

# Colonization pattern of abandoned croplands in mountain regions. A study case from Sierra Nevada

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## Abstract

Land abandonment is a major global change driver in the Mediterranean Region where anthropic activity has played an important role shaping landscape configuration. Understanding the woodland expansion towards marginal areas (abandoned crops) is critical to develop effective management strategies. In this work we analyze the colonization pattern of abandoned croplands by *Quercus pyrenaica* in Sierra Nevada. We aimed to assess differences among populations in the rear edge of its distribution. For this purpose we characterized (i) the colonization pattern of *Q. pyrenaica*, (ii) the structure of the seed source (mature forest), and (iii) the abundance of the main seed disperser (European jay, *Garrulus glandarius*). The study was conducted in five abandoned croplands located in two representative populations of *Q. pyrenaica* located in contrasting slopes. We sampled three habitat types: mature forest, edge-forest and abandoned cropland. A total of 83 plots (10 x 30 m) were sampled. In each plot all tree individuals were counted. Basal diameter and height of each tree specimen were measured and sapling abundance was calculated. Abundance of European jay was determined by bird census (7-year) (line-transect method). Sapling abundance was different between northern and southern *Q. pyrenaica* populations. However, no differences on sapling abundance were observed among habitat types. Abundance of jay does not differ significantly between sites. On the other hand, forest structure showed differences between populations. Differences in colonization pattern could be explained by different management histories and (different land-use intensities) before abandonment of the croplands (biological legacies) and cattle management practices.

## keywords

land-abandonment; colonization; *Quercus pyrenaica*; Sierra Nevada;

## Introduction

Land abandonment is a major global change driver in the Mediterranean Region where anthropic activity has played an important role shaping landscape configuration

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In this work we analyze the colonization pattern of abandoned croplands by *Quercus pyrenaica* in Sierra Nevada. We aimed to assess differences among populations in the rear edge of its distribution. For this purpose we characterized (i) the colonization pattern of *Q. pyrenaica*, (ii) the structure of the seed source (mature forest), and (iii) the abundance of the main seed disperser (European jay, *Garrulus glandarius*).

Land use and exploitation decreased, mostly at the onset of the nineteenth century, leaving much of the Mediterranean landscapes in an almost barren state, with poor vegetation cover. “Natural” vegetation started to recover spontaneously on abandoned agricultural land by secondary successional processes. In uncultivated landscape patches, but in which the vegetation had been severely degraded by wood-cutting or grazing, succession also commenced following a decrease in land exploitation (Debussche et al. 1999).

In Mediterranean area, cropland abandonment has been widespread during the second half of the last century (Pías et al. 2014; Valbuena-Carabaña et al. 2010).

Land-use change models predict an increase in this trend in the future (Rounseveld et al. 2006). In fact, land abandonment is considered one of the most powerful global-change drivers in developed countries (Escribano-Avila et al. 2012).

This finding is consistent with major social-ecological changes that occurred in the mountain region of Sierra Nevada, expressed by strong depopulation and land abandonment of annual and permanent crops (García Martínez, 1999). Mainly from 1956 to 1977, land abandonment in Sierra Nevada prevailed mostly at higher altitudes, being followed by specialization and intensification land use practices at lower elevations (a trend also verified in other mountain systems (e.g. Gellrich et al., 2007, Zimmermann et al., 2010).

Algunas montañas han sufrido un cambio dramático en los cambios de uso del suelo (eg) lo cual ha leading to changes in mountain ecosystems (see eg. R)

European Alps (Rutherford)

The abandonment of more marginal agricultural areas, in particular, has resulted in more homogenous landscape patterns (Tasser et al. 2007) and in the loss of biodiversity (Chapin et al. 2000; Zimmermann et al. 2010).

Rutherford GN, Bebi P, Edwards PJ, Zimmermann NE (2008) Assessing land-use statistics to model land cover change in a mountainous landscape in the European Alps. *Ecol Model* 212:460–471

Zimmermann P, Tasser E, Leitinger G, Tappeiner U (2010) Effects of land-use and landcover pattern on landscape-scale biodiversity in the European Alps. *Agric Ecosyst Environ* 139:13–22

The abandonment of agricultural land became widespread in many developed regions during the second half of the last century (Mottet et al., 2006, Rey Benayas et al., 2007), and land-use change models predict an increase in this trend in coming decades (Rounseveld et al., 2006).

The aim of this work is

Understanding the woodland expansion towards marginal areas (abandoned crops) is critical to develop effective management strategies.

In this work we analyze the colonization pattern of abandoned croplands by *Quercus pyrenaica* in Sierra Nevada

Our hypothesis is that combination of different land uses strongly affects to colonization pattern.

We studied the colonization pattern of *Q. pyrenaica* woodlands located in the rear edge of their distribution.

queremos estudiar como es el patron de colonización natural de los cultivos abandonados y cómo este se ve afectado por el uso del pasado. Para ello vamos a analizar

Nuestra hipótesis es que aquellos cultivos que fueron abandonados antes

For this purpose we explore the colonization pattern of

queremos saber si el patrón de colonización en esta región montañosa está mas determinado por las condiciones climáticas que por las el uso del suelo.

Nos gustaría inferir si el patrón de colonización hacia hábitats marginales, está mas condicionado por el uso del suelo que por las condiciones climáticas

Objectives: to analyze the structure of the seed source (mature forest) to analyze the colonization pattern of abandoned cropland by *Q. pyrenaica* to compare the abundance of the main seed disperser (European jay, *G. glandarius*)

Our specific goals are: (

to analyze the colonization pattern of abandoned cropland by *Q. pyrenaica*; to explore differences on colonization pattern a

Table 1: Abandonment cropland features

Site	Cropland		Elevation (m)	Area (ha)	Number of transects		
	Code	Abandonment Age (years)			Cropland	Edge	Forest
Robledal de Cádiz	CA1	> 60	1796-1866	3.29	6	3	4
	CA2	< 30	1789-1858	5.80	9	3	7
	CA3	40 - 60	1851-1892	1.56	3	3	4
Robledal de San Juan	SJ1	40 - 60	1507-1674	3.47	6	3	6
	SJ2	30 - 40	1575-1746	10.36	13	3	10

to compare the abundance of the main seed disperser (European jay, *G. glandarius*)

Our specific goals are to: (1) describe the patterns of natural regeneration of *Q. pyrenaica*; (2) experimentally estimate the survival probability of acorns and seedlings; (3) identify the mortality factors acting on the two life-cycle stages; and (4) experimentally test whether there are between microhabitat differences in the effect of the mortality agents.

## Material and methods

## Sampling description

We sampled 5 abandonment croplands located at two Pyrenean oak forests in contrasting slopes of Sierra Nevada (southern Spain): “Robledal de San Juan” (SJ), a xeric site located at the northern aspect (37°7’29.63”N, 3°21’54.60”W; Güejar-Sierra, Granada, Spain); and “Robledal de Cáñar” (CA), a wetter site located at the southern aspect (37°57’28.04”N, 3°25’57.1”W; Cáñar, Granada) (Figure 1; Table 1). Each cropland was delimited using land-use and land-cover map of Andalusia for 1956 (CMA 2007) combined with a detailed photographic interpretation of the black and white 1956 orthophotos (1-m spatial resolution) (see Navarro-González, Bonet-García, and Pérez-Luque 2012 for more details). The estimation of the age abandonment for each cropland were performed combining interpretation of orthophotographies with information from local neighbors. We compiled all available aerial orthophotographies of the study areas from Fototeca Digital of the Spanish National Geographic Institute (<http://fototeca.cnig.es/>). The approximate abandonment age for each cropland was estimated by comparing the sequence of orthophotographs. These dates were accurated using information about past land-use, compiled from local neighbours (by local workshops and interviews with retired elder: farmers, shepherds and loggers; see details in Ricardo A. Moreno-Llorca et al. 2014; R. A. Moreno-Llorca et al. 2016). The estimated rank of ages could be considered accurate (see Table 1).

For each abandonment cropland, linear vegetation transects (30 m x 10 m) were randomly distributed in the old field; at the forest edges; and inside the surrounding forests (Figure 2). The numbers of transect within the old fields and surrounding forests were proportional to abandonment cropland size (Table 1). Transects were sampled in autumn 2012.

In each vegetation transect all tree species were recorded, and tree height and diameter were measured. For each transect we computed the juvenile abundance as the number of individuals lower than 150 cm tall. We did not separate the generative and vegetative origins of young oaks, since it is difficult due to resprouting trait of this species. In addition to the juvenile abundance, we explored differences between several recruitment stages based on individual size (*e.g.* [Plieninger et al. 2010 Large Scale Patterns?](#)). We considered five size categories based in height (every 30 cm). All data were properly documented and published in an international repository (see [Perez Luque et al. 2015 Dataset MIGRAME?](#) for a detailed description of the dataset).

## Disperser community

To explore the disperser community in our study sites, we used bird censuses carried out by the Sierra Nevada Global Change Observatory. This dataset contains bird censuses at different ecosystems types of Sierra Nevada since 2008 (for more details see [BareaAzconetal2012PasseriformesOtrasa?](#); [PerezLuqueetal2016DatasetPasserine?](#)). We only used data for the Eurasian jay (*Garrulus glandarius*), since it is the main disperser of *Q. pyrenaica* ([Gomez2003ImpactVertebrate?](#)). As we are interested in the comparison of the Eurasian jay community between the two study sites, we computed the annual bird abundances (in terms of birds/10 ha) for each site during a 7-year period (2008-2013). For more details about bird censuses see ([BareaAzconetal2012PasseriformesOtrasa?](#)) and Zamora and Barea-Azc'on (2015).

## Data Analysis

We used the vegetation transects carried out inside the forest (habitat type = FOREST) to analyze the structure of the seed source (mature forest). Several parameters related to forests' structure and functioning were computed: tree density, juvenile abundance, tree species composition, tree size related statistics (*i.e.* mean, median, maximum, 75 and 90 percentiles of tree-height), and basal area (BA). Differences between sites were assessed using the non-parametric Mann–Whitney U-test, since data does not met normality and/or homocedasticity assumptions. We also compared whether there was variation within transects belong to the same locality. ANOVA analysis were performed to explore differences of Bird disperser abundance (*G. glandarius*) between sites and across years.

The variation of the juvenile abundance between study sites, habitat type, and their interaction (site-habitat type), was analyzed using Generalized Linear Models with a Tweedie distribution with a log link (cita libro). Study sites and habitat type were the explanatory variables. Prior to the analysis, data exploration was applied following protocols described by ([Zuuretal2010ProtocolData?](#)) and ([IenoZuur2015BeginnerGuide?](#)). As the dataset comprised count data, we initially used the Poisson and the Negative Binomial distribution. However, these models were overdispersed. A variance power parameter of 1.28 (1.20-1.40, 95% confidence interval) were used in the Tweedie GLM model. This parameter was estimated using the `tweedie.profile` function of the `tweedieciat` R package (cita). Model comparison (univariate models) were carried out using the Akaike's information criterion (AIC) (Burnham and Anderson 2002). The model accuracy was tested by Nagelkerke's pseudo-R<sup>2</sup> (Nagelkerke 1991), used as a measure of goodness of fit. The significance of the explanatory variables in the selected model was tested using the likelihood ratio tests (LRT). Wald z-tests and Tukey's HSD-corrected *post hoc* comparisons were used to test for differences in juvenile abundance among sites and habitat-type.

All statistical analyses were performed in R using ...

brglm v. 0.5–6 (Kosmidis 2007), lme4.0 v. 0.9999–2 (Bates et al. 2012), ggplot2 v. 0.9.0 (Wickham 2009), and multcomp v. 1.2–12 (Hothorn et al. 2008) for multiple comparisons–corrected P values.

### ## Results

A total of 83 vegetation transects were sampled in autumn 2012.

No significant differences for forest attributes were found in forest between study sites (Table 2). *Q. pyrenaica* woodland of CA site showed higher tree density but smallest tree heights (mean, median and percentiles) than SJ site (Table 2). In addition, higher contribution of juvenile abundance was found for CA site, with also showed greater basal area than SJ site (Table 2).

```
g <- data.frame(Variable = c("% of Q. pyrenaica", "Tree density (ind/ha)", "Juvenile abundance (ind/ha)",
"Maximum tree height (m)", "Tree height mean (m)", "Tree height median (m)", "Tree height 75 percenti

fs <- read_csv(here::here("data/forest_str_by_localidad.csv")) %>%
  dplyr::select(-c(alternative:conf.method)) %>%
  bind_cols(g) %>%
```

Table 2: Forest attributes of northern (SJ) and southern (CA) sites. U Mann-Withney statistics with significance at 0.05 level. Mean and SE are shown

Variable	Southern site (CA)	Northern site (SJ)	U statistic	p value
Tree density (ind/ha)	1671.11 $\pm$ 229.21	1587.5 $\pm$ 161.67	4.808111	0.9369620
Juvenile abundance (ind/ha)	1004.44 $\pm$ 195.72	883.33 $\pm$ 127.18	4.852030	0.7667391
Adult abundance (ind/ha)	584.44 $\pm$ 80.47	704.17 $\pm$ 63.31	4.448516	0.1780814
Maximum tree height (m)	13.93 $\pm$ 0.65	13.75 $\pm$ 0.71	4.824306	0.8736194
Tree height mean (m)	4.32 $\pm$ 0.6	5.09 $\pm$ 0.37	4.330733	0.0855255
Tree height median (m)	3.19 $\pm$ 0.83	3.57 $\pm$ 0.66	4.564348	0.3527368
Tree height 75 percentile (m)	5.73 $\pm$ 1.02	8.29 $\pm$ 0.6	4.343805	0.0922400
Tree height 90 percentile (m)	10.07 $\pm$ 0.95	11.22 $\pm$ 0.54	4.605170	0.4399915
Basal Area (m <sup>2</sup> /ha)	37.56 $\pm$ 4.23	33.58 $\pm$ 3.6	4.912655	0.5400805

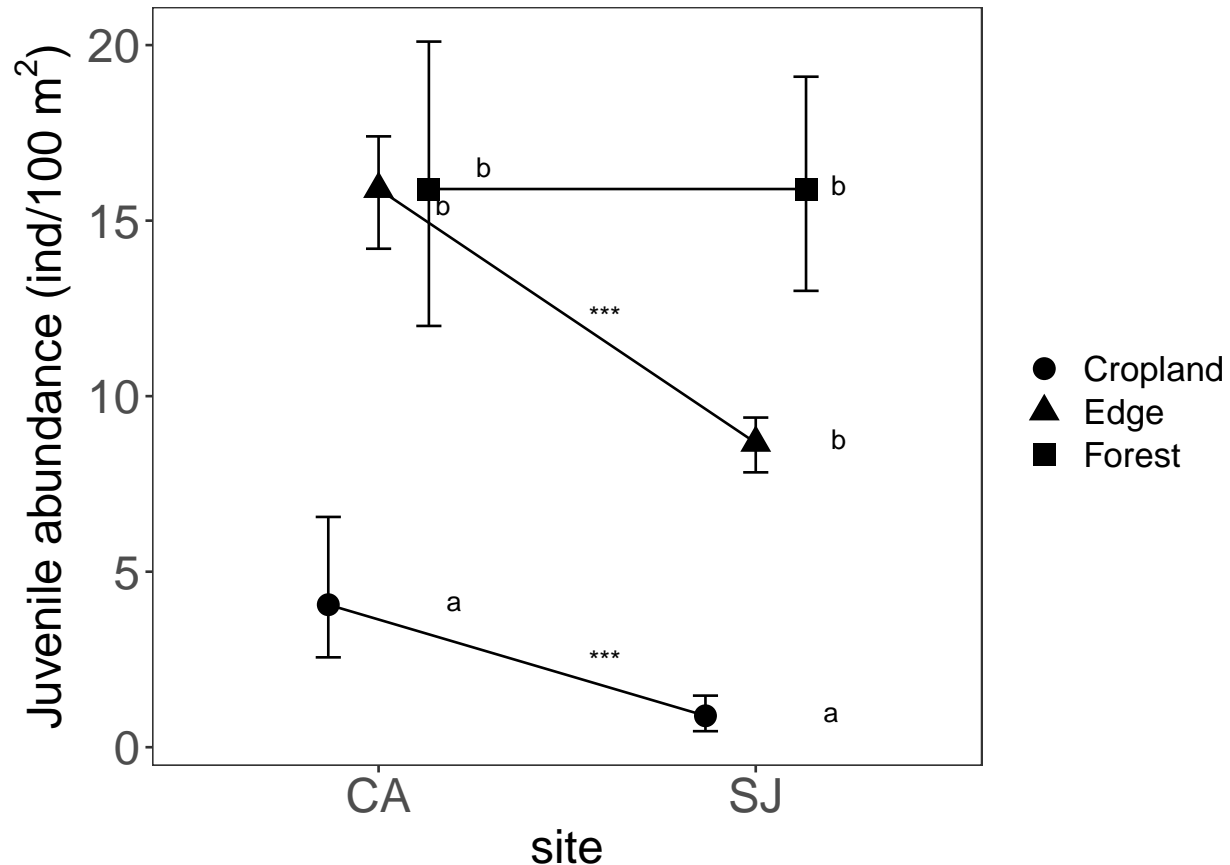
```
dplyr::select(-parameter2, -variable, -method) %>%
relocate(Variable)

fs %>%
  kbl(col.names = c("Variable",
                    "Southern site (CA)",
                    "Northern site (SJ)",
                    "U statistic",
                    "p value"),
      booktabs = T, linesep = "",
      align = "c", escape = FALSE,
      caption = "Forest attributes of northern (SJ) and southern (CA) sites. U Mann-Withney statistics v
  kable_styling(latex_options = c("scale_down"))

# %>%
#   collapse_rows(columns = 1) %>%
#   add_header_above(c(" " = 1, "Cropland" = 2, " " = 2, "Number of transects" = 3)) %>%
#   column_spec(column = 3, width = "8em")
```

Abundance of *Garrulus glandarius* was no different between study sites ( $F_{1,82}=2.387$ ;  $p = 0.126$ ; CA=1.69 $\pm$ 0.21 and SJ = 1.33 $\pm$ 0.22 birds/10ha), and no differences were found across years in the studied period (2008-2014) ( $F_{6,82}=1.234$ ;  $p = 0.297$ ). The interaction term was also no significant ( $F_{6,82}=1.26$ ;  $p = 0.284$ ).

```
knitr::include_graphics(here::here("ms/juvenile_interaction.pdf"))
```



→ menor competencia en CA

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