

Estimation of the Climate Preference Between Two Lineages of European Ground Squirrel Using Maximum Entropy Modeling

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Abstract – *Spermophilus citellus* (Linnaeus, 1766), commonly referred to as the European ground squirrel, exists in specific areas of Central Europe and the Balkans. The species is currently listed as “vulnerable” on the IUCN Red List of Threatened Species. Recently genetic studies have shown that the species has two main lineages; the *northern* and the *southern*. The *northern* lineage shows distribution range at the central and western part of the Balkans and Central Europe, whereas the *southern* lineage is spread in a more limited area, which includes the southern and eastern parts of the Balkans. The purpose of this study is to reveal the potential geographic distribution in Last Glacial Maximum (approximately 22 kya), present and future (average 2070) periods of these lineages using Maximum Entropy modeling (MaxEnt). This study also contributes to comparing the distribution of two lineages between past, present and future periods. The final MaxEnt with ten replicate runs was constructed based on 80 occurrence records from Austria, Bulgaria, Czech Republic, Greece, Hungary, Slovakia, Serbia, Macedonia, Moldova, Romania, Turkey and Ukraine, and twelve abiotic bioclimatic variables obtained from WorldClim. Thus, it was attempted to estimate the importance of bioclimatic factors influencing the potential geographical distribution for each lineage as well as assessing the area under curve values. This study showed that the two lineages of the European ground squirrel had different geographic distribution patterns for past, present and future periods. Moreover, the study will make important contributions to conservation studies such as management strategies, species action plans and translocation.

Keywords – Climatic preference, ecological niche modeling, European ground squirrel, geographic distribution, maxent, jack-knife test

1. Introduction

The Quaternary period witnessed many climatic and environmental changes at different stages until today. The current distribution of European species was shaped by the consecution of the glacial and interglacial periods in the Quaternary during which a large part of northern Europe was covered by ice (Hewitt, 2000). A large part of the area above 40° in Europe was covered by broad terrestrial ice-sheets at a temperature of about 10° C lower than today’s (Birks & Willis, 2008). Because of the changing ice sheets and ocean currents, the geographic ranges of the animal species were affected across Europe and Asia especially during the Last Glacial Maximum (LGM) (Peltier, 1994; Pollard & Thompson, 1997). LGM probably pushed many terrestrial species to survive in refugial areas in the Mediterranean peninsula. It is predicted that the European continent had three classical southern refugia in the Mediterranean (Iberian, Italian and Balkan) which made significant contributions to the re-colonization of northern Europe (Hewitt, 2000; Stewart et al., 2010). From these areas, the Balkan refugial area is undoubtedly the most effective in the re-population of eastern and western parts (Hewitt, 1996; 2000). Moreover, an area called “cryptic northern refugia” has been identified based on fossil and genetic evidence in northern Europe; this refugium had many different ecological characteristics from the South (Stewart & Lister, 2001; Stewart et al., 2010).

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Ecological niche modelings (ENM) are correlative approach methods that are used to predict the distribution of a species or evolutionary lineage across a given geographic area and time using bioclimatic variables or other variables such as soil type and wind speed. These methods are based on the fact that the localities where the species lives are known, the potential distribution area at unsampled locations of that species in the past, present, or future can be inferred by using environmental variables (Peterson et al. 2002; Hijmans & Graham, 2006; Elith et al., 2011). In recent years, ENM has been widely used in scientific fields such as conservation biology, ecology, phylogeography and evolution (Gür, 2013; Tzvetkov & Koshev, 2016; Zaharia et al., 2016; Gür et al., 2017; Qiao, Escobar, & Peterson, 2017). The information obtained from ENM is important for the protection of endangered species and the prevention of habitat loss (Guisan et al., 2013). The Maximum Entropy Algorithm (MaxEnt, Phillips et al., 2004, 2006, 2017a,b) is a presence-background method and is one of the most preferred methods for relating species records to bioclimatic variables (Elith et al., 2011). The algorithm is among the top-performing methods in terms of prediction accuracy and may remain effective despite small sample sizes (Pearson et al., 2006; Elith et al., 2006; Wisz et al., 2008).

Presently the European ground squirrel, *Spermophilus citellus* is spread from central to south-eastern Europe, but its distribution area is divided into two main geographical areas by the Carpathian Mountains (Kryštufek, 1999; Wilson & Reeder, 2005; Coroiu et al., 2008; Matějů et al., 2010). Phylogeographic studies focusing on individuals representing a large part of the distribution range of the species indicate that the European ground squirrel has two major genetically independent lineages with seven sublineages (Gündüz et al., 2007; Kryštufek et al., 2009; Říčanová et al., 2013). The *northern* lineage includes individuals from Austria, Bulgaria, Czech Republic, Slovakia, Hungary, Serbia, Macedonia, Moldova, Romania and Ukraine and the *southern* lineage consists of individuals from Bulgaria, Greece, Southern Macedonia, Romania and the European part of Turkey (Thrace). These lineages show sympatric distribution within a restricted area in Central and Eastern Bulgaria.

Říčanová et al. (2013) emphasized that the separation time of the *northern* and *southern* lineages dates back to the middle Pleistocene period (1.31-1.79 million years ago). Moreover, they proposed possible scenarios based on phylogenetic and biogeographical analyses about the ancestral areas of these lineages. According to these scenarios, Serbia and Macedonia haplotypes represent the oldest *S. citellus* population to the west of the Carpathians. Paleontology also supports the appearance of to the west of the Carpathians in Central and Western Europe in the Gunz glacial of Austria (c. 750 kya, Kurten, 1968). The other haplotypes colonized large areas during several later. The *southern* lineage originated probably in southeast Bulgaria and first colonized the European part of Turkey. The oldest species record is from the Yarimburgaz Cave in the European part of Turkey and is dated back to 1.323-0.885 Ma (Santel & von Koenigswald, 1998; Fortelius, 2011). Furthermore, the area around the Carpathian mountains has been a refuge area for many mammalian species (Benda & Ivanova, 2003; Mráz & Ronikier, 2016; Savić, Ćirović, & Bugarski-Stanojević, 2017) and is known to be an important source of genetic diversity, during the Quaternary period (Hewitt, 2000).

Until recently the European ground squirrel occurred in very large numbers in steppe and pasture areas with discontinuous shrubs and trees up to 2,500 m above sea level (Kryštufek & Vohralík, 2005; Popova et al., 2019). The population size of the European ground squirrel decreased rapidly due to high death rates caused by habitat fragmentation and anthropogenic effects such as agricultural and industrial activities (Zaharia et al., 2016). Today, the population has become fragmented, and even disappeared from peripheral parts of its previous range, as in Germany, Poland and Croatia (Coroiu et al., 2008). Therefore, action plans and reintroduction and conservation projects were prepared in different European countries where the species has been extinct (Balaz, Jancova, & Ambros, 2008; Matějů et al., 2010; 2012; Gedeon et al., 2011, 2012; Janák, Marhoul, & Matějů, 2013; Löbbová & Hapl, 2014; Koshev et al., 2019). As a result, *S. citellus* has been a protected species within the European legislation under the Bern Convention and EU Habitats and Species Directive. Moreover,

S. citellus is currently listed as “vulnerable” on the International Union for Conservation of Nature and Natural Resources Red List of Threatened Species (Coroiu et al., 2008).

Recently, ENM, fossil and molecular studies have focused on several ground squirrel species about their likely responses to global climate change (Musil, 1985; Gür, 2013; Řičanová et al. 2013; Gür et al., 2017). In these studies, they were tried to predict the responses of the species to global climate changes during glacial-interglacial cycles. The ENM's results in the past periods suggested that the range limit of *S. xanthoprimum* expanded rather than contracted throughout the glacial periods and contracted rather than expanded throughout the interglacial periods (Gür, 2013), contrary to the classical paradigm. Moreover, the results in the present period revealed that annual precipitation and temperature affect the geographical distribution of the species as well as plant productivity. But the *S. taurensis* showed a different geographical displacement. The results demonstrated that the species survived throughout Late Quaternary glacial-interglacial cycles by altitudinal migrations without a large range change movement (Gür et al., 2017). Furthermore, the present analysis result suggested winter temperature and precipitation affect the range limit of the species. These analyses revealed that as warming continues, the potential distribution of species will continue to shift towards higher altitudes, and its range area will be restricted in the future. In another study, the fossil record of *S. citellus* indicated that it had a wider distribution during the Pleistocene glacial periods than in the interglacial periods (Musil, 1985). Therefore, the current distribution of the species is restricted, which suggests that the European ground squirrel responds to global climatic changes along the oceanic–continental gradient (Stewart et al., 2010). Also, the continental refugia concept has been supported by molecular studies (Řičanová et al. 2013).

ENM can be an effective tool in identifying suitable habitats for the European ground squirrel (Zaharia et al., 2016; Tzvetkov & Koshev, 2016). Some climate differences observed among the modern geographic distribution of the northern and southern lineages indicate that climate is one of the main determinants of the presence of *S. citellus* in an area. Therefore, this study aims to find answers to the following questions by using niche analysis based on bioclimatic data.

- i) How was the potential distribution of *S. citellus* in central Europe and the Balkans in the Last Glacial Maximum?
- ii) Is the geographical distribution obtained from ENM of the species throughout the Late Quaternary period compatible with the continental gradient refugia concept, which is also supported by fossil evidence?
- iii) Which areas were potentially suitable habitats for *S. citellus* lineages?
- iv) What are the potential distribution areas, bioclimatic variables and their contribution values affecting the distribution of *S. citellus* today?
- v) Will the future distribution of *S. citellus* change compared to its current distribution?
- vi) How will *S. citellus* adapt to future climate change?
- vii) Can ENM improve the success rate of reintroduction and conservation projects on *S. citellus*?

2. Materials and Methods

2.1. Species Data

Known presence occurrence and translocation records of *S. citellus* were compiled from different resources including Katona, Váczi, & Altbäcker (2002); Harrison et al. (2003); Gündüz et al. (2007); Youlatos et al. (2007); Balaz, Jancova, & Ambros, 2008; Hoffmann, Turrini, & Brenner (2008); Hulová & Sedláček (2008); Koshev (2009); Kryštufek et al. (2009); Matějů et al. (2010, 2012); Gedeon et al. (2011), Řičanová et al. (2011, 2013); Haberl, Kryštufek, & Hoffmann (2012); Baltag et al. (2014); Löbbová & Hapl (2014); Diakou, Kapantaidakis, & Youlatos (2015); Barkaszi & Zagorodniuk (2018); Koshev et al. (2019); the Global Biodiversity Information Facility website (www.gbif.org) and field observations (Figure 1). From these records, locations of molecular-based studies were selected and georeferenced to ensure the precision of the data using Google Earth, version 7.1 (<http://www.google.com/earth>) and DIVA-GIS, version 7.5 (www.diva-gis.org) and the data set used in this study was constructed based on the sublineages (northern and southern)

characterized by mtDNA cytochrome *b* gene of *S. citellus*. Multiple presence records were spatially filtered and randomly removed within 20 km distance to correct sampling bias and ensure high geographical heterogeneity (Pearson et al., 2006; Fourcade et al., 2014). Geographic Distance Matrix Generator version 1.2.3 ([http:// biodiversityinformatics.amnh.org](http://biodiversityinformatics.amnh.org)) was used to calculate the spatial geographic distance among localities. Thus, 59 records for the *northern* lineage from nine countries (Austria, Bulgaria, Czech Republic, Hungary, Macedonia, Moldova, Romania, Serbia and Slovakia) and 21 records for the *southern* lineage from five countries (Bulgaria, Greece, Macedonia, Romania and Turkey) were used in this study.

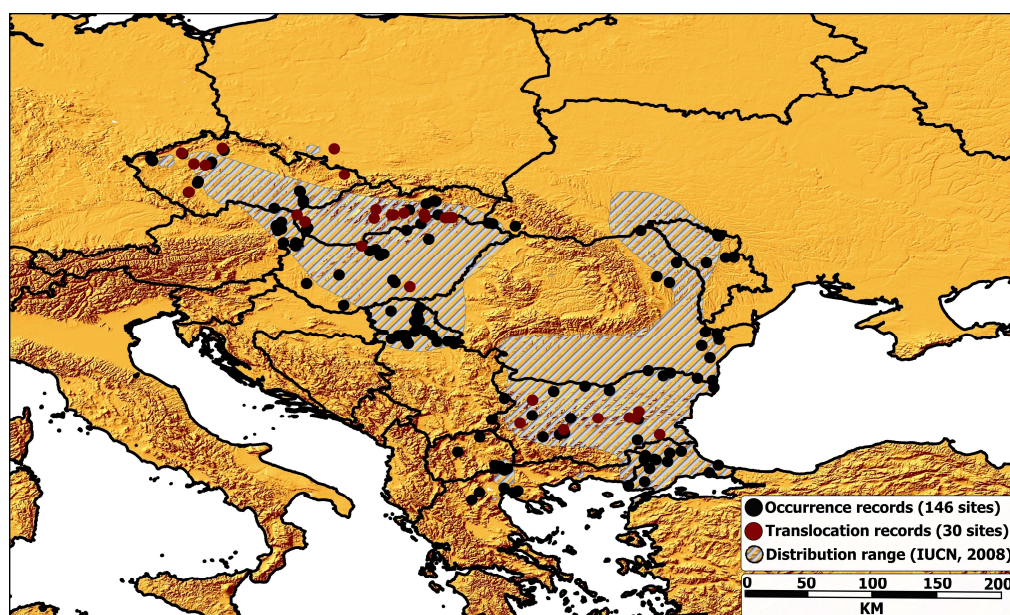


Figure 1. Map of known occurrence and translocation records of the European ground squirrel.

2.2. Bioclimatic Variables

19 bioclimatic variables were downloaded from WorldClim Version 1.4 (<http://www.worldclim.org/>) with a high resolution of 1x1 km (30 arc seconds) for the past (LGM, approximately 22 kya), the present data (1950-2000) and future (average 2070) under the RCP 4.5 emissions scenario (Hijmans et al., 2005). LGM data was based on two Global Climate Models (CCSM4: The Community Climate System Model and MIROC-ESM: The model for Interdisciplinary Research on Climate). Future data was also based on the above Global Climate Models with only presentative concentration pathways (RCP 4.5) predicting climate change emission scenarios. The downloaded file format was GeoTIFF. All these variables were masked to include only 09° to 37°E and 37° to 58°N. Variables which were highly correlated with each other were removed using Pearson correlation coefficients ($r > 0.85$) by the SDM toolbox, version 2.4 (Brown, 2014; Brown, Bennett, & French, 2017) to eliminate multicollinear variables, which can lead to overfitting problems (Dormann et al., 2013; Feng et al., 2019). GeoTIFF raster files were converted to ASCII format using SDM toolbox in ArcGIS version 10.2 (<https://www.esri.com>). Other file conversions and data processing was conducted using ArcGIS (<https://www.esri.com>) and DIVA-GIS software. Consequently, a dataset including twelve bioclimatic variables was selected to reveal the niche modeling of the European ground squirrel. MaxEnt version 3.4.1 (Phillips et al., 2006; 2017 a,b) was used for calculating the average of the area under the receiver operator curve (AUC), as well as for assessing the contribution of the environmental variables. In addition, Jack-knife testing was used to assesses the contribution of each environmental variable to the model. MaxEnt settings were logistic output format, 10 random replicate analyses with cross-validation method, minimum training presence threshold, random seed and fade by clamping subsets; all other options were left on default. The AUC is widely used to estimate the predictive accuracy of the developed model (Hanley & Mcneil, 1982). The AUC

has values that typically range from 0.5 to 1, where 1 indicates high performance while 0.5 indicates low performance (Luoto et al., 2005; Elith et al., 2006). If the AUC values are more than 0.80, the constructed model is applicable (Swets, 1988) but if these are less than 0.5, then the model fits worse than a random one (Engler, Guisan, & Rechsteiner, 2004). The AUC values with 10 replicate runs were calculated separately for the *northern* lineage, the *southern* lineage, and the combined data.

3. Results and Discussion

The average test AUC values of the constructed model with 10 replicate runs based on default setting in MaxEnt software showed high accuracy in all distribution areas of *S. citellus*. All AUC values detected in this study were higher than 0.80, indicating that the model was reliable. These values are shown in Table 1. The 12 bioclimatic variables predicting the present potential distribution of *S. citellus* are given in Table 2 together with their contribution values. The results of the Jack-knife test supported the MaxEnt results for whole species' range, *northern* lineage and *southern* lineage (Supplementary material, Figure S1-3).

Table 1

AUC values and standard deviation for whole species' distribution and sublineage's distribution models

Model	AUC	AUC stdv.
<i>northern</i> lineage	0.944	0.005
<i>southern</i> lineage	0.981	0.007
whole species' range	0.934	0.008

Table 2

Percentage contribution (Pc) and permutation importance (Pi) values of bioclimatic variables used for predicting the present potential distribution of *S. citellus*

Bioclimatic variable	<i>Northern line-</i> <i>age</i>		<i>Southern line-</i> <i>age</i>		Combined data	
	Pc (%)	Pi (%)	Pc (%)	Pi (%)	Pc (%)	Pi (%)
Annual mean temperature (Bio 1)	0.0	0.5	0.2	0.0	0.6	0.2
Mean diurnal range (Bio 2)	27	35.8	2.1	0.1	28.4	24.4
Temperature annual range (Bio 7)	10.6	17	10.1	3.0	9.8	15.5
Mean temperature of wettest quarter (Bio 8)	20.6	6.3	6.0	0.4	10.9	4.3
Mean temperature of driest quarter (Bio 9)	18.6	2.9	33.5	0.4	8.8	3.7
Mean temperature of warmest quarter (Bio 10)	2.1	5.2	6.8	3.5	4.3	8.9
Mean temperature of coldest quarter (Bio 11)	7.7	1.4	11.2	2.5	13.6	4.3
Annual precipitation (Bio 12)	1.7	1.3	1.8	1.6	11.2	10.7
Precipitation of wettest month (Bio 13)	0.5	0.5	6.4	1.8	1.0	2.0
Precipitation of driest quarter (Bio 17)	1.0	5.3	12.2	5.2	6.6	7.9
Precipitation of warmest quarter (Bio 18)	4.8	9.3	9.3	80.8	0.9	9.3
Precipitation of coldest quarter (Bio 19)	5.3	14.4	0.5	0.7	3.9	8.9

Although habitat information and ecology of the species was extensively researched in previous studies (Váczí & Altbäcker, 1999; Hoffmann et al., 2003; Kryštufek & Vohralík, 2005; Özkurt et al., 2005; Matějů et al., 2008; Janderková et al., 2011; Ramos-Lara et al., 2014), there has not been a clear distinction between the lineages. In contrast to previous studies, this study aimed to determine the particular niche requirements for each of the lineages based on bioclimatic data. The raw output of the MaxEnt, which is a continuous prediction

of environmental variables of certain geographical locations, was completed for *S. citellus* for three different time periods (the LGM, the present, and the future). The MaxEnt prediction for the present period (Figure 2A, Figure 2B and Figure 2C) nearly matched with the known geographical distribution of the European ground squirrel, suggesting that the distribution is probably closely linked to climatic conditions. The present period analysis also showed that the known geographical distribution of the European ground squirrel highly overlaps with previous studies (Kryštufek, 1999; Hoffmann et al., 2003; Wilson & Reeder, 2005; Gündüz et al., 2007; Coroiu et al., 2008, Kryštufek et al., 2009; Matějů et al., 2010; Řičanová et al., 2011; 2013; Tiryaki, 2015). However, MaxEnt results indicate the presence of other suitable habitats, particularly in Macedonia and western Greece. It seems that there are still localities waiting to be discovered for *S. citellus*. It is also known that there are no populations of *S. citellus* among climatically suitable areas including Poland, Germany, the Italian peninsula, the Crimean Peninsula, and the north-western Anatolia.

For the present period, the highest bioclimatic parameter (the percentage contribution or permutation importance) for the *northern* lineage and the whole species' range were the mean diurnal range (Bio 2). Bio 2 can help provide information pertaining to the relevance of temperature fluctuation for different species (O'Donnell & Ignizio, 2012). The value of this parameter can well reflect the climatic characteristics of a geographic area. If the mean diurnal range is relatively large, it implies that there are relatively high temperature and powerful sunlight during the day in region. The high temperature and the powerful light is conducive to plant photosynthesis and productivity thereby affecting life characteristics such as body mass, reproductive success, and survival of ground-dwelling squirrels (Van Horne, 2003). Also, the two parameters for the *southern* lineage were the mean temperature of the driest quarter (Bio 9) and the precipitation of warmest quarter (Bio 18). Bio 9 and Bio 18 provide mean temperatures and total precipitation during the driest and warmest three months of the year, which can be useful for examining how such environmental factors may affect the seasonal distribution of the species. Here, two parameters imply the summer temperature and precipitation which contribute to plant productivity and therefore to the nutrition of the species. These results also indicate that the *southern* lineage prefers arid and dry areas. Moreover, the *northern* lineage prefers to be present in areas where 'annual mean temperature' is between 5.49-11.89°C (approximately 9.74°C), and 'annual precipitation' is between 428-847 mm (approximately 597 mm). In contrast, the *southern* lineage prefers to be present in areas where 'annual mean temperature' is between 10.68-16.14°C (approximately 13.12°C), and 'annual precipitation' is between 438-703 mm (approximately 573 mm). These results support that the northern and southern lineages have adapted to different climatic conditions. This information is a good criterion in selecting suitable areas for translocation studies such as reinforcement and reintroduction. Thus, this study will help researchers to determine the areas where action plans and conservation project can be implemented to ensure the continued existence of the species.

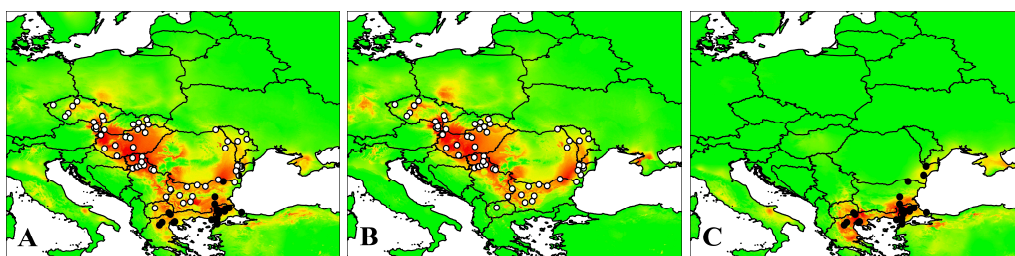


Figure 2. The MaxEnt modeling prediction for the present period (A. combined data, B. *northern* lineage, C. *southern* lineage). The open circle shows the occurrence records of the *northern* lineage, and the closed circle shows the occurrence records of the *southern* lineage

The combined data shows a potential distribution area between the latitudes of 39° to 53°N, and longitudes of 13° to 30°E throughout Europe (Figure 2A). The MaxEnt results also show that the *northern* lineage has a

potential distribution area between the latitudes of 41° to 53°N, and longitudes of 11° to 3°E in middle Europe (Figure 2B), whereas the *southern* lineage has a potential distribution area between the latitudes of 39° to 46°N, and longitudes of 21° to 29°E in the Balkan region (Figure 2C) under the present climatic conditions. However, the distribution map provided by the IUCN shows that *S. citellus* is distributed between the latitudes of 40° to 51°N, and longitudes of 13° to 29°E in Europe. That is, the IUCN coordinates are slightly different from predictions from this study. The results show that the potentially suitable climatic distribution of two *S. citellus* lineages is likely to expand under present climate scenarios, indicating that more suitable habitats will be available for the introduction and reintroduction of the species. These results are consistent with previous studies (Gür, 2013; Gür et al., 2017; Stojak et al., 2019). Nevertheless, it should not be ignored that species distributions are affected by complex dynamics (e.g. microclimate, competition, anthropogenic factors) as well as bioclimatic parameters acting on the distribution area.

The boundaries of the distribution of suitable geographic areas for *S. citellus* throughout central Europe and the Balkans, suggested by CCSM and MIROC paleoclimatic models, cover a more obvious wide area compared to the present period. This area is particularly noticeable in regions including Germany, the Czech Republic, and Romania. The MIROC model predicts (Figure 3A.2 and Figure 3B.2) more areas to be suitable than the CCSM model (Figure 3A.1 and Figure 3B.1) for the combined data and the *northern* lineage, but does not predict the same for the *southern* lineage (Figure 3C.2). Similarly, the western coast of the Black Sea is not predicted as a suitable area for the geographic distribution of the *southern* lineage, especially in the CCSM model (Figure 3C.1). Additionally, both models show that the *northern* lineage extended almost to the central regions of Germany, but did not reach Poland. These results are similar to those of Musil (1985) who suggest that the glacial periods were wider than the present interglacial period, and support “cryptic northern refugia” hypothesis for temperate species.

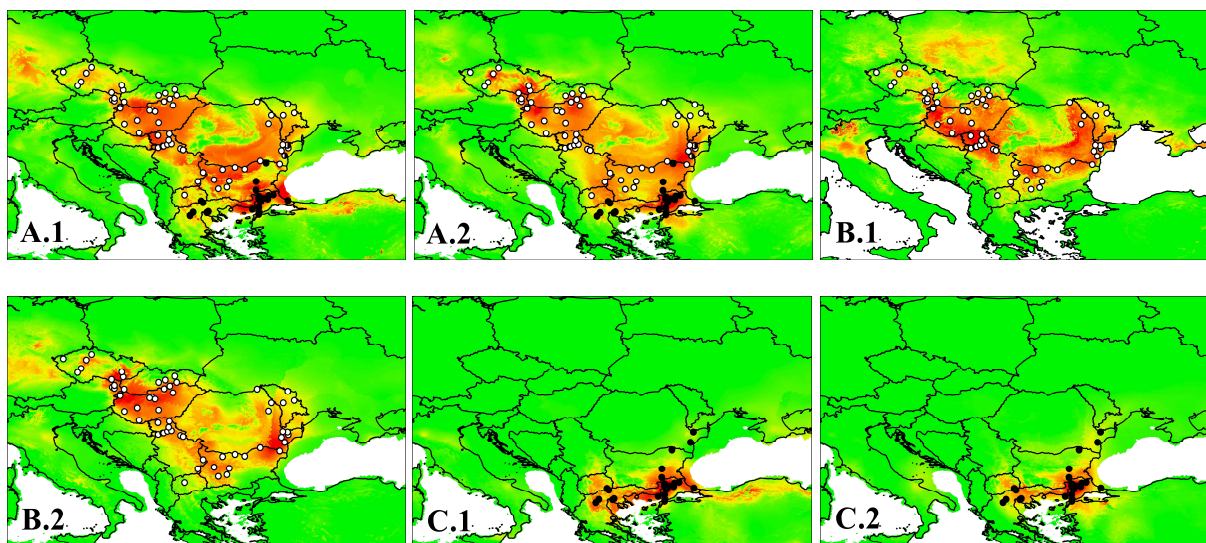


Figure 3. The MaxEnt modeling prediction for the LGM period (A.1. combined data with CCSM model, A.2. combined data with MIROC model, B.1. *northern* lineage with CCSM model, B.2. *northern* lineage with MIROC model, C.1. *southern* lineage with CCSM model, C.2. *southern* lineage with MIROC model).

MaxEnt predictions suggest two hot spots for the *northern* lineage at the Pannonian basin and the south-eastern part of the Carpathian Mountains. These regions probably refer to the most extensive suitable habitat areas during the LGM period (Figure 3B.1 and Figure 3B.2). The area around the Carpathian Mountains provided somewhat more temperate climatic conditions than the northern latitudes and formed two refuge areas for the *northern* lineage. These regions also contain unique fauna and flora elements today (Stewart & Lister, 2001; Stojak & Tarnowska, 2019). On the other hand, MaxEnt shows that the *southern* lineage occupies a single

hotpoint area around Bulgaria and European Turkey (Figure 3C.1 and 3C.2). This region includes the lowland Thrace, Rhodopes and Istranca Mountains and, also has many indigenous plant and animal species today (Petrova & Vladimirov, 2010; Valchovski & Mısırlıoğlu, 2017; Kryštufek et al., 2018). Moreover, these regions were also indicated as ancestral areas for the origin of the *S. citellus* lineages identified by Říčánová et al. (2013).

Interestingly, even though central Macedonia contained more suitable habitats for the *southern* lineage compared to the *northern* lineage, phylogenetic analysis indicated that the Macedonian sublineage was part of the *northern* lineage in LGM. It appears that this sublineage settled in this region much earlier than the *southern* lineage. This inference confirmed the molecular clock hypothesis that the separation of the sublineage within the *northern* lineage started between 0.80 and 1.10 million years ago (Říčánová et al., 2013). Conversely, north-eastern Bulgaria and south-eastern Romania contained more favorable habitats for the *northern* lineage compared to the *southern* lineage in LGM. Presumably, this spectacle suggests that the *southern* lineage began to settle in these regions immediately after the LGM period. Moreover, the phylogenetic analyses (Říčánová et al., 2013) which include samples from this region show that sublineages within the *northern* lineage furcated approximately 0.45 million years ago, while sublineages within the *southern* lineage furcated approximately 0.34 million years ago.

The combined data show a potential distribution area between the latitudes of 38° to 51°N and longitudes of 14° to 30°E throughout Europe (Figure 4A.1 and Figure 4A.2). The MaxEnt results also show that the *northern* lineage will have a potential distribution area between the latitudes of 41° to 52°N and longitudes of 10° to 29°E in central Europe (Figure 4B.1 and Figure 4B.2), and the *southern* lineage will have a potential distribution area between the latitudes of 38° to 45°N and longitudes of 20° to 28°E in the Balkan region (Figure 4C.1 and Figure 4C.2) under future climatic conditions. According to these results, the future potential distribution density of the *northern* lineage is likely to have a more fragmented structure compared to today. This indicates that the *northern* lineage is highly sensitive to the intensity of climate change. Thus, it can be predicted that the number of suitable habitats and local populations will decrease in the next 50 years. While the distribution of the *southern* lineage with the MIROC model is very similar to the present distribution, the CCSM model points to a different result. The CCSM model predicts a range of expansion in Macedonia and southern Greece compared to the present period. This means that the *southern* lineage is likely to be more resilient to climate change compared to the *northern* lineage, but its population trend should constantly be monitored and conservation measures should not be neglected. Therefore, it can be suggested that the conservation programs and action plans for the *northern* lineage are more urgent and of greater importance.

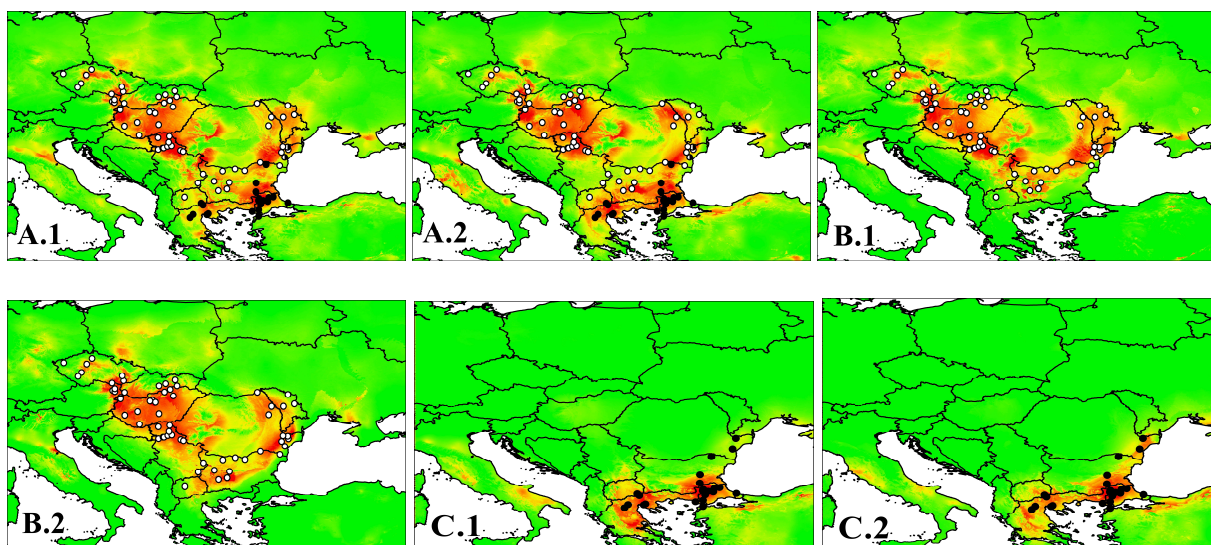


Figure 4. The MaxEnt modeling prediction for the future period (A1. combined data with CCSM model, A2. combined data with MIROC model, B1. *northern* lineage with CCSM model, B2. *northern* lineage with MIROC model, C1. *southern* lineage with CCSM model, C2. *southern* lineage with MIROC model)

4. Conclusion

This study estimated the habitat suitability and potential distribution probability of *S. citellus* in central Europe and the Balkans using the Maximum Entropy Model. MaxEnt fully described the observed present distribution of the European ground squirrel. Accordingly, it predicted which bioclimatic variables were more significant in the geographic distribution of both lineages belonging to the species. Furthermore, this study forecasted the past and future distribution patterns of the two lineages.

The continued survival of the European ground squirrel requires the evaluation of the species as a whole rather than as local populations. The performance of ongoing or completed reinforcement and reintroduction studies (Balaz, Jancova, & Ambros, 2008; Matějů et al., 2010; 2012; Gedeon et al., 2011; 2012; Löbbová & Hapl, 2014; Koshev et al., 2019) in European countries is closely linked to climatic change, therefore, the evaluation of climate change scenarios in relation to the potential distribution range of the species will allow researchers to develop possible strategies to increase conservation success. The results of this study indicate that suitable habitats for the two lineages will cover a narrower area compared to the present estimates, so, the regions where introduction and reintroduction studies will be done should not be selected randomly. Moreover, these assessments can be used for management strategies, conservation projects and species action plans.

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Author Contributions

Performed statistical analysis and wrote the paper.

Conflicts of Interest

The author has no conflict of interest.

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