE	NE	NE
C	3	1	NE	NE	1	NE
D	13	3	NE	NE	1	NE
E	NE	NE	NE	NE	1	NE
F	4	4	NE	NE	1	1
G	9	6	NE	NE	1	NE
H	14	6	NE	NE	1	NE
I	NE	NE	NE	NE	NE	NE
J	1	1	NE	NE	1	NE
K	1	1	NE	NE	1	1
L	2	2	NE	NE	1	1
M	3	2	NE	NE	1	1
N	NE	NE	NE	NE	NE	NE
O	NE	NE	NE	NE	NE	NE
P	NE	NE	NE	NE	NE	NE
Q	NE	NE	NE	NE	NE	NE
No Region Assigned	5	NE	NE	NE	1	NE
Total	**177**	**75**	**118**	**16**	**21**	**7**

(noMFE) = located outside a MFE forest stand, NE = non-existent

4.2. *Quercus ilex*

Figure 6 shows the final combined map for *Q. suber* from where we imparted the analysis.
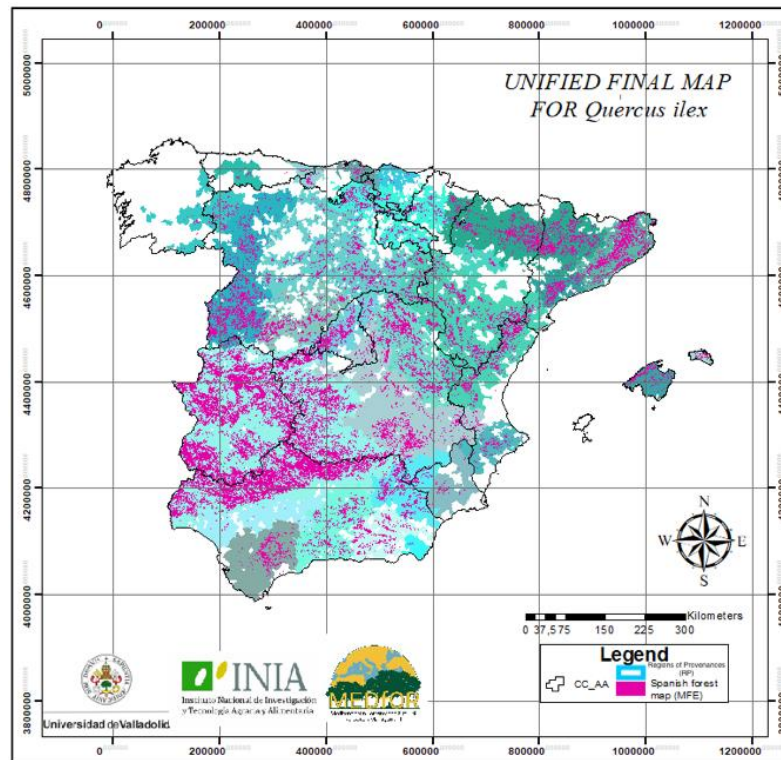
Figure 6: Unified final map for *Q. ilex*.

For *Q. ilex* the analysis was conducted similarly to *Q. suber*. Figure 7 shows the initial forest area where the species is present, according to the most updated MFE, and the total area of each region of provenance. Region RP 11, named Región Extremadurense, is by far the region with the largest forested surface for holm oak in Spain. It represents a total of 3,79 million ha, equivalent to more than 45 % of the total area of distribution for the species. The second largest forested area is located in the RP 10, Sistema Ibérico, but it only accounts for 8% of the total forest area. Similar to the forest surface, the largest RP is also the Región Extremadurense (RP 11), accounting for 23 % of the total area of the RPs. That corresponds to more than 9,3 million ha and covers great part of the west midlands of Spain. The second largest RP is also RP 10, although it does not cover even half of the surface covered by the previous region, accounting for about 10 % of the total area.
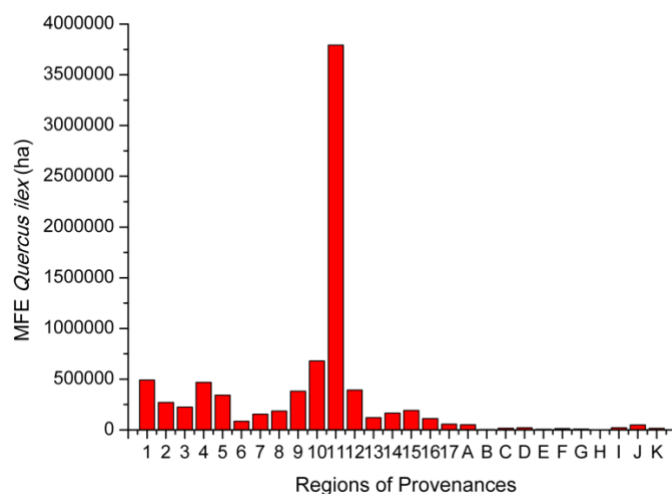

Figure 7: Total area forested with *Q. ilex* by Provenance Region based on MFE data.

The region Extremadurense RP 11 is by far the one that gained the largest amount of forest area after the unification when compared to the other regions, increasing its surface in about 285 thousand ha (Table 5). Although in net amounts it represents a vast area, when taking into consideration that this region is the largest RP and with the most forested area, this value only accounts for an increment of 8,12 % in relation to the its initial forested area. In proportional terms the RP that suffered the greatest change in area was Sierra Nevada - Filabres (RP 16), increasing its area by more than eighty-six percent of its initial forest surface, followed by the region of Sierras Béticas Valencianas ("J"), that decreased its woodlands by more than 46%. In terms of total change in forests surface in Spain, we can observe a loss of around 225 thousand ha of forests with *Q. ilex*, which represents a change of only 2,77% of the total area of occurrence in the country.

Table 5: Total reduced or gained area after the unifications of the regions of provenances with the most updated MFE for *Q. ilex*.

Region of Provenance	RP_aut Surface Area (ha)	Updated MFE Surface Area (ha)	Area Gained or Lost (ha)	Fraction of the Total(%)
1	501292	491996	-9296	-1,85
2	273610	271801	-1809	-0,66
3	211793	225725	13932	6,58
4	493431	469090	-24341	-4,93
5	355714	343223	-12491	-3,51
6	88939	86376	-2563	-2,88
7	157812	155950	-1862	-1,18
8	194505	187123	-7382	-3,80
9	382707	381968	-739	-0,19
10	786140	681418	-104721	-13,32
11	3508540	3793569	285029	8,12
12	427219	393823	-33396	-7,82
13	93784	122084	28300	30,18
14	129098	165720	36621	28,37
15	145452	193136	47685	32,78
16	60576	112737	52161	86,11
17	60831	57871	-2960	-4,87
A	50383	52141	1758	3,49
B	5092	4684	-408	-8,01
C	20588	17792	-2796	-13,58
D	22198	22506	308	1,39
E	6777	6571	-205	-3,03
F	14330	13529	-800	-5,59
G	6720	9157	2436	36,25
H	2193	2663	470	21,44
I	29625	21923	-7701	-26,00
J	92751	49639	-43112	-46,48
K	15901	16220	319	2,01
No Region Assigned	406	13110	12703	-
Total	**8138408**	**8363547**	**225139**	

When analyzing the results for *Q. ilex*, for the same reason as for *Q. suber*, the number of polygons also increased after the unification of the maps. In this case, there was found a small difference in the total area of the initial MFE and the updated MFE, that corresponds to an error of around 0,02%. This error is directly proportional to the area covered by the original maps and the number of divisions suffered by the polygons after unifying the maps. This is caused as the values of area tend to be an approximation and the decimals of each polygon accumulates a total error that when summing their values individually resulted in this final value. When comparing the original map of the regions of provenance with the updated MFE, the area increased in around 225 thousand ha. The results of the analysis provided by Table 6 presents the results considering the total area and the total number of polygons as being the ones presented by the updated MFE. The number of polygons and the area of the MFE(i) that felt outside the area covered by the RP map was relatively low, corresponding approximately to 0,26% of the total number of polygons and 0,09% of the total area. For the number of disappeared polygons and its corresponding area, the analysis shows they were also low, differing from the values found for the number of reduced polygons and its corresponding area, that represented 10,47 and 13,21% of the total. Finally, the area where the species is dominant also increased after the unification and only a 0,01% of this area did not correspond to any area of the RP map.

Table 6: Total number of polygons, total surface area and surface area where the species is dominant in the initial maps, the updated maps and the three categories of areas created for *Q. ilex*.

Maps / Categories	N° of polygons	Fraction of total (%)	Total surface area (ha)	Fraction of total (%)	Area of dominance (ha)	Fraction of total (%)
MFE$_{(i)}$	188338		8361335		5704302	68,22
RP_aut$_{(i)}$	67827		8138358		5657280	69,51
MFE$_{(upd)}$	303231		8363547		5704895	68,21
MFE$_{(noRP)}$	498	0,16	7240	0,09	780	10,78
RP_aut$_{(des)}$	5755	1,90	53656	0,64	30783	57,37
RP_aut$_{(red)}$	31735	10,47	1104728	13,21	517652	46,86

(i) = initial map – before union, (upd) = updated map – after union, (noRP) = forest surface outside the RP_diss map, (des) = disappeared area, (red) = reduced area

The last analysis of the updating of the RP and MFE maps that is presented in Table 7 is regarding the number of disappeared and reduced polygons. It shows that the majority of the disappeared polygons corresponds to polygons from the cartographic source of AND25, produced by the autonomous community of Andalucía. 7,52% of the polygons from this source completely disappeared after the unification of the maps. Similarly, this same cartographic source showed the second highest number of polygons that reduced its size after the unification: a total of 24,71% of their polygons, only behind the cartographic source of MF_RIOJA, generated by the La Rioja's autonomous community, that had 25,20% of their polygons diminishing in size. Similar to what occurred for *Q. suber*, when considering the dominance of the species, the results were more homogeneous. The number of polygons in which the species was dominant and non-dominant that disappeared counted for 2,85% and 1,67% of the total number of polygons. The polygons in which the species was dominant and non-dominant that completely disappeared counted for 13,78% and 13,13% respectively of the total.

Table 7: Total number of polygons according to each cartographic source and dominance of *Q. ilex* and its corresponding number of disappeared and reduced polygons.

Cartographic Source / Dominance	N° of Polygons	RP$_{(des)}$	(%)	RP$_{(red)}$	Fraction of Total (%)
AND25	54230	4076	7,52	13400	24,71
IFN	2883	35	1,21	225	7,80
MF_RIOJA	2583	45	1,74	651	25,20
MFE50	167603	1473	0,88	16890	10,08
MFRT	6674	126	1,89	569	8,53
Dominant	156812	4468	2,85	21601	13,78
Non-dominant	77162	1287	1,67	10134	13,13

AND25 = Andalucía25 , IFN = Forest National Inventory, MFE50 = most updated Spanish Forest Map, MFRT = Ruiz de la Torre forest map

The results of the analysis of the conservation indicators of the genetic resources for holm oak are presented in Table 8. For this species there was no selected BM, so the study was made with the source-identified BM and GCU. The number of source-identified BM for *Q. ilex* was very heterogeneous distributed within the different regions of provenances for the species. The region of Sistema Ibérico (RP 10) and the Extremadurense (RP 11) are the two regions with the highest number of BMs, the first with one-hundred-and-thirty-one and the second with two more BMs than the first one, the two of them representing more than 36% of the total number of BMs. The only region lacking in BM was Sierras Murcianas ("H"). Although regions of Galicia-El Bierzo ("A") and Menorca ("K") have one BM present in their area, both of them are not located in any forest stand. Furthermore, twenty-three out of the twenty-eight RPs have BMs that are located out of forest stands where the presence of the species is not dominant. The study of the genetic conservation units showed a more homogeneous distribution, where each of the RPs presents one GCU, except for region Galaico-Leonesa (RP 1), that have two GCUs and region of Mallorca and Menorca, that do not have any GCU. Moreover, nine of the RPs have their GCUs located out of a forest stand where the species is identified as one of the three main species.

Table 8: Number of Basic Materials and Genetic Conservation Units in each RP for *Q. ilex*

Region of Provenance	N° of Source-Identified MB	N° of Source-Identified MB (noMFE)	N° of GCU	N° of GCU (noMFE)
1	31	9	2	1
2	52	7	1	1
3	80	39	1	NE
4	22	6	1	1
5	19	3	1	NE
6	2	NE	1	NE
7	62	10	1	1
8	16	3	1	1
9	12	2	1	NE
10	131	46	1	NE
11	133	37	1	NE
12	30	13	1	NE
13	19	6	1	1
14	10	2	1	NE
15	26	4	1	NE
16	8	NE	1	NE
17	17	7	NE	NE
A	1	1	1	NE
B	3	2	1	1
C	7	4	1	NE
D	4	NE	1	NE
E	5	1	1	NE
F	2	1	1	1
G	1	NE	1	NE
H	NE	NE	1	1
I	4	1	1	NE
J	32	21	1	NE
K	1	1	NE	NE
Total	**730**	**226**	**27**	**9**

(noMFE) = located outside a MFE forest stand, NE = non-existent

5. DISCUSSION

With the results of this work, it was possible to infer about many aspects related to the current system of the regions of provenances in Spain, especially for the studied species; *Q. suber* and *Q. ilex*. By using the MFE50 as the latest data-source for the current species distribution in the country we could draw the changes in the forest since the creation of the regions of provenance's map, in 2009. Both species presented in general an increase in the forest area when taking into account the whole studied territory, meaning that the area of their current distribution of the MFE50 is larger than the original RP's map. Although holm oak in Spain is more broadly distributed when compared to cork oak, being its area almost six times greater, the changes in cork oak woodlands was more significant. While holm oak gained in total an area of 225159 ha, cork oak gained 305332 ha of forest area. A single RP of *Q. suber* is responsible for an increase of almost two-hundred-thousand ha of forests, the region of Sierra Morena Occidental (RP 5), located in the south-west region of Spain. For *Q. ilex*, the Extremadurense region (RP 11), also located

in the south-west of the country, was responsible for the greater increase in forest area of this species, gaining about 285 thousand ha of forests. Additionally, both species expanded their distribution range out of their limits of the RP_diss map, meaning new forest stands of holm and cork oak are now located in municipalities that before were not part of any RP. These stands need to be incorporated in a RP based on its location and edaphoclimatic characteristics.

Another important outcome of this work was taken by the analysis of the number of polygons that disappeared or reduced and its respective area. The disappeared polygons are related to areas where the forest does not exist in the MFE50 while the diminished ones are related to polygons that did not overlap completely well. In both cases the loss of forest area was mainly caused by miss-overlapping, which can be related to cartographic errors, misidentification or mislabelling and not actually a change in forest area. When we studied these aspects in respect to the cartographic source, in both cases the polygons extracted from Andalucía autonomous community (AND25) presented a high number of disappeared as well as reduced polygons. This could also indicate an error caused by a displacement of the polygons when overlapping with the MFE50, which could mean that vectors from this source might have suffered any kind of modification when incorporated to the RP_aut map.

When analysing the surface area where the species is dominant, we can notice that *Q. suber* experienced a greater change when comparing the RP_aut and MFE50 maps, gaining almost ten percent more area of dominance in the latest map. However, the area of dominance for *Q. ilex* almost did not change, being 69,51% of the total area of the RP_aut map and 68,22 in the MFE50 map. This can also be explained when investigating the area where the species is dominant that is located outside any RP, which reached almost 20% of the total area outside any RP, while for *Q. ilex* this value was only about 10%. For both species, still considering the area where the species is dominant, the area related to the disappeared polygons tended to be slightly higher in relative terms than the area related to the reduced polygons, meaning that removed forest stands are more related to stands where the species are dominant. For *Q. ilex*, more than 57% of the disappeared area was forest stands where this species was dominant, which indicates a positive relationship between both aspects. Similarly, in both cases, the number of disappeared polygons where the species were dominant tended to be slightly higher when compared to the number of disappeared polygons where the species were non-dominant, indicating also a positive relationship between these two factors. Nevertheless, the number of reduced polygons did not show a significant difference between areas of dominance and non-dominance for the two species.

When analysing the conservation indicators of the genetic resource for *Q. suber* the major issue found was the problem related to the RPs with no MBs. Besides the RPs that do not present any forest area detected in the MFE (restricted area provenance regions I, N, O, P, Q,), Moncayo (E) also lacks in source-identified BMs. Furthermore, regions of Litoral Onubense (RP6), Cuenca del Navia (B), Alpujarras (J), Pais Vasco (K), and Pinet (L) have all their source-identified BMs located outside the *Q. suber* forested areas. This fact implies an inconvenience at the time of collection of reproductive materials to be used in forest plantations inside the same RP, as this, together with the selected MB, are the only ways to guarantee the origin and quality of the reproductive forest material and thus to facilitate the selection of the most appropriate area of collection. For *Q. ilex*, only region of Sierra Almerienses (H) do not have any BM located inside the RP. Also, two other restricted area provenance regions present all their BMs out of a forest area detected in the MFE (Galicia-El Bierzo (A) and Menorca (K)). Especially for holm oak, besides the fact that these three RPs (H, A and K) present a small forest area, this implies an added problem as this species do not have any selected BM, being the source-identified BM the only way to provide to stakeholder the information on the characteristics of the reproductive forest material.

The Genetic Conservation Units analysis for *Q. suber* also showed some problems with its distribution and locations. Even though region of Cuenca de Navia (B) is the only RP without a GCU, besides the ones without forest area, many others RPs have their GCUs mismatching any forest area of the, which is the case of Sierra Morena Oriental (4), Litoral Onubense (RP 6), Galicia-El Bierzo (A), Sierra de Guadarrama (F), País Basco (K), Pinet (L) y Duero Medio (M). Coincidently some of these regions (RP 6, K and L) also had all their BMs location not in MFE forest stand and it is important to confirm and revise this information on the field to guarantee if these problems are related to a cartographic error or if the forest stand have been actually removed from the area. The results for *Q. ilex* also highlighted some problems related to the GCUs. Again, one RP do not have any GCU in their area, which is the case of Mallorca (RP 17), and a total of eight regions have their GCU in a location that do not coincide with the MFE50 map, which is the case of regions Cuenca Central del Duero (RP 2), Prepirineo (RP 4), Sierras de Ávila y Segovia RP° 7), Sur de Guadarrama (RP 8), Sierra de Cádiz-Ronda (RP 13), Asturias (B), Monegros (F), Sierras Almerienses (H). Some of these mismatch cases would be related to the accuracy of the coordinates collected from the bibliography on studies with genetic markers of this species. In any case, field work will be necessary for establishing the location and dimension of the forest stands that could be designed as GCUs.

6. CONCLUSIONS

With the main outcomes of this study it was possible to conclude that exists some unresolved questions regarding the updating of information. The analysis shows that the current data available are not satisfactory coupled. With the first part of this study we could notice that the RP_aut map and the MFE50 present some significative differences and this could be due to updating mistakes in-between forest inventories, misidentification, cartographic errors or actually a change in the species distribution area, therefore these mismatches are areas that should be revised in the field. Moreover, the system of the Regions of Provenances in Spain should also be revised, not only for the studied species relevant in this work but also for other species that had their distribution range modified in last few years. It is clear that not only forest areas disappeared from the RP map but also many new forest areas are now present in the MFE50, especially in locations that were not part of the system of RP. After the confirmation that these are new areas in which the species is present but with no RP assigned to them, they should then be incorporated in the RP map throughout an evaluation of its location and its edaphoclimatic characteristics. In the case of *Q. suber*, the regions "I", "N", "O", "P" and "Q" should be given special attention for the fact that they do not present any forest area located in the MFE50 and an inspection has to be done to confirm this situation. The second part of this study revealed important aspects related to the Conservation Indicators of the Forest Genetic Resources. Besides the fact that some of the RPs do not present any source-identified Basic Material, many of the RPs have all BMs located in areas that do not coincide with a forest stand from the MFE50 map. This is similar when considering the Genetic Conservation Units. Furthermore, some regions do not present any GCU and also have a BM located out of a forest area, which is the case of or region Cuenca de Navia ("B") for *Q. suber* and Menorca ("K") for *Q. ilex* and a special attention should be given to them, as their location is known to be situated in autochthonous forest stands.

Last but not least, another important outcome was the creation of scripts to for the automatization of the analysis in order to evaluate the changes in forest area and, in addition, to incorporate in the MFE50 map's table of attributes a field that is related to the origin of the forest stands. This should therefore be used in the future National Forest Inventories in order to make this information available in the forthcoming Spanish Forest Maps.

7. AKNOWLEDGEMENTS

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ANNEX 1 – RP_DISS MAP FOR *QUERCUS SUBER*
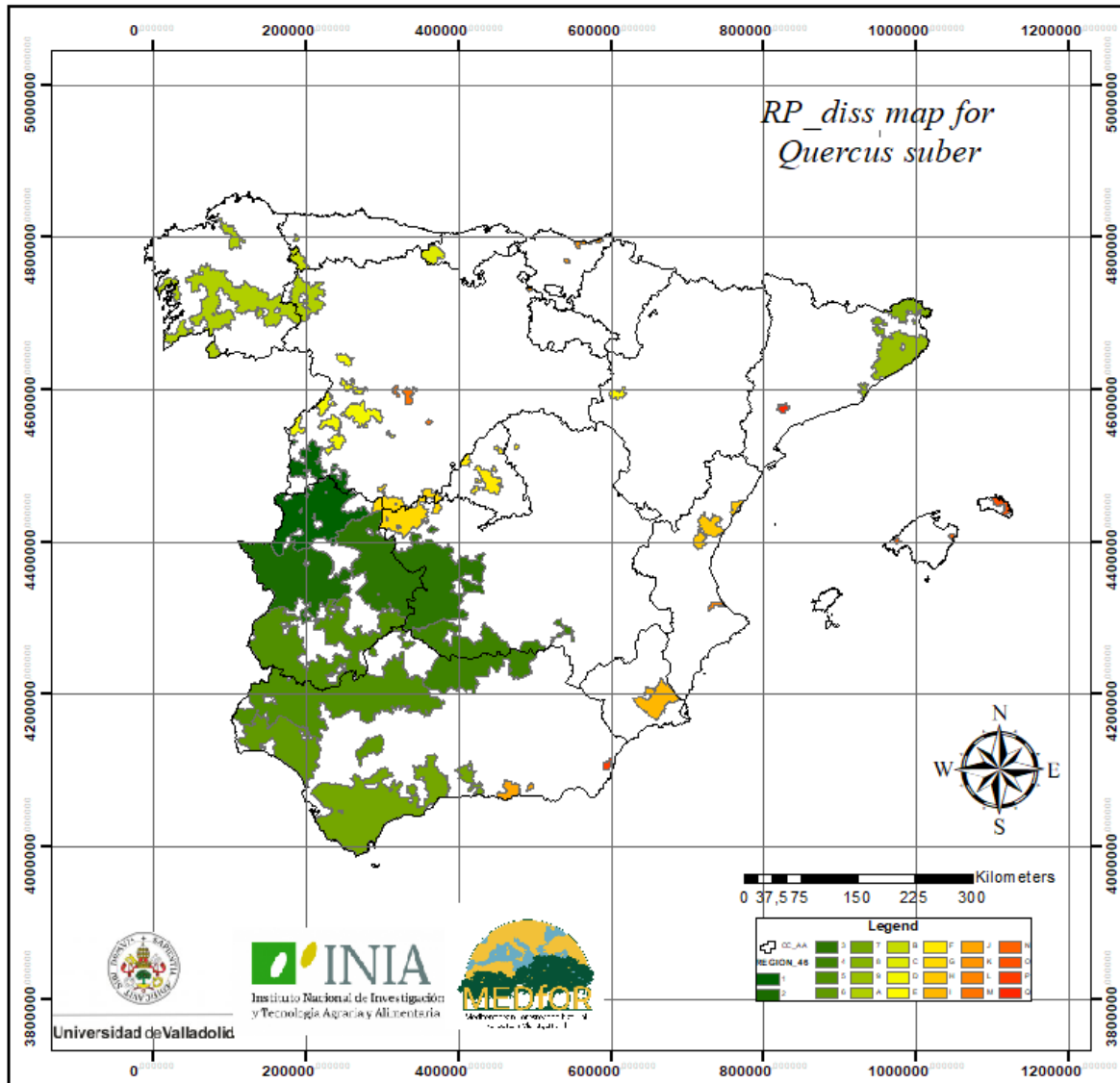
ANNEX 2 – RP_AUT MAP FOR *QUERCUS ILEX*
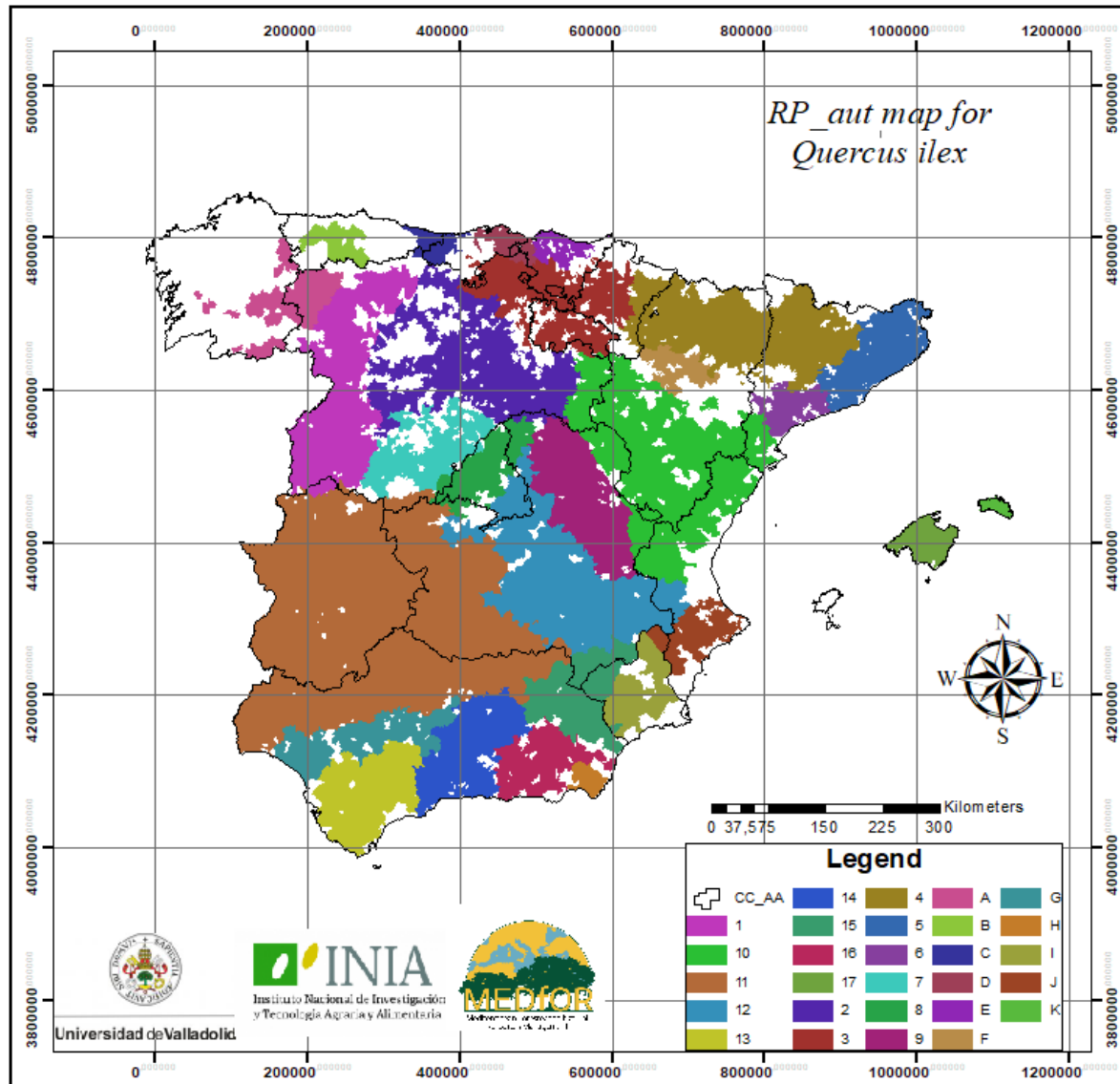
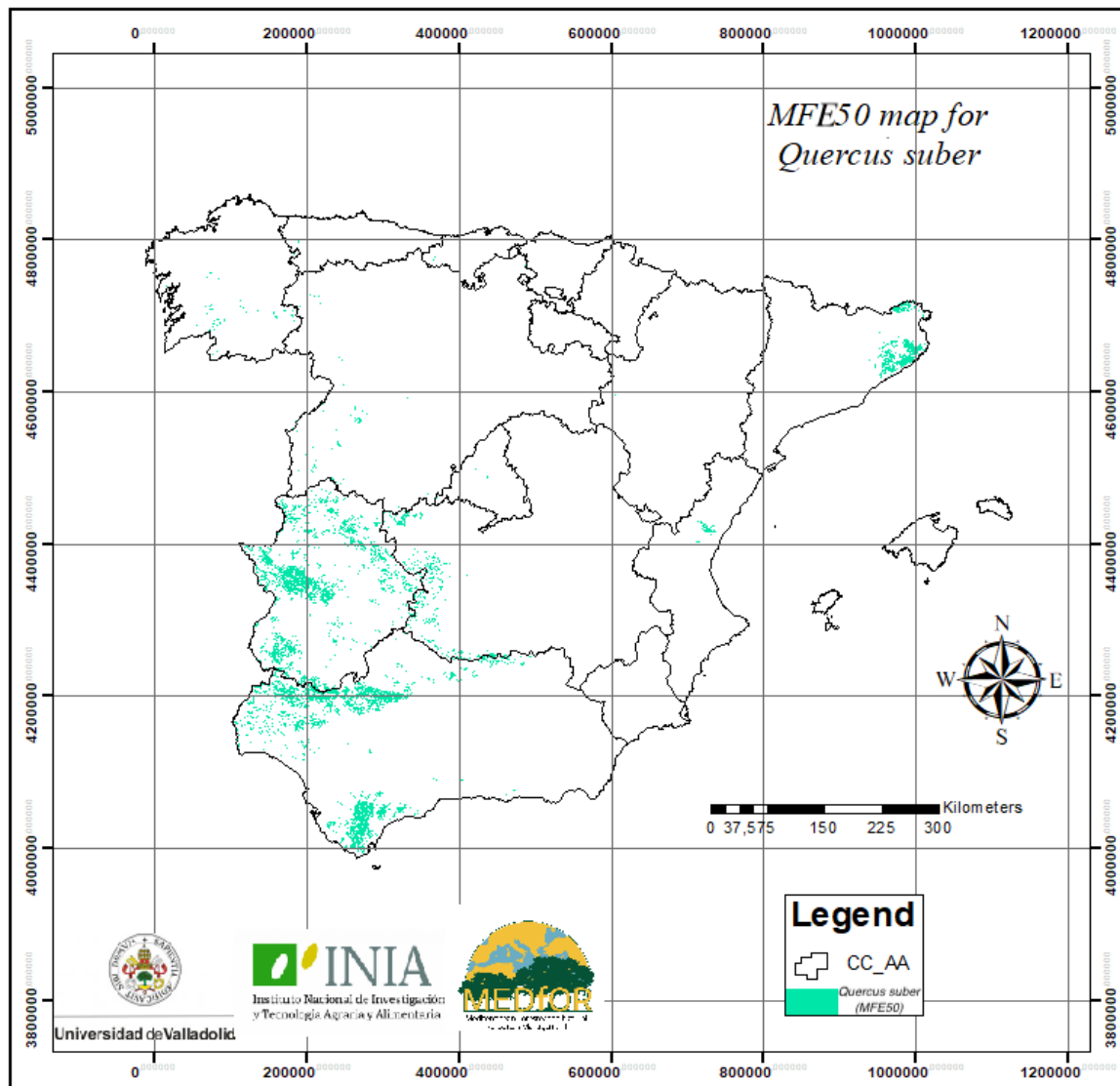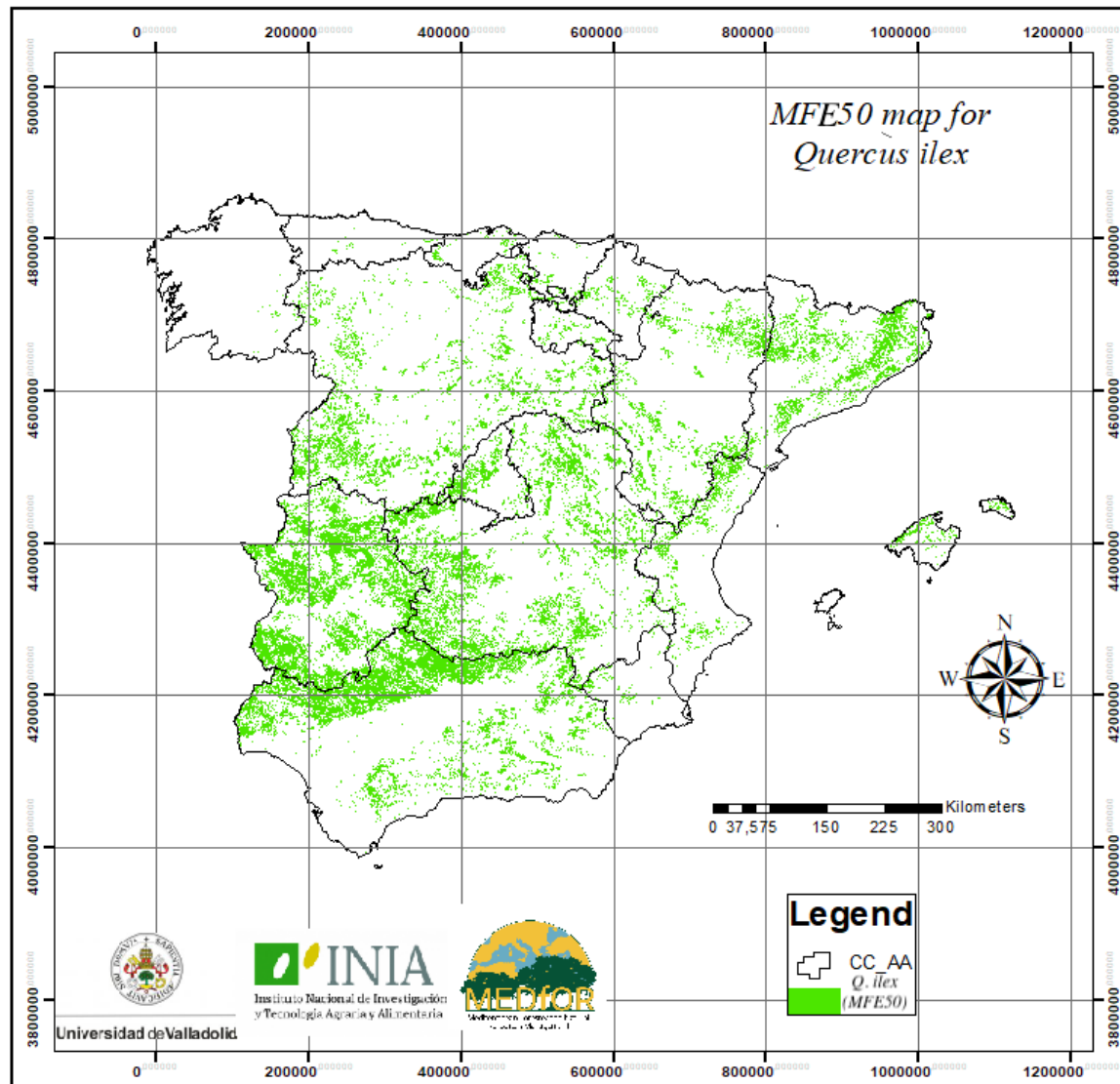## ANNEX 3 – RP_AUT MAP FOR *QUERCUS Suber*
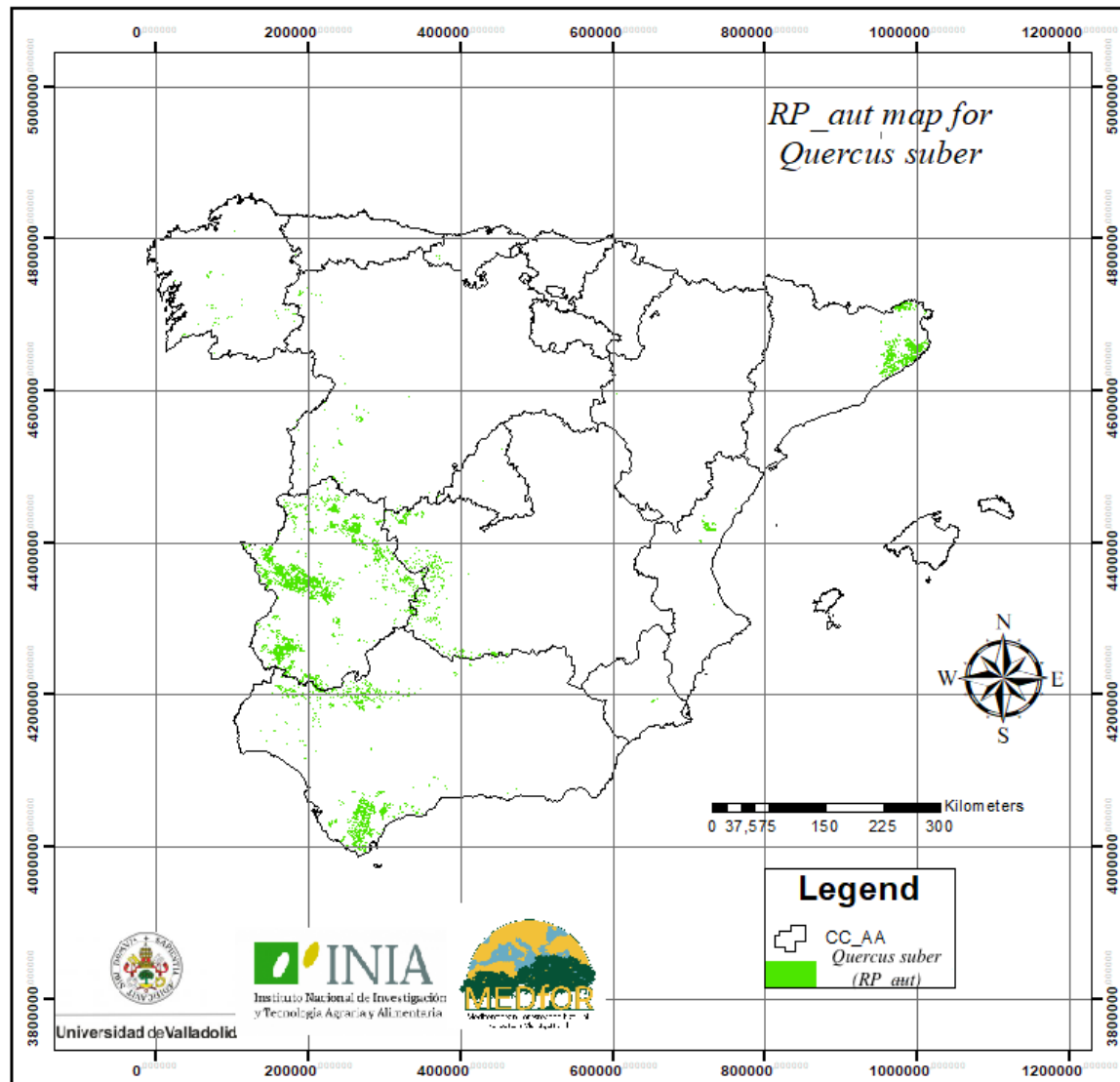
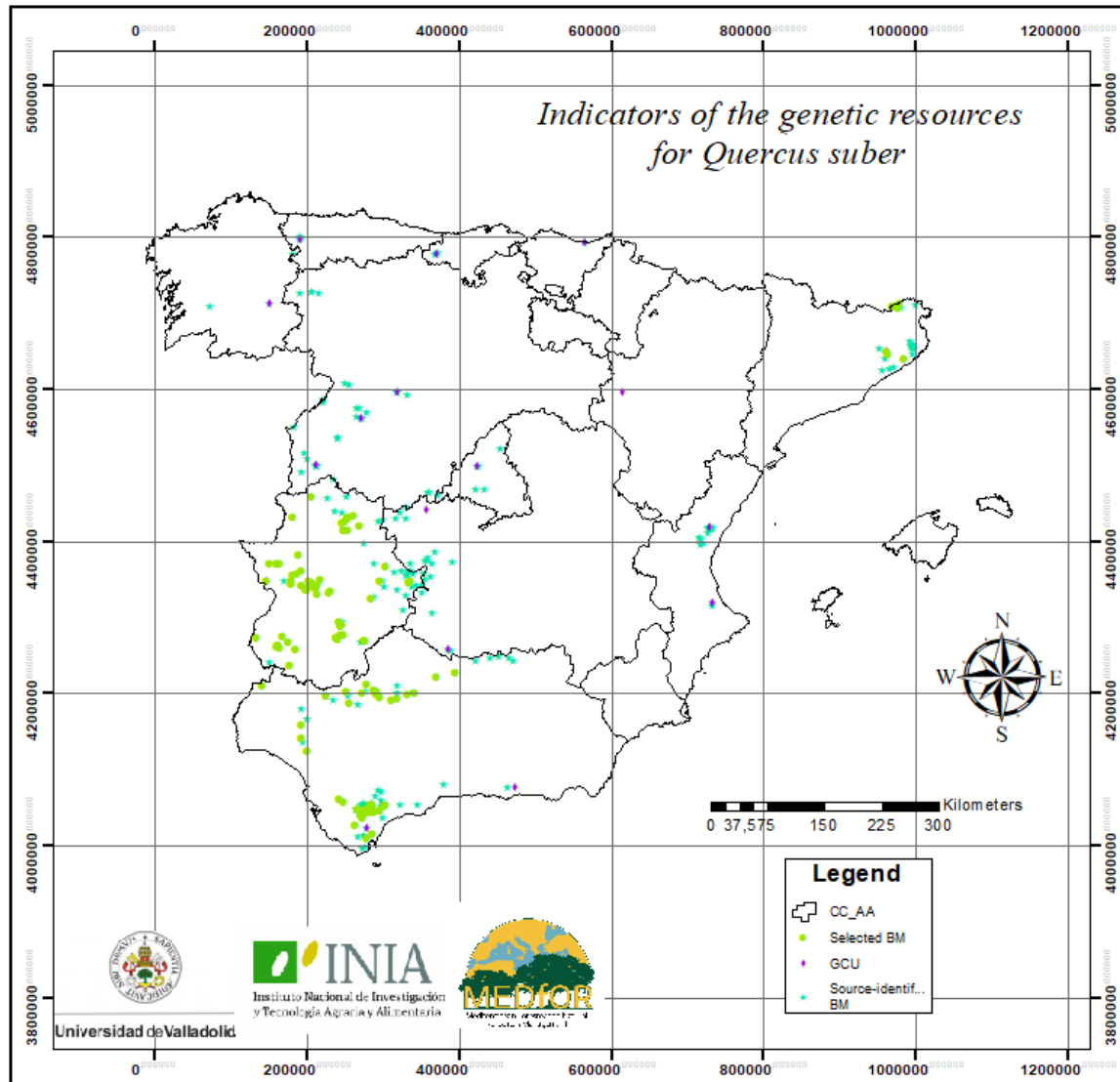## ANNEX 4 – RP_AUT MAP FOR *QUERCUS ILEX*
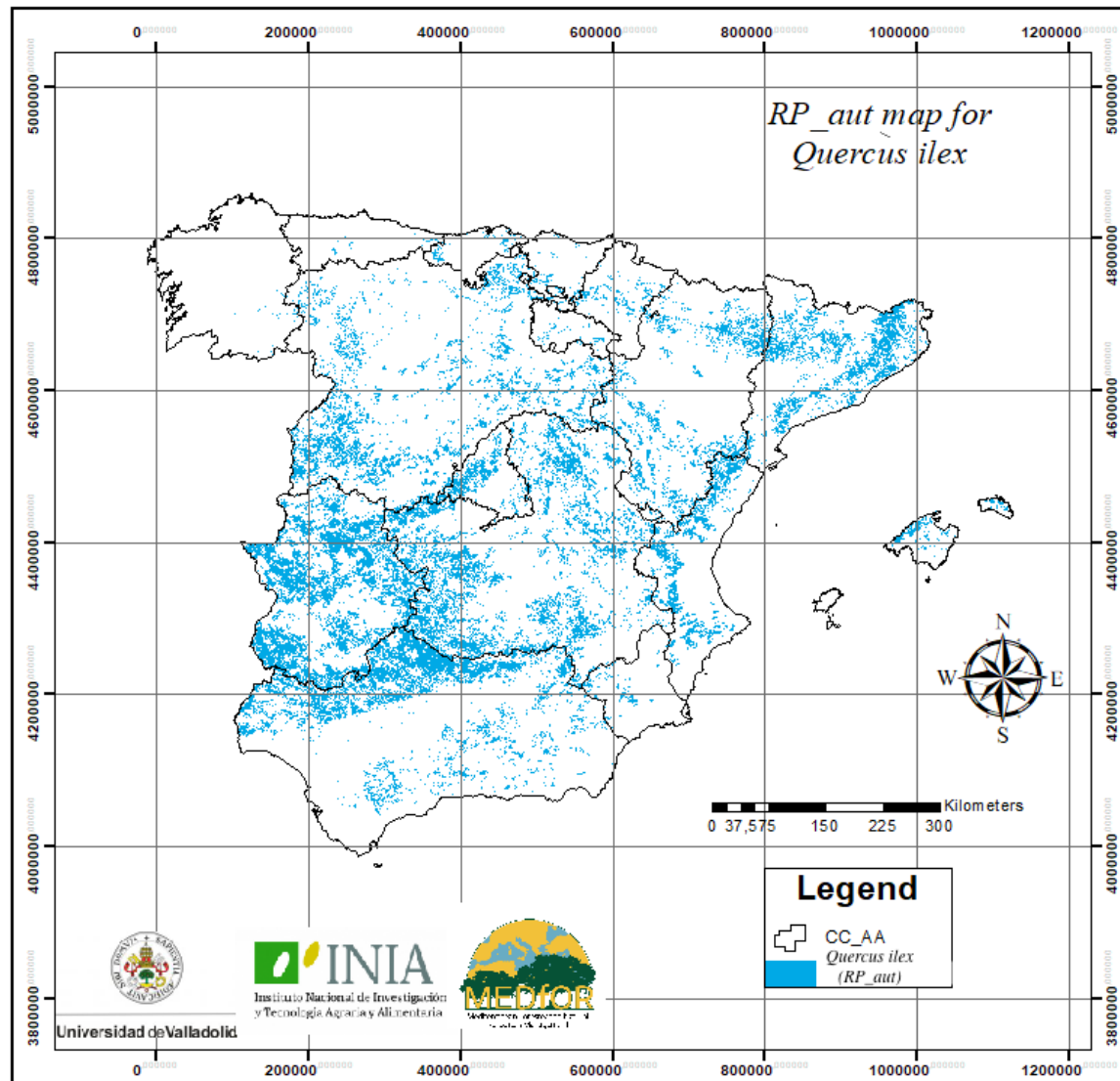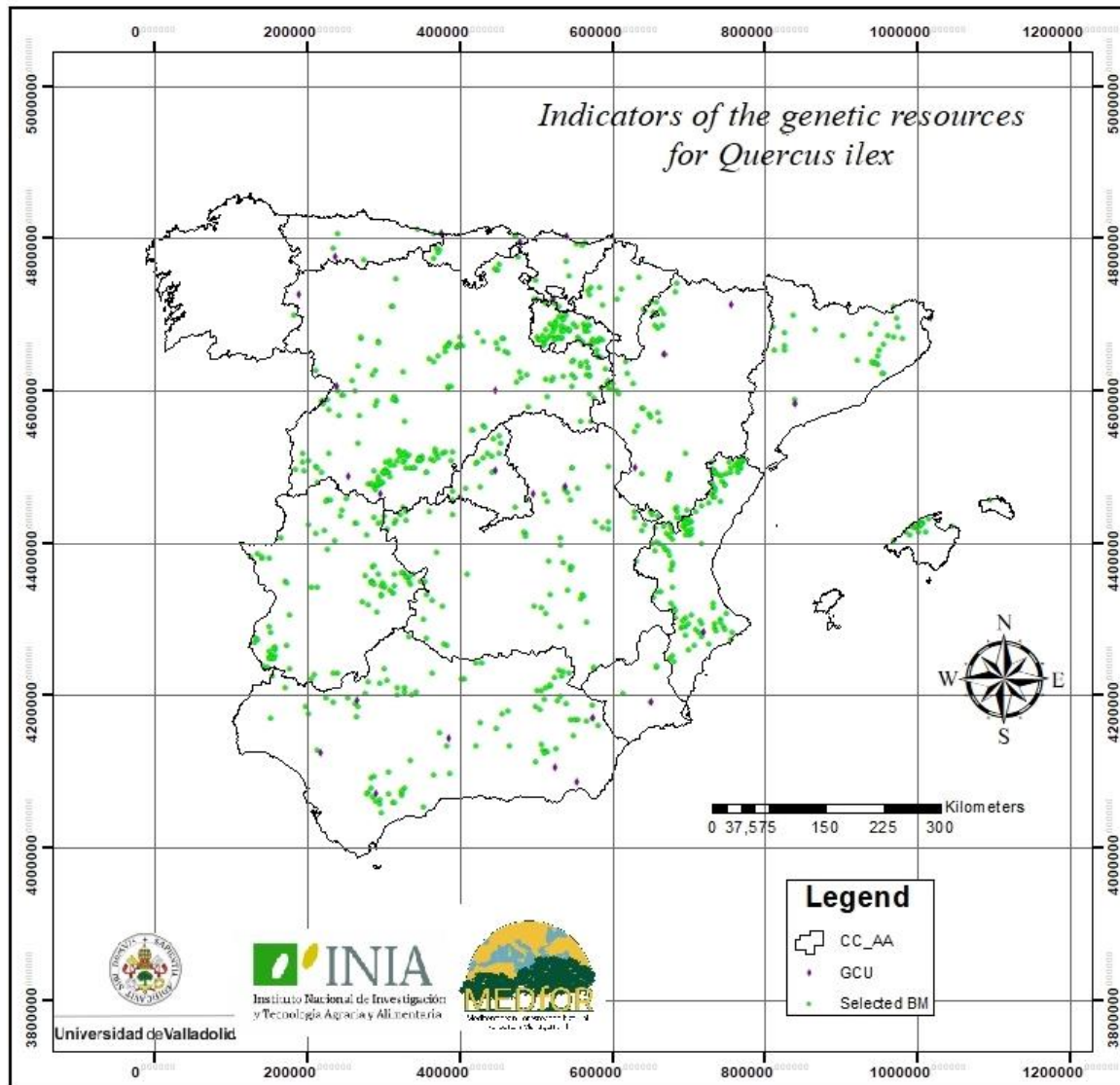
ANNEX 5 – MFE50 MAP FOR *QUERCUS SUBER*

ANNEX 6 – MFE50 MAP FOR *QUERCUS ILEX*

ANNEX 7 – DISTRIBUTION MAP OF THE INDICATORS OF THE GENETIC RESOURCES FOR *QUERCUS SUBER*

ANNEX 8 – DISTRIBUTION MAP OF THE INDICATORS OF THE GENETIC RESOURCES FOR *QUERCUS ILEX*

Indicators of the genetic resources for Quercus ilex

ANNEX 9 – R SCRIPT FOR MAP ANALYSIS AND UPDATING FOR *QUERCUS SUBER*

```r
############# ACTUALIZACIÓN MAPAS REGIONES DE PROCEDENCIA SEGUN MAPA FORESTAL ESPAÑOL######

############################### Librerias #############################################
library(foreign) #importar dbf
library(rgdal)
library(sp)
library(dplyr)
library(openxlsx)#requiere instalar Rtools en el ordenador


###############################################################################################
#Establecer directorio
setwd("C:/")



###################### Fase 1: explorar datos cartografia inicial ########################


tablas<-list.files(pattern = ".dbf")
tablas

########## Mapa de las Regiones de Procedencia
RP_diss <-read.dbf("Quercuessuber_diss.dbf")
names(RP_diss)
levels(RP_diss$REGION_46)
RP_diss$REGION_46 <- factor(RP_diss$REGION_46,
            levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "A",
                    "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L",
                    "M", "N", "O", "P", "Q", "No"))
RP_diss$REGION_46[is.na(RP_diss$REGION_46)] <- "No"
View(RP_diss)


########## Mapa Forestal Español Especie objetivo
MFE_Sp<-read.dbf("Species_dist_46.dbf")
names(MFE_Sp)


######### Mapa Regiones de Procedencia autóctonas
RP_Sp_aut<-read.dbf("QuercussuberRP.dbf")
names(RP_Sp_aut)



######## Mapa RP autóctonas con Cod_RP
RP_Sp_cod<-read.dbf("RP_Qsuber_cod.dbf")
names(RP_Sp_cod)
# Ver qué regiones hay y añadir valor "no" para evitar problemas con NA no explícitos
levels(RP_Sp_cod$REGION_46)
RP_Sp_cod$REGION_46 <- factor(RP_Sp_cod$REGION_46,
                levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "A",
                        "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L",
                        "M", "N", "O", "P", "Q", "No"))

RP_Sp_cod$REGION_46[is.na(RP_Sp_cod$REGION_46)] <- "No"
```

```
View(RP_Sp_cod)



# Captura datos iniciales: núm polígonos, Superficie total, superficie sp dominante
Mapa_nombre_i <- c("MFE(i)", "RPaut(i)")
Num_pol_i<-c(nrow(data.frame(MFE_Sp)), nrow(data.frame(RP_Sp_aut)))
Sup_tot_i<-c(sum(MFE_Sp$Shape_Area),sum(RP_Sp_aut$Shape_Area))


#Extraer polígonos con la sp dominante
MFE_Dom<-subset(MFE_Sp, SP1=="46")
RP_aut_Dom<- subset(RP_Sp_aut, FIRST_DOMI=="D")
Sup_Dom_i<-c(sum(MFE_Dom$Shape_Area), sum(RP_aut_Dom$Shape_Area))


############# Fase2: Importar datos Unión de mapas MFE con RP según escenarios ###############

# Importo datos según escenarios en bruto definidos en GIS
MFE_RP<-read.dbf("Qsuber_MF_RP.dbf")
names(MFE_RP)
View(MFE_RP)
# Renombrar variables para usar script genérico
MFE_RP <- MFE_RP %>% rename(FID_MFE ="FID_Specie", Region = "REGION_46",
            FID_RP = "FID_Quercu", Escenario = "SCOPE",
            Dominancia = "FIRST_DOMI", FID_RPaut = "FID_Quer_1")
names(MFE_RP)


####
# Ver qué regiones hay y añadir valor "no" para evitar problemas con NA no explícitos
levels(MFE_RP$Region)
MFE_RP$Region <- factor(MFE_RP$Region,
        levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "A",
            "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L",
            "M", "N", "O", "P", "Q", "No"))
MFE_RP$Region[is.na(MFE_RP$Region)] <- "No"
View(MFE_RP)


#Lista codigo de la RP de la especie
Cod_RP<-list(unique(MFE_RP$Region))
Cod_RP


### Subset segun escenarios
#  MFE sin unión con RP (MFE_solo)
MFE_solo = subset(MFE_RP, Escenario == 1)
# RP sin unión con MFE (RP_solo)
RP_solo = subset(MFE_RP, Escenario ==2)
# MFE unido RP
MFE_RP_solo= subset(MFE_RP, Escenario ==3)


########## Fase 3: Actualización de mapas #########################################
# 1º Mapa MFE actualizado con RP
MFE_RP_merge = merge(MFE_solo, MFE_RP_solo, all= TRUE)
#sumo areas mismo FID_MFE
```

```r
mut1<-mutate(group_by(MFE_RP_merge, FID_MFE), total_area=sum(AREA_M2))
#Extraigo polig cuya area ha aumentado
MFE_RP_act<-subset(mut1, FID_RP > -1 | total_area>AREA_M2)
View(MFE_RP_act)# RP actualizado


#MFE completo con RP actualizadas
MFE_Act<-mutate(mut1, RPactual = if (FID_RP >=0 | total_area>AREA_M2) {
 "RP"
} else {
 "noRP"
})
warnings()
View(MFE_Act)
#Exportar a excel
write.xlsx(MFE_Act,"~/Desktop/Thesis/Results/MFE_Act_Qsuber.xlsx", asTable = FALSE)


#Paso 2
MFE_RP_act<- mutate(MFE_Act, Origen = if(Orig_num <=1.9){
 "A"
} else if (RPactual == "noRP"){
 "NoRP"
} else {
 "R"
})
View(MFE_RP_act)
#Exportar a excel
write.xlsx(MFE_Act,"~/Desktop/Thesis/Results/MFE_Act_Qsuber.xlsx", asTable = FALSE)
# Versión corta
MFE_Act_exp <- data.frame(id=c(MFE_RP_act$IdFF2015),area=c(MFE_RP_act$total_area),Origen=c(MFE_RP_act$Origen))
MFE_Act_exp<- distinct(MFE_Act_exp, id, area, Origen)
View(MFE_Act_exp)
write.xlsx(MFE_Act_exp,"~/Desktop/Thesis/Results/MFE_Act_exp_Qsuber.xlsx", asTable = FALSE)
summary(MFE_Act_exp$Origen)


#Error: control variación en area total MFE antes y después
E_Sup_MFE <- sum(MFE_Sp$Shape_Area) -sum(MFE_Act$AREA_M2)
E_Sup_MFE


# 2º Identificacion RP poblaciones desaparecidas/disminuidas.
#Unico archivo para exportar
RP_Desap<-mutate(RP_solo, RPactual = if_else (RP_solo$Shape_Area > RP_solo$AREA_M2, "RP_dism","RP_desap"))
View(RP_Desap)
write.xlsx(RP_Desap,"~/Desktop/Thesis/Results/RP_Desap_Qsuber.xlsx", asTable = FALSE)


################ Analisis de resultados #####################################
## Separo Regiones de Procedencia autóctonas y no autóctonas
# Mapa MFE Actualizado
MFE_Act
MFE_noRP <- subset (MFE_Act, RPactual == "noRP") #polígonos MFE sin RP asociada
# Mapa RP desaparecidas/disminuidas
RP_desap <- subset(RP_Desap, RPactual== "RP_desap" & FID_RPaut >0)
View(RP_desap)
```

```r
RP_dism <- subset(RP_Desap, RPactual== "RP_dism" & FID_RPaut >0)
View(RP_dism)


######### Estudio de superficies ######################################
Mapa_nombre_f<- c("MFE_act", "MFE(noRP)","RP(desap)", "RP(dism)")
Num_pol_f<- c(nrow(MFE_Act), nrow(MFE_noRP), nrow(RP_desap),
        nrow(RP_dism))


Sup_tot_f<- c(sum(MFE_Act$AREA_M2), sum(MFE_noRP$AREA_M2),
        sum(RP_desap$AREA_M2), sum(RP_dism$AREA_M2))


### Superficies según dominancia
RP_act_SP1 <-subset(MFE_Act, SP1==46)
MFE_noRP_SP1 <-subset(MFE_noRP, SP1==46)
RP_desap_SP1 <-subset(RP_desap, Dominancia == "D")
RP_dism_SP1 <-subset(RP_dism, Dominancia == "D")
SUP_Dom_f <- c(sum(RP_act_SP1$AREA_M2),sum(MFE_noRP_SP1$AREA_M2),
        sum(RP_desap_SP1$AREA_M2),sum(RP_dism_SP1$AREA_M2))


#### Generar Data frame con resultados de superficies
Mapas<-c(Mapa_nombre_i,Mapa_nombre_f)
Num_polig<-c(Num_pol_i, Num_pol_f)
Sup_total<-c(Sup_tot_i, Sup_tot_f)
Sup_Domin<-c(Sup_Dom_i, SUP_Dom_f)
Data_analisis<-data.frame(Mapas,Num_polig, Sup_total,Sup_Domin)
View(Data_analisis)


######## Estudio de poblaciones desap/dism
# Segun fuente cartográfica
#Crear mapa fuentes donde solo haya FID_RPaut >-1
MFE_Act_FUENTES= subset(MFE_RP, FID_RPaut >=0)
Fuentes <- data.frame(RP_des=c(summary(RP_desap$FUENTE)),
          RP_dis=c(summary(RP_dism$FUENTE)))
Total_Fue=c(summary(MFE_Act_FUENTES$FUENTE))
View(Fuentes)
View(Total_Fue)
# Según dominancia
Dominanc <- data.frame(RP_des=c(summary(RP_desap$Dominancia)),
            RP_dis=c(summary(RP_dism$Dominancia)))
Total_Dom=c(summary(MFE_RP$Dominancia))
View(Dominanc)
View(Total_Dom)
##### Exportar  resultados como libro excel
wb<-createWorkbook()


addWorksheet(wb, "Superficies")
writeData(wb, "Superficies", Data_analisis)
addWorksheet(wb, "Fuentes")
writeData(wb, "Fuentes", Fuentes, rowNames= TRUE)
addWorksheet(wb, "Dominancia")
writeData(wb,  "Dominancia", Dominanc,rowNames= TRUE)
```

```r
saveWorkbook(wb, "~/Desktop/Thesis/Results/Datos_Qsuber.xlsx", overwrite = TRUE)
#####
# Superficies Por Regiones de Procedencia
# MFE_Act
Reg_MFE_Act<-mutate(group_by(MFE_Act, Region), SupRP=sum(AREA_M2))
SupRP_act<-unique(data.frame(CodRP = c(Reg_MFE_Act$Region),SupMFEact=c(Reg_MFE_Act$SupRP)))
View(SupRP_act)
write.xlsx(SupRP_act,"~/Desktop/Thesis/Results/SupRP_act_Qsuber.xlsx", asTable = FALSE)
#MFE(i)
MFEiRP= subset(MFE_RP, FID_MFE >=0)
Reg_MFEi<-mutate(group_by(MFEiRP, Region), SupMFEiRP=sum(AREA_M2))
SupMFEi<-unique(data.frame(CodRP = c(Reg_MFEi$Region),SupMFEi=c(Reg_MFEi$SupMFEiRP)))
View(SupMFEi)
write.xlsx(SupMFEi,"~/Desktop/Thesis/Results/SupMFE(i)_Qsuber.xlsx", asTable = FALSE)
#RP(i)
Reg_RPi<-mutate(group_by(RP_diss, REGION_46), SupRPi=sum(Shape_Area))
SupRPi<-unique(data.frame(CodRP = c(Reg_RPi$REGION_46),SupRPi=c(Reg_RPi$SupRPi)))
View(SupRPi)
write.xlsx(SupRPi,"~/Desktop/Thesis/Results/SupRP(i)_Qsuber.xlsx", asTable = FALSE)
#RP(i)RP
RPiRP= subset(RP_Sp_cod, FID_Autoct >=0)
Reg_RPiRP<-mutate(group_by(RPiRP, REGION_46), SupRPiRP=sum(Shape_Area))
SupRPiRP<-unique(data.frame(CodRP = c(Reg_RPiRP$REGION_46),SupRPiRP=c(Reg_RPiRP$SupRPiRP)))
View(SupRPiRP)
write.xlsx(SupRPiRP,"~/Desktop/Thesis/Results/SupRP(i)RP_Qsuber.xlsx", asTable = FALSE)
#MFE_RP
Reg_MFE_RP<-mutate(group_by(MFE_RP, Region), Sup_MFE_RP=sum(AREA_M2))
SupMFE_RP<-unique(data.frame(CodRP = c(Reg_MFE_RP$Region),SupMFE_RP=c(Reg_MFE_RP$Sup_MFE_RP)))
View(SupMFE_RP)
write.xlsx(SupMFE_RP,"~/Desktop/Thesis/Results/SupMFE_RP_Qsuber.xlsx", asTable = FALSE)


#RPaut_Desap
Reg_RP_Desap<-mutate(group_by(RP_desap, Region), SupRP=sum(AREA_M2))
Sup_RP_Desap<-data.frame(CodRP=c(Reg_RP_Desap$Region), SupRPDes=c(Reg_RP_Desap$SupRP))
Sup_RP_Desap<-unique(Sup_RP_Desap)
View(Sup_RP_Desap)
write.xlsx(Sup_RP_Desap,"~/Desktop/Thesis/Results/Sup_RP_Desap_Qsuber.xlsx", asTable = FALSE)


#RP_dism
Reg_RP_Dism<-mutate(group_by(RP_dism, Region), SupRP=sum(AREA_M2))
Sup_RP_Dism<-data.frame(CodRP=c(Reg_RP_Dism$Region), SupRPDis=c(Reg_RP_Dism$SupRP))
Sup_RP_Dism<-unique(Sup_RP_Dism)
View(Sup_RP_Dism)
write.xlsx(Sup_RP_Dism,"~/Desktop/Thesis/Results/Sup_RP_Dis_Qsuber.xlsx", asTable = FALSE)


###### Sup x RP
Sup_RP<- data.frame(MFE_Act =c(unique(Reg_MFE_Act$SupRP)),
          RP_Desap =c(unique(Reg_RP_Desap$SupRP)),
          RP_Dism=c(unique(Reg_RP_Dism$SupRP)))


##### Num poligonos x RP
Npol_data <- data.frame(MFE_Act = c(summary(MFE_Act$Region)),RP_Desap =c(summary(RP_desap$Region)),
```

```
            RP_Dism=c(summary(RP_dism$Region)))
```

```
View(Npol_data)
```

```
write.xlsx(Npol_data,"~/Desktop/Thesis/Results/Npol_data_Qsuber.xlsx", asTable = FALSE)
```

ANNEX 10 - R SCRIPT FOR MAP ANALYSIS FOR *QUERCUS ILEX*

############ ACTUALIZACIÓN MAPAS REGIONES DE PROCEDENCIA SEGUN MAPA FORESTAL ESPAÑOL######

############################## Librerias ######################################

```r
library(foreign) #importar dbf
library(rgdal)
library(sp)
library(dplyr)
library(openxlsx)#requiere instalar Rtools en el ordenador


#############################################################################################
#Establecer directorio
setwd("C:/Users/User/Desktop")
#getwd()

##################### Fase 1: explorar datos cartografia inicial #######################
#Explorar directorio
tablas<-list.files(pattern = ".dbf")
tablas

########## Mapa de las Regiones de Procedencia
RP_diss <-read.dbf("Qilex_diss.dbf")
names(RP_diss)
levels(RP_diss$Region45)
RP_diss$Region45 <- factor(RP_diss$Region45,
            levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "10",
                  "11", "12", "13", "14", "15", "16", "17", "A", "B", "C", "D",
                  "E", "F", "G", "H", "I", "J", "K", "No"))
RP_diss$Region45[is.na(RP_diss$Region45)] <- "No"
View(RP_diss)


########## Mapa Forestal Español Especie objetivo
MFE_Sp<-read.dbf("Species_dist_45.dbf")
names(MFE_Sp)


######### Mapa Regiones de Procedencia autóctonas
RP_Sp_aut<-read.dbf("QuercusilexRP.dbf")
names(RP_Sp_aut)


######## Mapa RP autóctonas con Cod_RP
RP_Sp_cod<-read.dbf("RP_Qilex_cod.dbf")
names(RP_Sp_cod)
# Ver qué regiones hay y añadir valor "no" para evitar problemas con NA no explícitos
levels(RP_Sp_cod$Region45)
RP_Sp_cod$Region45 <- factor(RP_Sp_cod$Region45,
            levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "10",
                  "11", "12", "13", "14", "15", "16", "17", "A", "B", "C", "D",
                  "E", "F", "G", "H", "I", "J", "K", "No"))

RP_Sp_cod$Region45[is.na(RP_Sp_cod$Region45)] <- "No"
View(RP_Sp_cod)
```

```r
# Captura datos iniciales: núm polígonos, Superficie total, superficie sp dominante
Mapa_nombre_i <- c("MFE(i)", "RPaut(i)")
Num_pol_i<-c(nrow(data.frame(MFE_Sp)), nrow(data.frame(RP_Sp_aut)))
Sup_tot_i<-c(sum(MFE_Sp$Shape_Area),sum(RP_Sp_aut$Shape_Area))


#Extraer polígonos con la sp dominante
MFE_Dom<-subset(MFE_Sp, SP1=="45")
RP_aut_Dom<- subset(RP_Sp_aut, FIRST_DOMI=="D")
Sup_Dom_i<-c(sum(MFE_Dom$Shape_Area), sum(RP_aut_Dom$Shape_Area))


############## Fase2: Importar datos Unión de mapas MFE con RP según escenarios ################

# Importo datos según escenarios en bruto definidos en GIS
MFE_RP<-read.dbf("MFE_RP_Qilex.dbf")
names(MFE_RP)
View(MFE_RP)
# Renombrar variables para usar script genérico
MFE_RP <- MFE_RP %>% rename(FID_MFE ="FID_Specie", Region = "Region45",
            FID_RP = "FID_Quercu", Escenario = "SCOPE",
            Dominancia = "FIRST_DOMI", FID_RPaut = "FID_Quer_1")
names(MFE_RP)


####
# Ver qué regiones hay y añadir valor "no" para evitar problemas con NA no explícitos
levels(MFE_RP$Region)
MFE_RP$Region <- factor(MFE_RP$Region,
            levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "10",
                "11", "12", "13", "14", "15", "16", "17", "A", "B", "C", "D",
                "E", "F", "G", "H", "I", "J", "K", "No"))
MFE_RP$Region[is.na(MFE_RP$Region)] <- "No"
View(MFE_RP)


#Lista codigo de la RP de la especie
Cod_RP<-list(unique(MFE_RP$Region))
Cod_RP


#####Generar un campo binario para hacer la union de la tabla al mapa


### Subset segun escenarios
#  MFE sin unión con RP (MFE_solo)
MFE_solo = subset(MFE_RP, Escenario == 1)
# RP sin unión con MFE (RP_solo)
RP_solo = subset(MFE_RP, Escenario ==2)
# MFE unido RP
MFE_RP_solo= subset(MFE_RP, Escenario ==3)


########## Fase 3: Actualización de mapas ###############################################
# 1º Mapa MFE actualizado con RP
MFE_RP_merge = merge(MFE_solo, MFE_RP_solo, all= TRUE)
```

```r
#sumo areas mismo FID_MFE
mut1<-mutate(group_by(MFE_RP_merge, FID_MFE), total_area=sum(AREA_M2))


#Extraigo polig cuya area ha aumentado
MFE_RP_act<-subset(mut1, FID_RP > -1 | total_area>AREA_M2)
View(MFE_RP_act)# RP actualizado
#MFE completo con RP actualizadas
MFE_Act<-mutate(mut1, RPactual = if (FID_RP >=0 | total_area>AREA_M2) {
 "RP"
} else {
 "noRP"
})
warnings()
View(MFE_Act)
#Exportar a excel
write.xlsx(MFE_Act,"~/Desktop/Thesis/Results/MFE_Act_Qilex.xlsx", asTable = FALSE)


#Paso 2
MFE_RP_act<- mutate(MFE_Act, Origen = if(Orig_num <=1.9){
 "A"
} else if (RPactual == "noRP"){
 "NoRP"
} else {
 "R"
})
View(MFE_RP_act)
#Exportar a excel
write.xlsx(MFE_Act,"~/Desktop/Thesis/Results/MFE_Act_ilex.xlsx", asTable = FALSE)
# Versión corta
MFE_Act_exp <- data.frame(id=c(MFE_RP_act$IdFF2015),area=c(MFE_RP_act$total_area),Origen=c(MFE_RP_act$Origen))
MFE_Act_exp<- distinct(MFE_Act_exp, id, area, Origen)
View(MFE_Act_exp)
write.xlsx(MFE_Act_exp,"~/Desktop/Thesis/Results/MFE_Act_exp_Qilex.xlsx", asTable = FALSE)
summary(MFE_Act_exp$Origen)


#Error: control variación en area total MFE antes y después
E_Sup_MFE <- sum(MFE_Sp$Shape_Area) -sum(MFE_Act$AREA_M2)
E_Sup_MFE
#2º Identificacion RP poblaciones desaparecidas/disminuidas.
#Unico archivo para exportar
RP_Desap<-mutate(RP_solo, RPactual = if_else (RP_solo$Shape_Area > RP_solo$AREA_M2, "RP_dism","RP_desap"))
View(RP_Desap)
write.xlsx(RP_Desap,"~/Desktop/Thesis/Results/RP_Desap_Qilex.xlsx", asTable = FALSE)


############### Analisis de resultados ######################################
## Separo Regiones de Procedencia autóctonas y no autóctonas
# Mapa MFE Actualizado
MFE_Act
MFE_noRP <- subset (MFE_Act, RPactual == "noRP") #polígonos MFE sin RP asociada
# Mapa RP desaparecidas/disminuidas
RP_desap <- subset(RP_Desap, RPactual== "RP_desap" & FID_RPaut >0)
View(RP_desap)
```

```r
RP_dism <- subset(RP_Desap, RPactual== "RP_dism" & FID_RPaut >0)
View(RP_dism)
########## Estudio de superficies ########################################
Mapa_nombre_f<- c("MFE_act", "MFE(noRP)","RP(desap)", "RP(dism)")
Num_pol_f<- c(nrow(MFE_Act), nrow(MFE_noRP), nrow(RP_desap),
         nrow(RP_dism))


Sup_tot_f<- c(sum(MFE_Act$AREA_M2), sum(MFE_noRP$AREA_M2),
         sum(RP_desap$AREA_M2), sum(RP_dism$AREA_M2))


### Superficies según dominancia
RP_act_SP1 <-subset(MFE_Act, SP1==45)
MFE_noRP_SP1 <-subset(MFE_noRP, SP1==45)
RP_desap_SP1 <-subset(RP_desap, Dominancia == "D")
RP_dism_SP1 <-subset(RP_dism, Dominancia == "D")
SUP_Dom_f <- c(sum(RP_act_SP1$AREA_M2),sum(MFE_noRP_SP1$AREA_M2),
         sum(RP_desap_SP1$AREA_M2),sum(RP_dism_SP1$AREA_M2))


#### Generar Data frame con resultados de superficies
Mapas<-c(Mapa_nombre_i,Mapa_nombre_f)
Num_polig<-c(Num_pol_i, Num_pol_f)
Sup_total<-c(Sup_tot_i, Sup_tot_f)
Sup_Domin<-c(Sup_Dom_i, SUP_Dom_f)
Data_analisis<-data.frame(Mapas,Num_polig, Sup_total,Sup_Domin)
View(Data_analisis)


######## Estudio de poblaciones desap/dism
# Segun fuente cartográfica
#Crear mapa fuentes donde solo haya FID_RPaut >-1
MFE_Act_FUENTES= subset(MFE_RP, FID_RPaut >=0)
Fuentes <- data.frame(RP_des=c(summary(RP_desap$FUENTE)),
            RP_dis=c(summary(RP_dism$FUENTE)))
Total_Fue=c(summary(MFE_Act_FUENTES$FUENTE))
View(Fuentes)
View(Total_Fue)
# Según dominancia
Dominanc <- data.frame(RP_des=c(summary(RP_desap$Dominancia)),
              RP_dis=c(summary(RP_dism$Dominancia)))
Total_Dom=c(summary(MFE_RP$Dominancia))
View(Dominanc)
View(Total_Dom)
##### Exportar resultados como libro excel
wb<-createWorkbook()


addWorksheet(wb, "Superficies")
writeData(wb, "Superficies", Data_analisis)
addWorksheet(wb, "Fuentes")
writeData(wb, "Fuentes", Fuentes, rowNames= TRUE)
addWorksheet(wb, "Dominancia")
writeData(wb,  "Dominancia", Dominanc,rowNames= TRUE)


saveWorkbook(wb, "~/Desktop/Thesis/Results/Datos_Qilex.xlsx", overwrite = TRUE)
```

```
#####
# Superficies Por Regiones de Procedencia
# MFE_Act
Reg_MFE_Act<-mutate(group_by(MFE_Act, Region), SupRP=sum(AREA_M2))
SupRP_act<-unique(data.frame(CodRP = c(Reg_MFE_Act$Region),SupMFEact=c(Reg_MFE_Act$SupRP)))
View(SupRP_act)
write.xlsx(SupRP_act,"~/Desktop/Thesis/Results/SupRP_act_Qilex.xlsx", asTable = FALSE)
#MFE(i)
MFEiRP= subset(MFE_RP, FID_MFE >=0)
Reg_MFEi<-mutate(group_by(MFEiRP, Region), SupMFEiRP=sum(AREA_M2))
SupMFEi<-unique(data.frame(CodRP = c(Reg_MFEi$Region),SupMFEi=c(Reg_MFEi$SupRP)))
View(SupMFEi)
write.xlsx(SupMFEi,"~/Desktop/Thesis/Results/SupMFE(i)_Qilex.xlsx", asTable = FALSE)
#RP(i)
Reg_RPi<-mutate(group_by(RP_diss, Region45), SupRPi=sum(Shape_Area))
SupRPi<-unique(data.frame(CodRP = c(Reg_RPi$Region45),SupRPi=c(Reg_RPi$SupRPi)))
View(SupRPi)
write.xlsx(SupRPi,"~/Desktop/Thesis/Results/SupRP(i)_Qilex.xlsx", asTable = FALSE)
#RP(i)RP
RPiRP= subset(RP_Sp_cod, FID_Autoct >=0)
Reg_RPiRP<-mutate(group_by(RPiRP, Region45), SupRPiRP=sum(Area_RP))
SupRPiRP<-unique(data.frame(CodRP = c(Reg_RPiRP$Region45),SupRPiRP=c(Reg_RPiRP$SupRPiRP)))
View(SupRPiRP)
write.xlsx(SupRPiRP,"~/Desktop/Thesis/Results/SupRP(i)RP_Qilex.xlsx", asTable = FALSE)
#MFE_RP
Reg_MFE_RP<-mutate(group_by(MFE_RP, Region), Sup_MFE_RP=sum(AREA_M2))
SupMFE_RP<-unique(data.frame(CodRP = c(Reg_MFE_RP$Region),SupMFE_RP=c(Reg_MFE_RP$SupRP)))
View(SupMFE_RP)
write.xlsx(SupMFE_RP,"~/Desktop/Thesis/Results/SupMFE_RP_Qilex.xlsx", asTable = FALSE)


#RPaut_Desap
Reg_RP_Desap<-mutate(group_by(RP_desap, Region), SupRP=sum(AREA_M2))
Sup_RP_Desap<-data.frame(CodRP=c(Reg_RP_Desap$Region), SupRPDes=c(Reg_RP_Desap$SupRP))
Sup_RP_Desap<-unique(Sup_RP_Desap)
View(Sup_RP_Desap)
write.xlsx(Sup_RP_Desap,"~/Desktop/Thesis/Results/Sup_RP_Desap_Qilex.xlsx", asTable = FALSE)




#RP_dism
Reg_RP_Dism<-mutate(group_by(RP_dism, Region), SupRP=sum(AREA_M2))
Sup_RP_Dism<-data.frame(CodRP=c(Reg_RP_Dism$Region), SupRPDis=c(Reg_RP_Dism$SupRP))
Sup_RP_Dism<-unique(Sup_RP_Dism)
View(Sup_RP_Dism)
write.xlsx(Sup_RP_Dism,"~/Desktop/Thesis/Results/Sup_RP_Dis_Qilex.xlsx", asTable = FALSE)

###### Sup x RP
Sup_RP<- data.frame(MFE_Act =c(unique(Reg_MFE_Act$SupRP)),
          RP_Desap =c(unique(Reg_RP_Desap$SupRP)),
          RP_Dism=c(unique(Reg_RP_Dism$SupRP)))

##### Num poligonos x RP
Npol_data <- data.frame(MFE_Act = c(summary(MFE_Act$Region)),RP_Desap =c(summary(RP_desap$Region)),
```

```
              RP_Dism=c(summary(RP_dism$Region)))

View(Npol_data)

write.xlsx(Npol_data,"~/Desktop/Thesis/Results/Npol_data_Qilex.xlsx", asTable = FALSE)
```

ANNEX 11 – R SCRIPT FOR BASIC MATERIAL ANALYSIS

```
############ ANÁLISIS DE LOS MATERIALES DE BASE #########


############################## Librerias ############################################
library(foreign) #importar dbf
library(openxlsx)#requiere instalar Rtools en el ordenador


####################################################################################################
#Establecer directorio
setwd("C:/Users/User/Desktop ")
#getwd()


##################### Fase 1: explorar datos cartografia inicial ########################


tablas<-list.files(pattern = ".dbf")
tablas


########## MFE con MB o RIUS
MB_Qilex <-read.dbf("MB_Identificados_Qilex.dbf")
#Seleccionar solamente poligonos con MB o RIUS
MB_Qilex_Exc = subset(MB_Qilex, AUTO >= 0)
write.xlsx(MB_Qilex_Exc,"~/Desktop/Thesis/Results/MB_Qilex.xlsx", asTable = FALSE)


#Importar tabla excel


#Quitar valores NA's
levels(MB_Qilex$Region45)
MB_Qilex$Region45 <- factor(MB_Qilex$Region45,
            levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "10",
                "11", "12", "13", "14", "15", "16", "17", "A", "B", "C", "D",
                "E", "F", "G", "H", "I", "J", "K", "No"))
MB_Qilex$Region45[is.na(MB_Qilex$Region45)] <- "No"
View(MB_Qilex)


#Tabla con numeros de poligonos en cada region
Npol_MB_Qilex=c(summary(MB_Qilex$Region45))
View(Npol_MB_Qilex)
write.xlsx(Npol_MB_Qilex,"~/Desktop/Thesis/Results/Npol_MBSelc_Qilex.xlsx", asTable = FALSE)


#Tabla con poligonos fuera del MFE
#Sacar valoes de FID_Specie =-1
MB_Qilex_noMFE <- subset (MB_Qilex, FID_Specie == "-1")
MBSel_Qilex_noMFE=c(summary(MB_Qilex_noMFE$Region45))
View(MBSel_Qilex_noMFE)
write.xlsx(MBSel_Qilex_noMFE,"~/Desktop/Thesis/Results/Npol_MBSel_Qilex_noMFE_Qsuber.xlsx", asTable = FALSE)
```

ANNEX 12 – R SCRIP FOR GENETIC CONSERVATION UNITS ANALYSIS

```
############# ANÁLISIS DE LAS UNIDADES DE CONSERVACIÓN GENÉTICA #######

############################### Librerias ##############################################
library(foreign) #importar dbf
library(rgdal)
library(sp)
library(dplyr)
library(openxlsx)#requiere instalar Rtools en el ordenador


##############################################################################################
#Establecer directorio
setwd("C:/Users/User/Desktop ")
#getwd()


###################### Fase 1: explorar datos cartografia inicial #######################
# Explorar directorio

tablas<-list.files(pattern = ".dbf")
tablas
#Importar datos shapefile
#myShape <- readOGR(dsn = "myShapefileDir", layer = "myShapefile")


########## MFE con MB o RIUS
RIUS <-read.dbf("RIUS_Union_Qsuber.dbf")
#Seleccionar solamente poligonos con MB o RIUS
RIUS_Exc = subset(RIUS, AUTO >= 0)
write.xlsx(RIUS_Exc,"~/Desktop/Thesis/Results/RIUS_Qsuber.xlsx", asTable = FALSE)


#Importar tabla excel


#Quitar valores NA's
levels(RIUS_Qsuber$REGION_46)
```

```
RIUS_Qsuber$REGION_46 <- factor(RIUS_Qsuber$REGION_46,
          levels = c( "1", "2", "3", "4", "5", "6", "7", "8", "9", "A",
                "B", "C", "D", "E", "F", "G", "H", "I", "J", "K", "L",
                "M", "N", "O", "P", "Q", "No"))
RIUS_Qsuber$REGION_46[is.na(RIUS_Qsuber$REGION_46)] <- "No"
View(RIUS_Qsuber)


#Tabla con numeros de poligonos en cada region
Npol_RIUS=c(summary(RIUS_Qsuber$REGION_46))
View(Npol_RIUS)
write.xlsx(Npol_RIUS,"~/Desktop/Thesis/Results/Npol_RIUS_Qsuber.xlsx", asTable = FALSE)


#Tabla con poligonos fuera del MFE
#Sacar valoes de FID_Specie =-1
RIUS_noMFE <- subset (RIUS_Qsuber, FID_Specie == "-1")
RIUS_noMFE=c(summary(RIUS_noMFE$REGION_46))
View(RIUS_noMFE)

write.xlsx(RIUS_noMFE,"~/Desktop/Thesis/Results/Npol_RIUS_noMFE_Qsuber.xlsx", asTable = FALSE)
```