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DOI

[10.1111/ddi.12573](https://doi.org/10.1111/ddi.12573)

Publication date

2017

Document Version

Final published version

Published in

Diversity and distributions

License

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[Link to publication](#)

Citation for published version (APA):

Aguirre-Gutiérrez, J., van Treuren, R., Hoekstra, R., & van Hintum, T. J. L. (2017). Crop wild relatives range shifts and conservation in Europe under climate change. *Diversity and distributions*, 23(7), 739-750. <https://doi.org/10.1111/ddi.12573>

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Crop wild relatives range shifts and conservation in Europe under climate change

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Funding information

Dutch Ministry of Economic Affairs, Grant/Award Number: KB-21-004-001

Editor: Tomas Vaclavik

Abstract

Aim: Climate change is expected to have a great impact on the distribution of wild flora around the world. Wild plant species are an important component of the genetic resources for crop improvement, which is especially important in face of climate change impacts. Still, many crop wild relatives (CWRs) are currently threatened in their natural habitat and are poorly represented in gene bank collections. To guide in situ conservation measures and to prioritize species for ex situ conservation, predictions are needed about future species distributions as a result of climate change.

Location: Europe.

Methods: Using species occurrence data and present and future climatic information, we investigated the possible impacts of future climate change on the European distribution of a selection of CWRs red-listed in the Netherlands using a species distribution modelling framework. The representation of the CWRs in European protected areas was investigated for the current and future climatic conditions. The models were created based on an optimistic (RCP 2.6) and pessimistic (RCP 8.5) climate change scenario.

Results: A shift in distribution range, mostly towards northern locations, was observed for all investigated species. A loss of distribution area of up to 61.10% (full dispersal assumption) and 68.91% (no dispersal) according to RCP 2.6 was observed for some species. A distribution area loss of up to 90.92% (full dispersal) and 98.36% (no dispersal) was predicted for the most affected species under the RCP 8.5. Based on the predicted distribution in protected areas, present occupation in nature reserves appeared to be no guarantee for the species' future protection and persistence.

Main conclusions: We conclude that in situ conservation measures, ignoring the effects of climate change, will not be effective for many CWRs and that large-scale ex situ conservation actions are needed to safeguard CWRs.

KEYWORDS

climate change, ecological niche models, genetic diversity loss, protected areas, range shift, species distribution models

1 | INTRODUCTION

Present-day food crops were developed from selections of wild plants, which gradually were adapted to human cultivation and consumption.

As a result of this domestication process, the majority of cultivated crops show only poor phenotypic similarity with their wild predecessors, but nevertheless have remained interfertile to various extents (Vincent et al., 2013). Due to this interfertility, crop-related wild species are an

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indispensable source of useful traits for crop improvement when these traits are not found in the cultivated species (Van de Wouw, Kik, van Hintum, van Treuren, & Visser, 2010). For instance, resistance breeding against new pests and diseases relies to a large extent on the presence of traits in crop wild relatives (CWRs) (Hajjar & Hodgkin, 2007; Van Treuren, Van der Arend, & Schut, 2013). Crop productivity and food security may be endangered when wild genetic resources are no longer available; therefore, the safeguarding of CWRs is widely regarded as a high priority (Maxted et al., 2010). Despite their high ecological and economic value for food and agriculture given by their trait availability, wild species are currently severely underrepresented in ex situ genetic resource collections (Castañeda-Álvarez et al., 2016; Commission on Genetic Resources for Food and Agriculture, 2010). In their natural habitats, the survival of many species is at risk due to human influences, such as urbanization and pollution. During the last decades, the in situ survival of species has become a growing concern as a result of climate change (Bilz, Kell, Maxted, & Lansdown, 2011; Dempewolf et al., 2014).

Changes in the earth climate system since the 1950s are undisputed. Increased temperatures have been recorded in nearly all regions of the world and changes in precipitation patterns are now evident (Stocker et al., 2013). It is considered extremely likely that these changes are predominantly human driven and that further changes can be expected in the future due to continued greenhouse gas emissions (Stocker et al., 2013). The magnitude of the expected changes depends on many factors, and therefore, different climate scenarios have been developed, denoted as the Representative Concentration Pathways (RCPs). Four RCPs (2.6, 4.5, 6.0 and 8.5) have been established based on the approximate radiative forcing in the year 2100 relative to the preindustrial conditions with baseline in 1750 (van Vuuren et al., 2011). The radiative forcing is defined as the influence of a factor for disturbing the incoming and outgoing energy in the earth's atmosphere (IPCC, 2007). RCPs are greenhouse gas concentration trajectories of which RCP 2.6 represents an optimistic scenario (greenhouse gas emissions decline after 2020) and RCP 8.5 a pessimistic scenario (greenhouse gas emissions continue to increase). According to the optimistic RCP 2.6, the global mean surface temperature is expected to increase 0.3–1.7°C in the period between 2081 and 2100, whereas for the pessimistic RCP 8.5, the changes in temperature range between 2.6 and 4.8°C (Stocker et al., 2013).

It is expected that climate change will affect agricultural productivity and the survival probability of plant species in their natural habitats (Jarvis, Lane, & Hijmans, 2008). For wild relatives of peanut, potato and cowpea, it has been estimated that due to climate change 16%–22% of their wild relatives will go extinct, while most species are expected to lose more than 50% of their distribution range (Jarvis, Upadhyaya, et al., 2008). Therefore, predictions about the future distribution of wild species are essential for the development of sound conservation strategies (Maxted et al., 2015). Effects of climate change on future species distributions can be estimated through the use of species distribution models (SDMs), in which the presence of a species at geographic locations is related to the environmental conditions at those sites. SDMs can thus render insights into the effects of the underlying environmental conditions on species distribution. Subsequently, this

relationship is used to predict the probability of species occurrence at thus far unexplored geographical locations. For this reason, SDMs have been used to identify gaps in genetic resources collections and to support collecting missions (Cobben et al., 2015; Parra-Quijano, Iriando, & Torres, 2012; Teeling, Maxted, & Ford-Lloyd, 2012). When projections of climate change scenarios are incorporated in SDMs, the probability of occurrence under future environmental conditions can be estimated. Effects of climate change on the species distribution range can then be analysed by comparing present and future projected distributions (Jarvis, Upadhyaya, et al., 2008; Thuiller et al., 2011).

Here, we use a set of spatially explicit species occurrence records of the known natural distribution of eight wild species related to wheat, turnip, rapeseed, mustard, pea, cyprus-vetch, alfalfa, mint, raspberry, blackberry, dewberry, black salsify and corn salad (Table 1). These species were selected based on their relationship with food crops, their current protection level and their representation of different habitat types, life history, reproduction, pollinator vector, seed dispersal, rarity and availability of species occurrence data (see Section "2"; Table 1). We analysed the current representation of the study species in ex situ collections in Europe. Present and future climatic information was used along with species occurrences to investigate the impact of climate change on their distribution in Europe.

Given the current and predicted changes in climatic conditions in the next decades (Moss et al., 2010; Stocker et al., 2013), we expect that the CWRs show future range contraction of their current distribution if the current environmental conditions to which they are adapted become scarcer (Thuiller, Lavorel, Araujo, Sykes, & Prentice, 2005). Additionally, given the greater projected warming and dryness in southern European regions in comparison with northern areas (Kovats et al., 2014), we expect range shifts for the species towards northern latitudes following their climatic niche. As we expect climate change to contract the distribution range of the studied species and to shift their spatial distribution, we also address these effects on the representation of the species in European protected areas.

2 | METHODS

2.1 | Study region and selected species

Western Europe represented the main study area, focussing on species selected from a CWR inventory in the Netherlands. The eight selected species are *Bromus secalinus*, *Erucastrum gallicum*, *Lathyrus japonicus*, *Medicago polymorpha*, *Mentha pulegium*, *Rubus saxatilis*, *Scorzonera humilis* and *Valerianella rimosa* (Table 1). *Erucastrum gallicum* belongs to the secondary gene pool of rapeseed and turnip and to the tertiary gene pool of Ethiopian cabbage and mustard. In the absence of gene pool information for the other study species, their relationship to the crops presented in Table 1 is classified as "belonging to the same genus" with the exception of the relationship of *B. secalinus* to barley, wheat and rye. The CWR species were selected from a group of 53 species, red-listed in the Netherlands, that resulted from an inventory of Dutch wild relatives of agricultural and horticultural crops important world-wide or to the Netherlands

TABLE 1 Characteristics of the study species and their threat status in the Netherlands, Germany, Flanders and England. Data on rarity and trends in occurrence in the Netherlands are also presented, as well as the number of occurrence data points that were used as input for the construction of the species distribution models

Data characteristics	Species							
	<i>Bromus secalinus</i>	<i>Erucastrum gallicum</i>	<i>Lathyrus japonicus</i>	<i>Medicago polymorpha</i>	<i>Mentha pulegium</i>	<i>Rubus saxatilis</i>	<i>Scorzonera humilis</i>	<i>Valerianella ramosa</i>
Related crop	Barley, Brome grass, Rye, Wheat	Ethiopian cabbage, Mustard, Rapeseed, Turnip	Cyprus-vetch, Pea, Spanish vetchling, Tuberous pea	Alfalfa	Mint	Blackberry, Dewberry, Raspberry	Black salsify	Corn salad
Habitat	Poor lime fields	Nutrient-rich brushwood	Coastal dunes	Nutrient-rich brushwood	Disturbed habitats	Forests, dry acidic soil	Dry heaths	Calcareous fields
Life history	Annual	Annual	Perennial	Annual	Perennial	Perennial	Perennial	Annual
Reproduction	Allogamous	Autogamous	Allogamous	Autogamous	Allogamous	Allogamous	Allogamous	Autogamous
Pollination vector	Wind	No data	Insects	No data	Insects	Insects	Insects	No data
Seed dispersal	Animals and humans	No data	Water	Animals	Wind and water	Birds	Wind	No data
Netherlands Rarity	Rare	Rather rare	Very rare	Very rare	Rare	Very rare	Very rare	Very rare
Netherlands trend since 1950	Reduction 75%–100%	Reduction 50%–75%	Stable or increase	Stable or increase	Reduction 25%–50%	Reduction 75%–100%	Reduction 50%–75%	Reduction 75%–100%
Netherlands threat status	Endangered	Vulnerable	Near Threatened	Near Threatened	Vulnerable	Critically Endangered	Endangered	Critically Endangered
Germany threat status	Least Concern	Least Concern	Not Evaluated	Not Evaluated	Endangered	Least Concern	Vulnerable	Vulnerable
Flanders threat status	Least concern	No data	Extinct	No data	Critically Endangered	No data	Endangered	Critically Endangered
England threat status	Near Threatened	No data	Least Concern	Least Concern	Critically Endangered	Least Concern	Vulnerable	Endangered
Number of species' occurrences at the European level	3,621	1,274	656	3,597	3,036	10,645	4,518	1,147

in particular (CWRnl, 2016). The crop domain considered in that inventory was defined by the world primary crop list of the Food and Agriculture Organization of the United Nations, supplemented with crops of economic importance to the Netherlands using data on crop production areas and economic revenues per hectare. The crop inventory was further supplemented with crops included in Annex 1 of the International Treaty on Plant Genetic Resources for Food and Agriculture, the European Union database of registered plant varieties and the Dutch variety list. Altogether, the crop domain consisted of 207 agricultural and horticultural crops. Wild species occurring in the Netherlands and relating to these crops were identified based on the genus name of the crop or on published data on interfertility in case of different genera, revealing 214 species of which 53 were red-listed in the Netherlands (van Treuren et al., in prep.). From these Dutch red list CWRs, the species for the present study were selected to encompass a wide variation in habitat, life history, reproduction, pollination vector and seed dispersal characteristics. Additional selection criteria included variation in rarity, occurrence trend and threat status in the Netherlands (NDFV Verspreidingsatlas, 2016), while also variation in IUCN red list status (www.iucnredlist.org) in Germany (Floraweb, 2016), Flanders (Van Landuyt et al., 2006) and England (Stroh et al., 2014) was considered (Table 1). The species status in neighbouring regions was considered important given that such areas may act as source and sink locations for the establishment of new populations. To examine the current representation of the study species in ex situ collections maintained in Europe, data were downloaded from the search catalogue EURISCO (<http://eurisco.ecpgr.org>) on 2 February 2017. Investigations were restricted to records with sample status "wild" (code 100) or "weedy" (code 200) and a documented origin country located in Europe. Despite their partial location in Europe, the Russian Federation and Turkey were included in the analyses.

2.2 | Species distribution data

Geographic occurrence data of the eight selected species for Central-Western Europe were obtained from the database of the Global Biodiversity Information Facility (GBIF, 2015). Records with missing geographic information were discarded. All species occurrence records were compiled at a resolution of 5×5 km grid cells to accommodate the higher uncertainty in geographic coordinates of the older records relative to the higher location accuracy of the more recent records. Multiple observations for the same grid cell were reduced to one, in order to obtain only unique records per species per grid cell. To account for possible spatial autocorrelation between closely located species presence records, only presence locations that were separated from each other by at least one grid cell were used. A total of 28,494 presence records were obtained for the eight species, ranging from 656 to 10,645 records per species (Table 1).

2.3 | Environmental data

Current bioclimatic conditions related to temperature and precipitation at a grid size resolution of 5×5 km were obtained for Europe

from the WorldClim dataset (Hijmans, Cameron, Parra, Jones, & Jarvis, 2005). The bioclimatic variables represent annual trends in climatic conditions, seasonality and climate extremes, which may impact the reproduction and survival of vegetation (Hijmans et al., 2005). In addition, data on soil pH and topsoil organic carbon were obtained. These variables may directly constrain the establishment and development of vegetation (FAO, IIASA, ISRIC, ISSCAS & JRC, 2012). In order to avoid high collinearity between predictors and to avoid potential model overfitting from the 19 bioclimatic variables originally available, we selected a set of seven with pairwise absolute Pearson's correlation coefficients $<.75$ (Fig. S1). The selected seven bioclimatic and two soil variables were precipitation of the wettest quarter (mm), precipitation of the driest month (mm), precipitation seasonality (coefficient of variation), temperature seasonality ($SD \times 100$), mean temperature of the wettest quarter ($^{\circ}C$), minimum temperature of the coldest month ($^{\circ}C$), maximum temperature of the warmest month ($^{\circ}C$), top soil organic carbon (%) and soil pH ($-\log(H^+)$).

Downscaled climatic conditions for the time period 2070 (average 2061–2080) for RCP 2.6 and RCP 8.5 were obtained from the Coupled Model Intercomparison Project phase 5 (CMIP5) as presented by the Intergovernmental Panel on Climate Change (Stocker et al., 2013). The data were acquired from the Worldclim dataset (www.worldclim.org). The results of the different climate models may differ (Murphy et al., 2004; Pierce, Barnett, Santer, & Gleckler, 2009), so to account for their variability, an ensemble of average values from 14 different climate models for the RCP 2.6 and 8.5 was used (Table S1). Details on the different climate models are provided by Flato et al. (2013). The same set of bioclimatic variables as used for predicting current distributions was used to predict future distributions. The soil-related variables were assumed to be constant across time and were only used to delimit the potential distribution of the species under current and future conditions. All analyses were carried out in R (<https://www.r-project.org>) using the RASTER package.

2.4 | Species distribution modelling

We used an ensemble modelling approach based on a recent study comparing modelling algorithms and measures of model performance (Aguirre-Gutiérrez et al., 2013). The ensemble model was also used to account for the variability in model predictions obtained by different algorithms. For the ensemble approach, three modelling algorithms were selected, namely generalized linear models (GLM) (McCullagh & Nelder, 1989), MaxEnt (Phillips & Dudik, 2008) and Random Forest (Breiman, 2001). Single and quadratic terms were included for GLM, while linear and quadratic features were used for MAXENT to avoid overparameterization (Merow, Smith, & Silander, 2013). Five hundred trees were used for Random Forest. To account for the within-algorithm model variation when different sets of data are used for model fitting, we computed distribution models for each species using ten model repetitions with a bootstrap approach where 80% of the presence data were used for model training and 20% for model testing.

As real absence data were unavailable, randomly distributed pseudo-absences or background data (for MAXENT) in the study area were

generated (Barbet-Massin, Jiguet, Albert, & Thuiller, 2012). The importance of each environmental variable for driving the species distribution was evaluated through a correlation analysis between the originally obtained model and a model for which the values of the variable of interest were randomized across the species locations. The variable importance equals one minus the correlation value, with higher values indicating more important variables (Thuiller, Lafourcade, Engler, & Araújo, 2009).

From the 30 constructed models (three algorithms \times 10 model repetitions) per species, a final model ensemble was created using the median suitability score of the predictions. The median score was used because of the lower sensitivity to extreme values compared to other statistics such as the average score. Through this methodology, the most consistent model predictions of the species distribution can be captured as well as the within and between algorithm variation (Thuiller, 2014). The models' performance was assessed by the area under the curve (AUC) value (Hanley & McNeil, 1982). The obtained ensemble model was then used to predict species distribution under the future climatic conditions (RCP 2.6 and 8.5). All analyses were carried out in R (<https://www.r-project.org>) with the BIOMOD2 package (Thuiller et al., 2014).

2.5 | Species range shifts

To investigate possible range changes between the current and future distributions (RCP 2.6 and 8.5), the species ensemble models were converted to a presence/absence binary prediction using the threshold that maximizes their sensitivity and specificity (Jiménez-Valverde & Lobo, 2007). The range change was calculated as the percentage gain minus the percentage loss in species distribution range. Areal range changes were calculated for both a no dispersal and a full dispersal (no dispersal constrains) scenario. The latitudinal range shifts (north–south) were assessed using the centroids of the predicted (binary) present and future (RCP 2.6 and 8.5) species distributions and calculating the difference in latitudinal location (in kilometres). For these calculations, the directional distribution tool in ARCGIS (v10.1; ESRI Redlands, CA, USA) was used. Values of zero reflect no change in the centroid of a species range distribution, values above zero indicate range shifts towards northern locations and values below zero show range shifts towards the south. To evaluate the importance of nature reserves for the current and future species in situ conservation, we determined the degree of overlap between the present and future species distributions and the protected areas covered by the Natura 2000 network (Evans, 2012) and the Common Database on Designated Areas (CDDA) of protected European sites (European Environment Agency, 2017). Range shifts were evaluated under the assumption of unrestricted dispersal abilities of the investigated species. All analyses were carried out with the BIOMOD2 package (Thuiller et al., 2014).

3 | RESULTS

3.1 | Species representation in ex situ collections

The representation of wild or weedy accessions of European origin in ex situ collections in Europe varied among the study species, ranging

from 0 for *E. gallicum* to 504 for *M. polymorpha* (Table 2). Only for the latter species, a relatively high number of accessions was observed, mainly originating from southern European countries. Five of the eight study species were represented in EURISCO with <10 accessions and only three species presented information about their geographic collection location (Tables 2 and S2).

3.2 | Model performance and variable importance

Based on the present predictions of species distribution, all models showed high performance with AUC values of at least 0.95 and values for model sensitivity of at least 0.84 (Table 3). The included variables with the highest importance for driving the species distribution differed between species (Table 3). For the species *B. secalinus*, *E. gallicum*, *L. japonicus* and *S. humilis*, the two main variables were related to temperature, often to the temperature seasonality and to the maximum temperature of the warmest month (Fig. S2). Moreover, most species had higher projected suitability values on moderately seasonal environments and where the maximum temperature of the warmest month was between 20 and 25°C. For *M. polymorpha*, *M. pulegium*, *R. saxatilis*, *Valerianella rimosa*, the two main variables were related not only to temperature but also to precipitation, often related to the precipitation of the driest month (Table 3). However, the threshold at which each variable delimited the distributions varied per species, underpinning their adaptation to often dissimilar environmental conditions (Fig. S2).

3.3 | Species range changes

Range contractions were predicted for six of the eight study species under RCP 2.6 (optimistic scenario), ranging from almost 21% loss for *V. rimosa* to 61% for *B. secalinus* under the full dispersal assumption. Only *M. polymorpha* and *M. pulegium*, representing two of the most widely distributed study species under the current conditions, showed an increase in distribution area of almost 22% and 1%, respectively (Table 4). Under the no dispersal assumption, all species showed contractions, ranging from ~9% (*M. polymorpha*) to nearly 70% (*B. secalinus*) of their current predicted distribution. The range change analysis, assuming full dispersal, showed that the majority of the species experienced losses of suitable habitat in their southern locations, while remaining relatively stable in the central and northern parts of their distribution (Figure 1). All species, except for *L. japonicus*, showed shifts in their predicted centroid of distributional ranges of between 46 and 360 kilometres towards more northern locations under the optimistic scenario (Figure 2).

Except for *M. polymorpha*, all species showed more severe range contractions under RCP 8.5 (pessimistic scenario) both for the model with full dispersal and for the model with no dispersal. *B. secalinus*, *E. gallicum* and *V. rimosa* were predicted to lose more than 85% of their current distribution in Europe under RCP 8.5 and assuming full dispersal capacity. A similar loss was observed for *S. humilis* when assuming no dispersal capacity (Table 4). Under RCP 8.5, *M. polymorpha* is still expected to expand its range by around 22% when assuming

TABLE 2 Number of ex situ samples of the study species included in the search catalogue EURISCO with sample status denoted as wild or weedy and known origin country located in Europe

Country	<i>Bromus secalinus</i>	<i>Erucastrum gallicum</i>	<i>Lathyrus japonicus</i>	<i>Medicago polymorpha</i>	<i>Mentha pulegium</i>	<i>Rubus saxatilis</i>	<i>Scorzonera humilis</i>	<i>Valerianella rimosa</i>
Austria	5							
Bulgaria				4				
Croatia					1			
Cyprus				32				
Czech Republic (former) Czechoslovakia	1			7				
Denmark	2							
France	1			10	1		1	
Germany	1			4	1			
Great Britain	3		5	5				6
Greece				10				
Hungary				4				
Iceland			1			2		
Italy				46	1			
Norway	1							
Poland	4							
Portugal				67	1			
Romania	1							
Russian Federation	3		2	1				
Slovakia	7				1			
Spain				312	7			
Sweden	2		1					
Switzerland								1
Turkey				1				
Ukraine				1				
Total	31	0	9	504	13	2	1	7

full dispersal. Most species showed losses in the southern regions and mild expansions in northern locations as also observed for the optimistic scenario (Figure 1). Patterns in range shift were similar for the two climate change scenarios, but more drastic under the pessimistic scenario. For RCP 8.5 and assuming full dispersal capacity, a latitudinal shift in the centroid of distribution of at least 712 km towards the north was predicted for seven species assuming they track their suitable habitat. *L. japonicus* was the only species with slight shifts in its centroid of distribution towards the south, mainly as a result of northern range contractions (Figure 2).

3.4 | Role of protected areas

Under current environmental conditions, the predicted presence of the study species in the Natura 2000 and CDDA network of protected sites ranges from 10% (*M. polymorpha*) to 21% (*E. gallicum*) of the total predicted distribution area. Under RCP 2.6, the presence

of the eight CWRs in protected sites is predicted to decrease, often to less than half of the protected area under current conditions, such as observed for *B. secalinus* and *E. gallicum* (Table 5). This finding is even more severe under RCP 8.5. Under this pessimistic scenario, the expected occurrence of *B. secalinus*, *E. gallicum*, *S. humilis* and *V. rimosa* in protected areas reduces to 1.5%, 2.5%, 9.7% and 6.2%, respectively, of the predicted distribution in protected areas under current conditions (Table 5). However, *M. polymorpha* and *M. pulegium* are expected to expand their occurrence in protected areas under this pessimistic climate change scenario (Table 5). Our results indicate that effects of climate change on CWRs distribution patterns need to be analysed on a species-by-species basis, and that the present occurrence in protected areas does not provide any guarantee for future persistence. Moreover, following the information from EURISCO, only three (of the eight) species have been extracted for ex situ collections from inside European protected areas (Table S2).

TABLE 3 Evaluation scores, area under the curve (AUC) and sensitivity, for the species distribution ensemble models constructed and the importance value of each of the selected climatic and soil-related variables for SDMs of the modelled species. Importance values per variable can range from 0 to 1. The two highest importance values per species are italicized

	<i>Bromus secalinus</i>	<i>Erucastrum gallicum</i>	<i>Lathyrus japonicus</i>	<i>Medicago polymorpha</i>	<i>Mentha pulegium</i>	<i>Rubus saxatilis</i>	<i>Scorzonera humilis</i>	<i>Valerianella ramosa</i>
Evaluation metric								
AUC	0.97	0.98	0.99	0.97	0.98	0.95	0.98	0.99
Sensitivity	85.09	91.92	94.06	88.10	94.57	90.76	93.74	92.59
Environmental variable								
Precipitation of the wettest quarter	0.11	0.03	0.28	0.31	0.15	0.07	0.02	0.04
Precipitation of the driest month	0.15	0.20	0.08	0.16	0.07	0.14	0.04	0.48
Precipitation seasonality	0.08	0.04	0.15	0.21	0.28	0.09	0.11	0.04
Temperature seasonality	0.26	0.33	0.35	0.16	0.51	0.05	0.33	0.62
Mean temperature wettest quarter	0.03	0.14	0.01	0.01	0.01	0.02	0.02	0.01
Min. temperature coldest month	0.05	0.03	0.70	0.41	0.19	0.09	0.08	0.02
Max. temperature warmest month	0.32	0.27	0.97	0.03	0.17	0.65	0.26	0.17
Soil organic carbon	0.01	0.01	0.01	0.01	0.01	0.03	0.01	0.01
Soil pH	0.01	0.02	0.08	0.01	0.01	0.02	0.01	0.01

TABLE 4 Predicted range changes of the studied species for the 2070s in Europe based on climate change scenario RCP 2.6 and RCP 8.5, respectively. Range sizes are presented as the number of grid cells (2.5 arc-minutes resolution at the equator) in which the species was predicted to occur

Species	Current range	RCP 2.6		RCP 8.5	
		Range 2070	Range change % (FD)	Range 2070	Range change % (ND)
<i>Bromus secalinus</i>	71,231	27,706	-61.10	6,470	-97.17
<i>Erucastrum gallicum</i>	57,596	27,048	-53.04	5,479	-98.36
<i>Lathyrus japonicus</i>	62,396	42,435	-31.99	37,420	-58.32
<i>Medicago polymorpha</i>	102,834	124,961	21.52	125,857	-15.73
<i>Mentha pulegium</i>	111,894	113,430	1.37	98,437	-32.7
<i>Rubus saxatilis</i>	168,338	101,109	-39.94	67,695	-66.35
<i>Scorzonera humilis</i>	76,827	44,926	-41.52	25,590	-88.85
<i>Valerianella ramosa</i>	41,624	32,956	-20.83	5,428	-93.34

FD, Full dispersal capacity assumption; ND, no dispersal capacity assumption.

4 | DISCUSSION

4.1 | Areal range changes and latitudinal shifts of crop wild relatives

Previous studies have shown that the diversity of CWRs is not well represented in gene banks and that Western Europe is among the areas suffering from significant collection gaps (Castañeda-Álvarez et al., 2016; see also eurusco.ipk-gatersleben.de). These collection gaps represent a major challenge to genetic resource conservation given the current lack of knowledge about the impact of climatic changes on the future distribution of food crops and their CWRs (Brown & Funk, 2008; Ford-Lloyd et al., 2011). Our study shows

strong range contractions in Europe for most of the examined species under the two climate change scenarios and the two dispersal models. Moreover, shifts towards northern locations are predicted for most species independent of the climate change scenario considered. We also show that the predicted areal range changes and latitudinal shifts may severely reduce the presence of species within the European network of protected sites.

The predicted range changes for the analysed species are largely related to the expected changes in maximum temperature of the warmest month, temperature seasonality and the precipitation in the driest month (Table 3; Fig. S2). Such relationships can be expected as most of the analysed species are majorly distributed in temperate regions, which are expected to become warmer and drier as a result of

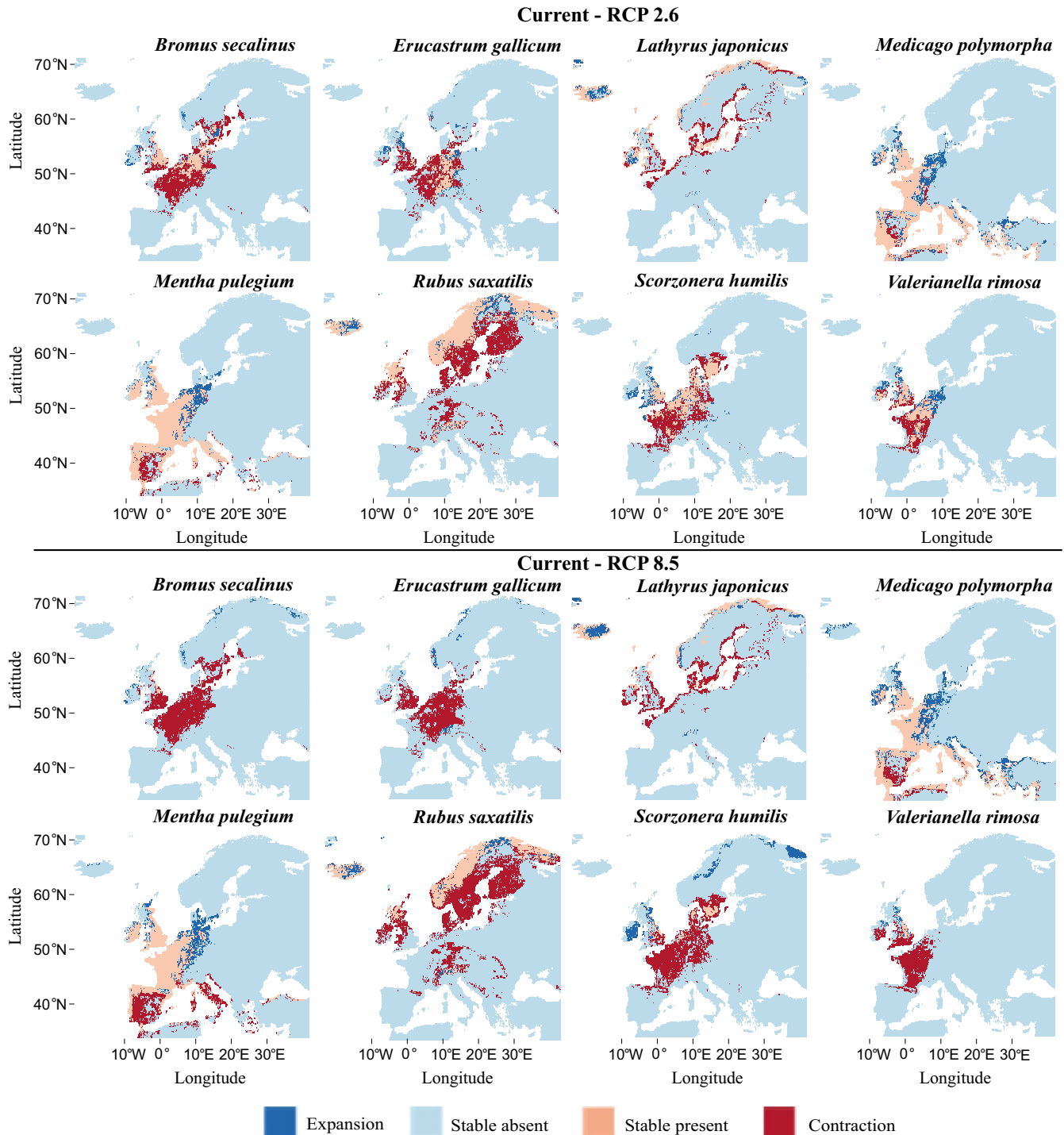


FIGURE 1 Predicted distribution area under climate change scenario RCP 2.6 (upper panel) and RCP 8.5 (lower panel) for the year 2070 as compared to current predictions. [Colour figure can be viewed at wileyonlinelibrary.com]

climate change, especially in southern Europe (Stocker et al., 2013). The increase in temperature in the current distribution area is expected to shift the species towards more northern areas where the conditions are expected to become more suitable in the future. Seven of the eight analysed species are expected to shift their centroid of distribution up to 500 km towards the north by the period 2070, mainly due to southern range contractions and range expansions in northern Europe under RCP 2.6 and even further north under RCP

8.5. However, as these results are based on the assumption of full dispersal, it remains uncertain whether species are actually capable of reaching new areas within the given timeframe. Limited dispersal abilities of species and natural barriers may call for assisted migration measures to facilitate range shifts (Minteer & Collins, 2010). In case of limited natural migration, we expect the future distribution ranges to be considerably smaller than predicted in the present study for the full dispersal model. As observed for the no dispersal model, all study

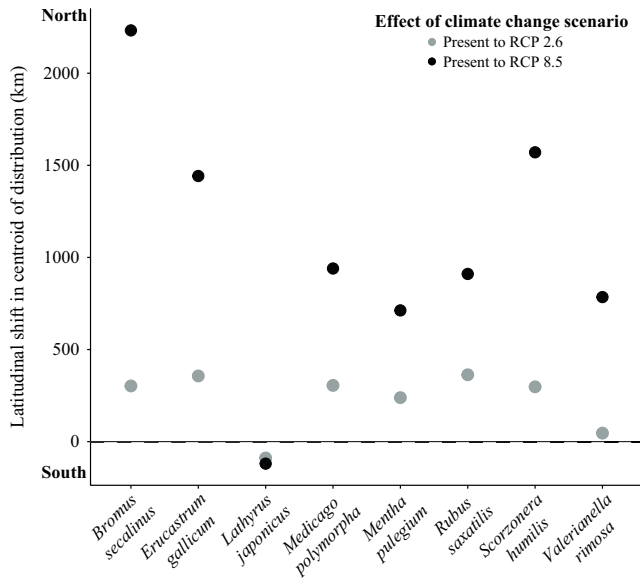


FIGURE 2 Comparison of the species latitudinal distribution between the current prediction and those under climate change scenario RCP 2.6 and RCP 8.5 for the year 2070, respectively, under the full dispersal capability assumption. Values above zero represent shifts towards the north and values below zero represent distributional shifts towards the south. [Colour figure can be viewed at wileyonlinelibrary.com]

TABLE 5 Predicted area included in the protected Natura 2000 network or Common Database on Designated Areas (CDDA) of protected sites in Europe for the eight crop wild relatives analysed. The protected area was predicted under current environmental conditions and under the climate change scenarios RCP 2.6 and RCP 8.5

Species	Area protected (km ²) ^a		
	Present	RCP 2.6	RCP 8.5
<i>Bromus secalinus</i>	144,132.91	44,724.13	2,160.45
<i>Erucastrum gallicum</i>	119,091.33	51,598.29	3,030.24
<i>Lathyrus japonicus</i>	58,276.05	30,498.82	28,338.37
<i>Medicago polymorpha</i>	125,053.61	169,062.27	172,962.30
<i>Mentha pulegium</i>	172,232.80	207,852.18	194,735.16
<i>Rubus saxatilis</i>	192,111.75	129,627.03	95,143.99
<i>Scorzonera humilis</i>	132,418.78	73,960.36	12,850.47
<i>Valerianella rimosa</i>	61,979.68	53,309.82	3,843.91

^aThe overlap analysis was carried out using the ETRS89 LAEA Europe geographic projection.

species experienced range contractions irrespective of the considered climate change scenario. Considering our finding that a large part of the current distribution area is expected to become unsuitable, this stresses the urgent need for conservation measures. As shown for the American and African continent, species extinctions as a result of climate change can be expected in the near future, in the absence of adequate in situ and ex situ conservation measures (Jarvis, Upadhyaya, et al., 2008; Ureta, Martínez-Meyer, Perales, & Álvarez-Buylla, 2012).

Apart from dispersal aspects, other population biological factors may play a role in the future distribution of species. Crop wild relatives may show high phenotypic plasticity, which means that species may be able to cope with higher environmental variation than expected based on observed distribution patterns (Merilä & Hendry, 2014). Moreover, the successful establishment of a species in new areas may depend on the interaction with other species occurring at suitable sites. In case of limited competitive abilities, migrating species may be out-competed by the indigenous species at new locations, preventing their establishment. Vice versa, the survival of indigenous flora may be jeopardized when migrating species possess strong colonizing abilities (Pyšek et al., 2012). A species may also rely on specific insects for its reproduction, which means that successful establishment at new locations depends on the presence or comigration of suitable pollinators. Largely due to the limited availability of data, species interactions are lacking from most modelling frameworks (but see Giannini, Chapman, Saraiva, Alves-dos-Santos, & Biesmeijer, 2013).

Species distribution modelling relies to a large extent on the quality of the input data and this includes the sampled species occurrences. The dataset used in the present study included a relatively low number of species occurrences from Eastern Europe. However, as most of the investigated species have their main distribution area in Western Europe, we expect to have covered most of their ecological niches. Evidently, predictions of future distributions as a result of climate change depend on which scenario will be the most likely in the forthcoming years. Here, we examined both an optimistic and pessimistic scenario to obtain insight in the expected range. The most likely climate change scenario for the next decades will highly depend on the outcome and implementation of international agreements regarding the emission of greenhouse gasses. In addition to the changing climate, also non-climatic factors, such as habitat destruction, will influence the future distribution of species.

Notwithstanding the uncertainties related to niche modelling and future climate change scenarios, it remains undisputed that the climate is changing and that this will impact the distribution and survival of species. Considering the importance of wild relatives for crop improvement, we cannot afford to await actual distribution changes and associated loss of diversity. Instead, we need to anticipate the changes by developing sound conservation strategies.

4.2 | Implications for conservation

Despite their importance for plant breeding, many CWRs are poorly represented in ex situ collections. This was also observed for the species examined in the present study, with the exception of *M. polymorpha* that showed a relatively large number of accessions included in EURISCO, albeit that its distribution area in Central Europe was relatively undersampled. Only five of the identified accessions of the study species were denoted in EURISCO as being part of the Multilateral System (MLS) of the International Treaty on Plant Genetic Resources for Food and Agriculture, while only a single accession was denoted as being conserved in the European Genebank Integrated System (Engels & Maggioni, 2011). Therefore, it remains to be

determined how many of the accessions of the study species included in EURISCO are actually unique, properly conserved and available for distribution. Considering the low representation in European ex situ collections, the uncertainties regarding conservation status and the expected loss of large parts of the European distribution area due to climate change, a high sampling priority for ex situ conservation is recommended for *B. secalinus*, *E. gallicum*, *L. japonicus*, *R. saxatilis*, *S. humilis* and *Valerianella rimosa*. The methodology for the selection of taxa and geographical areas with highest priority for conservation could be enhanced by the use of a gap analysis approach as that presented by Ramírez-Villegas, Khoury, Jarvis, Debouck, and Guarino (2010) to better identify the gaps in CWR gene pools in ex situ collections.

Protected areas are considered suitable habitats to safeguard biodiversity against direct human impacts. However, their efficacy for long-term conservation has been questioned (but see Maxted, 2008) as the changing climate may cause environmental changes and species shifts towards other locations (Beale, Baker, Brewer, & Lennon, 2013). Current protected areas may facilitate species range expansions under climate change by acting as stepping stones that facilitate colonizations at the leading edge of the species distribution. In the case of the study species, the fact that for most of them only few accessions of ex situ collection exist and that only three species have been collected from inside protected areas (see Table S2) may suggest a lack of protection for these genetic resources in face of future environmental changes. To maintain the role protected areas carry out, they should be of sufficient size and provide a large variety in suitable habitats (Thomas et al., 2012). Moreover, for protected areas to work as in situ reservoirs of CWR, one of their main considerations should be to preserve the species genetic diversity based on the development and implementation of a set of sound management and conservation plans (see Iriondo et al., 2012).

In Europe, the Natura 2000 and CDDA network of protected sites currently covers over 25% of the EU's land territory. Although not all human activities are excluded from these sites, the network provides a sustainable approach for biodiversity conservation (European Commission, 2016). While at least 10% of the distribution of the analysed species is predicted to be within protected areas under current conditions, climate change, especially under RCP 8.5, is expected to reduce this representation for most species. Thus, current protected areas are no guarantee for future species survival. Species may even go extinct on a regional scale, such as predicted for *B. secalinus* and *R. saxatilis* in the Netherlands (Figure 1). Therefore, our results call for the application of national-level CWR genetic resources protection strategies that encompass in situ and ex situ conservation programmes. The adopted national-level conservation strategies should not be forgotten as it is first of national interest to conserve the genetic resources that are fundamental for food security (see Phillips et al., 2017). Moreover, we also show the need of applying an integrated transnational conservation strategy for important CWRs as that presented by the European Cooperative Programme for Plant Genetic Resources (ECPGR, Maxted et al., 2015). This strategy should not only encompass in situ conservation measures in protected areas (Meilleur & Hodgkin, 2004) but also ex situ conservation measures to guarantee the survival of these genetic resources.

To allow for the development of effective conservation strategies, more insight in the probability of survival of CWRs in their natural habitats under climate change conditions is needed. Therefore, the impact of climate change on the distribution of CWRs that may be used to improve the adaptation of crops to environmental changes, as climate change, should be determined. This approach should be combined with long-term monitoring programmes. This is especially important for rare and narrowly distributed species that due to their small range size and limited data availability are not well suited for range change analyses. Based on the outcome, genetic reserves can be identified where relatively stable populations occur (Maxted et al., 2015). For all species that appear vulnerable, seed samples should be collected and stored ex situ as backup collections to secure the option of future restoration and use. The preservation of these genetic resources is of primary importance as CWRs are valuable genetic resources that will help to improve our crops (Dempewolf et al., 2014; Nevo & Chen, 2010).

5 | CONCLUDING REMARKS

Our study predicts substantial changes in the distribution of eight CWRs in Europe for the 2070s based on two climate change scenarios. These changes include pronounced range contractions and range shifts towards northern areas for most of the studied species. These changes can be expected to result in loss of genetic diversity. We therefore suggest to investigate the impact of climate change on CWRs and to combine the results with long-term monitoring programmes and collecting of CWRs for ex situ backing up. These backup collections will secure the option of future restoration of wild populations and the use of these valuable resources in research and plant breeding.

ACKNOWLEDGEMENTS

This study was part of the Fundamental Research Programme on Sustainable Agriculture (KB-21-004-001) funded by the Dutch Ministry of Economic Affairs. The authors thank Tomas Vaclavik and two anonymous referees for their constructive comments that greatly improved this article.

AUTHOR CONTRIBUTIONS

J.A.G., R.V.T., R.H., T.V.H. conceived and designed the analyses. J.A.G. and R.H. gathered the data and prepared it for the analyses. J.A.G. performed the analyses and together with all other authors interpreted the results. The text was drafted by J.A.G. and R.V.T., and all other authors provided corrections to manuscript drafts and discussed ideas within it.

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BIOSKETCH

Jesús Aguirre-Gutiérrez (jesusaguirregutierrez.myfreesites.net) is interested in the effects that environmental changes, as climate and land-use modifications, have on the species distributions across time and space. He is also interested in the application of remote sensing techniques for biodiversity conservation. The team of authors is interested in the crop wild relative genetic resources and how these resources are affected by global change.

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

How to cite this article: Aguirre-Gutiérrez J, van Treuren R, Hoekstra R, van Hintum T.J.L. Crop wild relatives range shifts and conservation in Europe under climate change. *Diversity Distrib.* 2017;23:739–750. <https://doi.org/10.1111/ddi.12573>