MACIS

Minimisation of and Adaptation to Climate change Impacts on biodiverSity

Deliverable 3.5:
Report on the results of the run of improved modelling to Europe

Specific targeted research project (STREP)

Contract period 01 November 2006 – 31 October 2008
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Authors

Wilfried Thuiller & Bruno Lafourcade (CNRS
and MACIS Co-ordination Team

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Project Website www.macis-project.net

D3.5. Report on the results of the run of improved modelling to Europe

Written by Wilfried Thuiller & Bruno Lafourcade (CNRS)

One of the main objectives of WP3 was to further develop a series of biodiversity and habitat models that address biodiversity impacts, and are capable of calculating the consequences of the changes in the trends in drivers as specified by the narrative scenarios provided by the IPCC. For this deliverable, we focus on further developing BIOMOD, a well tested and developed modelling platform, which has been improved to deal with ensemble forecasting and applied it to European atlases (herptiles, birds, mammals and plants). For D3.3, we only delivered the preliminary results for mammals. For this D3.5, we deliver all the results for the different European atlases. The results for the mammals will thus be the same than for D3.3.

We build our analysis based on by modelling the current and future distribution of all the European amphibians, reptiles, breeding birds and mammals and a fraction of the European plants. Previous projections have highlighted the discrepancies between models, global change scenarios but they have not built a comprehensive study to include uncertainty into the modelling approach and have not used a wide range of GCM and scenarios.

Because projections might differ into the future, we pursue the development of an ensemble forecasting approach implemented in R called BIOMOD. We give here the advantage and pros of BIOMOD. BIOMOD offers a platform for ensemble forecasting (Figure 1) using freeware and open-source R software. It overcomes some of the limitations of existing software (e.g. being able to fit and compare different models) and incorporates several features for testing models (e.g. *k*-fold cross validation) and for examining species-environment relationships (e.g. using randomization tests).

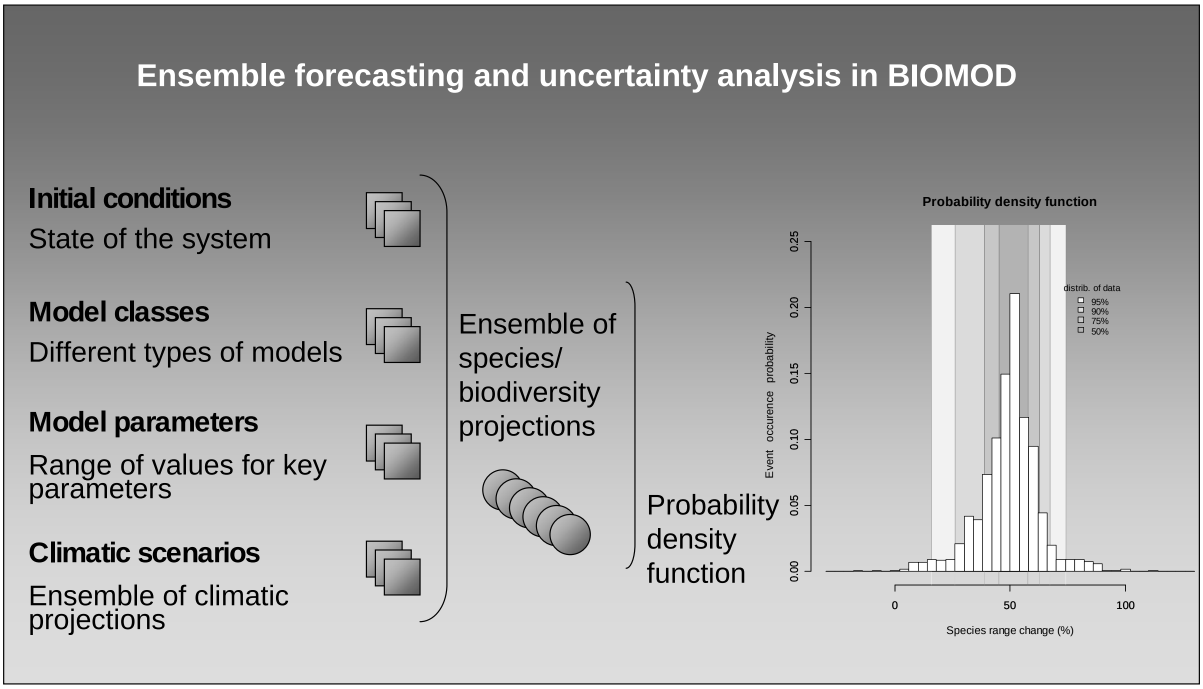


Figure 1: The probabilistic approach to forecasting biodiversity (adapted from Thuiller 2007)

Earlier implementations of BIOMOD provided limited ensemble simulations across model classes (i.e., four modelling techniques) and boundary conditions (i.e., up to five climate scenarios). Currently, BIOMOD enables large simulations across initial conditions (i.e., by sampling species distribution data and fitting different models for each sample), nine model classes (Generalised Linear Models (GLM), Generalised Additive Models (GAM), Multivariate Adaptive Regression Splines (MARS), Classification Tree Analysis (CTA), Mixture Discriminant Analysis (MDA), Artificial Neural Networks (ANN), Generalised Boosted Models (GBM), Random Forests , and one rectilinear envelop similar to BIOCLIM (SRE), a variable number of model parameterizations (e.g., polynomials and smoothing splines of different orders in general linear or additive models, nodes in classification trees, hidden layers in neural nets), and a virtually unlimited number of boundary conditions.

Evaluation of models in BIOMOD includes two sorts of analysis: assessments of the goodness-of-fit (= explanatory power) and of model accuracy (=predictive power). The former uses standard approaches associated with each technique; for example, ANOVA decomposition and AIC are available for both GLM and GAM, whereas rate of misclassification is used for CTA. The latter can be performed with three different procedures: the area under the relative operating characteristic curve (AUC), the Cohen's *K*, and True Skill Statistic (TSS). The AUC is most widely used as it is not dependent of thresholds for transforming modelled probabilities of occurrence into presence and absence. In contrast, Cohen's *K* and TSS require the estimation of thresholds, which are necessary for generating a misclassification matrix and providing a measure of model accuracy. BIOMOD estimates the optimal thresholds that maximise the Cohen's *K* and TSS respectively. Cohen's *K* has been criticized for being strongly influenced by the prevalence of the species in the data and the TSS has been introduced to palliate this problem.

In an ideal world, model accuracy (e.g. AUC/Kappa/TSS) should always be evaluated with independent data. When independent data are not available, an alternative is to use data-splitting procedures, whereby a proportion of the original data are used for training the models and the withheld data are used for model evaluation. A single random splitting of data was available in earlier implementations of BIOMOD but it proved to be a non negligible source of variability in prediction making. Currently, BIOMOD allows much greater flexibility. Apart from the ability to define the size of the training and test sets, BIOMOD also allows *k* number of data splitting runs to be computed, effectively providing a k-fold cross validation procedure. BIOMOD also allows jack-knifing (and other forms of bootstrapping). Users simply need to define the training sets as 100% of the data minus 1 record and then repeating the procedure a user-defined number of times (e.g. 1000 times). When non-independent data are used for model evaluation, variability in model accuracy should be interpreted as a measure of the sensitivity of model results to the initial conditions rather than as a measure of predictive ability.

Assuming that no modelling procedure is always best, selecting the best model for each situation might be a useful option. The alternative ensemble forecasting paradigm draws on the assumption that model accuracy on non-independent test data is not representative of model accuracy on independent situations. In such cases, committee averaging of model predictions (giving the same weight to all predictions) can be implemented to derive a consensus prediction; an alternative is to combine models using some form of weighting (e.g. using PCA score value). There are a range of approaches to do this, but in BIOMOD weights are currently calculated on the basis of models' predictive accuracy on test data (i.e., a form of 'stacking'). An empirical testing of consensus forecasting under climate change has shown that weighted approaches are promising.

This new BIOMOD is available on request to Wilfried Thuiller (wilfried.thuiller@ujf-grenoble.fr). A paper presenting the software is accepted for publication in Ecography:

Thuiller, W., B. Lafourcade, R. Engler, and M. B. Araujo. 2008. BIOMOD – A platform for ensemble forecasting of species distributions. Ecography.

This new BIOMOD platform has thus been used to re-analysis impacts of climate change on European biodiversity. We run the 9 models presented in BIOMOD for all herptiles (120 spp.), birds (600 spp.), mammals (141 spp.) and plants (1500 spp.). The distribution of the each species has then been projected under 3 global change models (CGCM2, CSIRO, HadCM3) for 4 SRES scenarios (A1FI, A2, B1, B2) under 2020, 2050 and 2080. The probabilities of occurrence from each model have then been transformed into presence absence using three different procedures (ROC, TSS, Kappa). It leads us to:

9 x 4 x 3 x 3 = 108 projections for each species, making 270,000 projections overall (several hundred of Gigs of data).

Methods applied to all the European taxa: Species relying on marine or freshwater ecosystems have preliminary been removed to the database as well as species with a too low number of occurrence (<20). To avoid multi-colinearity and over-calibrating the models, we selected only four uncorrelated variables for all European species: ratio potential over actual evapo-transpiration, growing degree days, minimum temperature of the coldest month, and annual precipitation.

A 10-fold cross-validation has been carried out for each species to estimate the predictive accuracy of the models. To avoid displaying thousand of maps, we deliver an ensemble of prediction for each species. This was done by averaging across the 9 models (weighted by the predictive accuracy of the model).

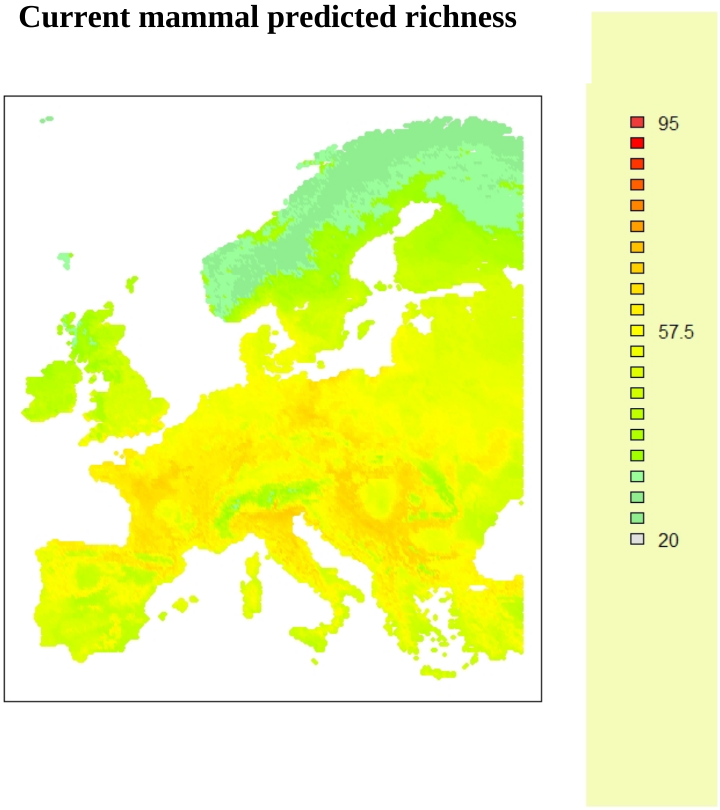
RESULTS

MAMMALS

Although species tended to respond in an idiosyncratic way, most of the species were predicted to gain potential habitats in the future. Quite logically, patterns of changes and divergence between scenario and GCMs were accentuated with projection time (2020, 2050 and 2080) (file Mammals Range Change.xls).

Expected species turnover is moderately low according to all GCMs, scenarios and time frame (see Figure below). There is obvious increase with time (correlated with the increase of climate change after 2050). Species turnover differed according to GCM as well. In general HadCM3 seems the most harmful for mammal communities. There is no obvious geographic pattern in the divergence between GCMs. The pattern is similar for species richness

In general, the effects of global climate change on European mammal communities may be most noticeable not as a loss of species from their current ranges, but instead as a fundamental change in community composition.

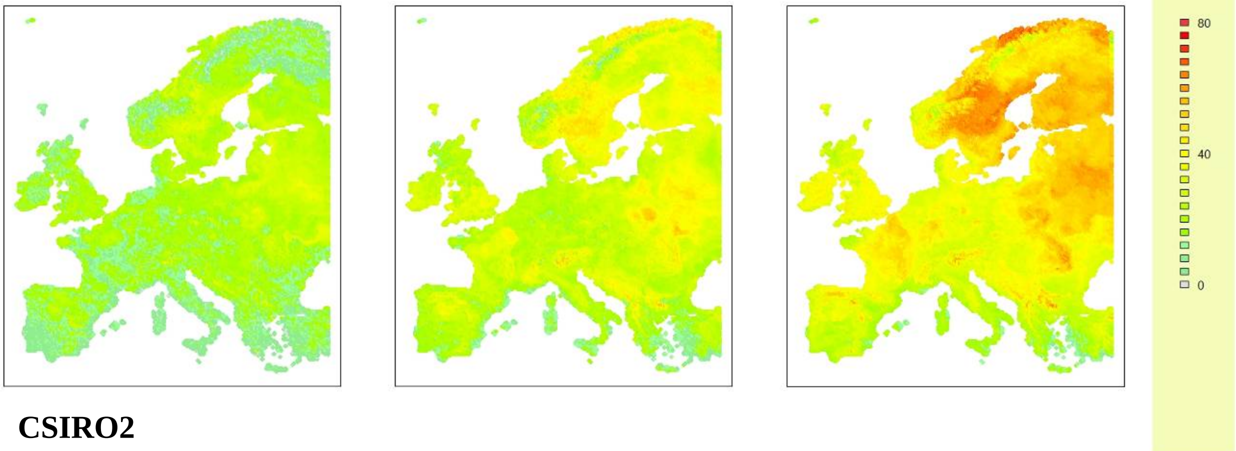

Current mammal predicted richness

A1

SPECIES TURNOVER IN MAMMAL COMMUNITIES

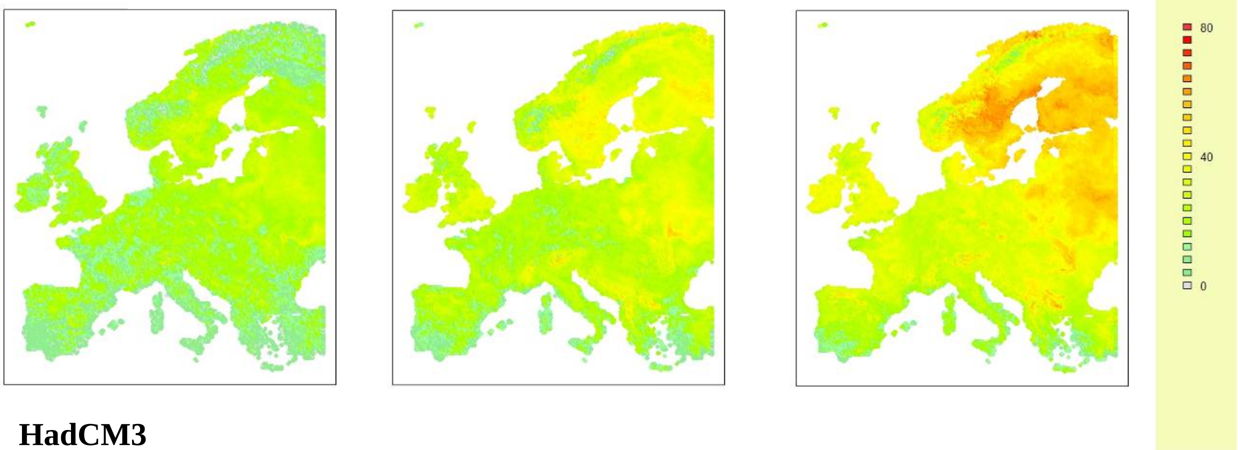
CGCM2

2020 2050 2080



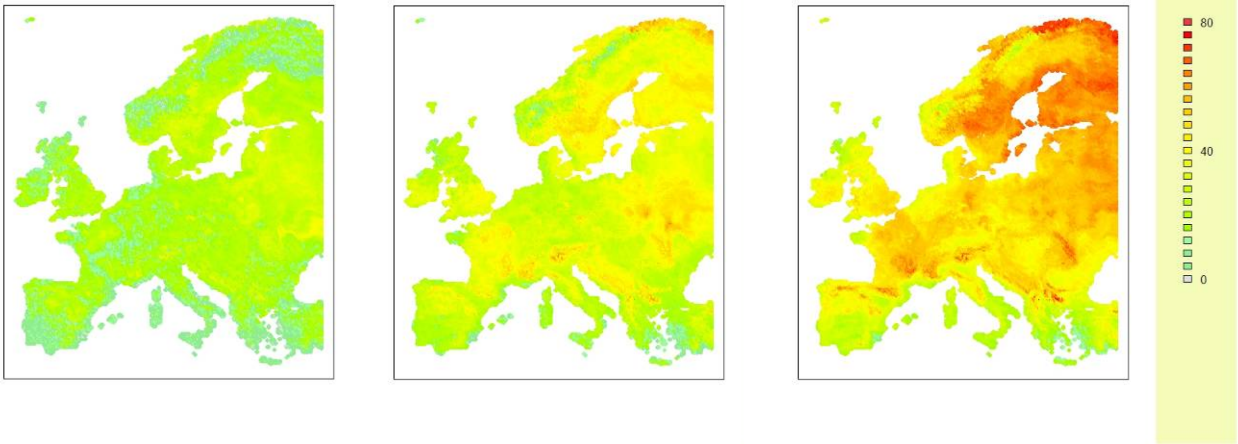
CSIRO2

2020 2050 2080



HadCM3

2020 2050 2080

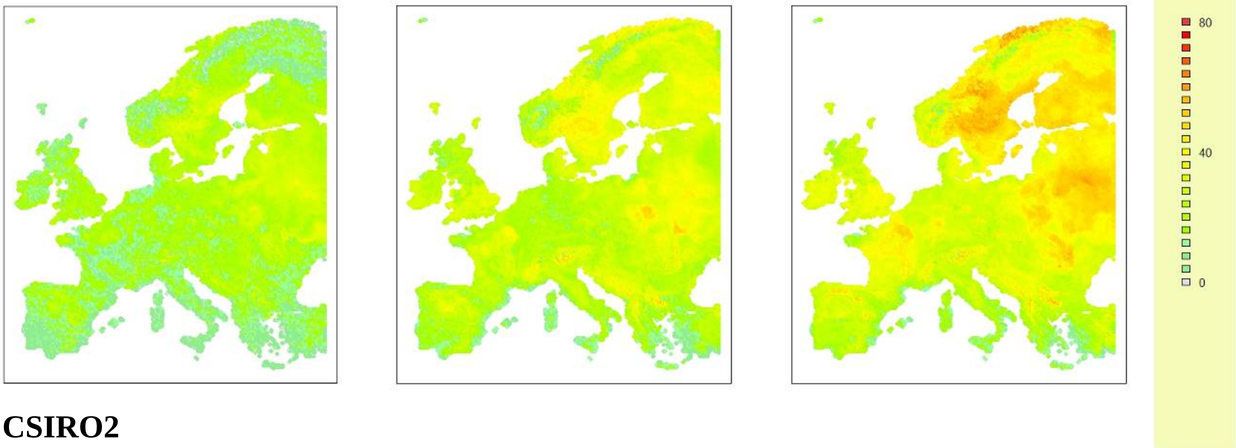


A2

SPECIES TURNOVER IN MAMMAL COMMUNITIES

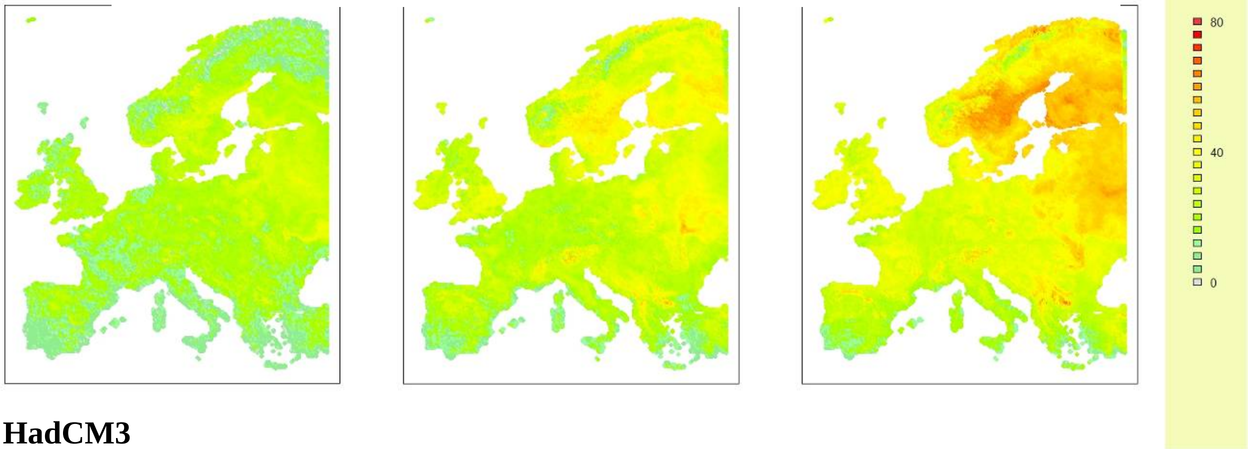
CGCM2

2020 2050 2080



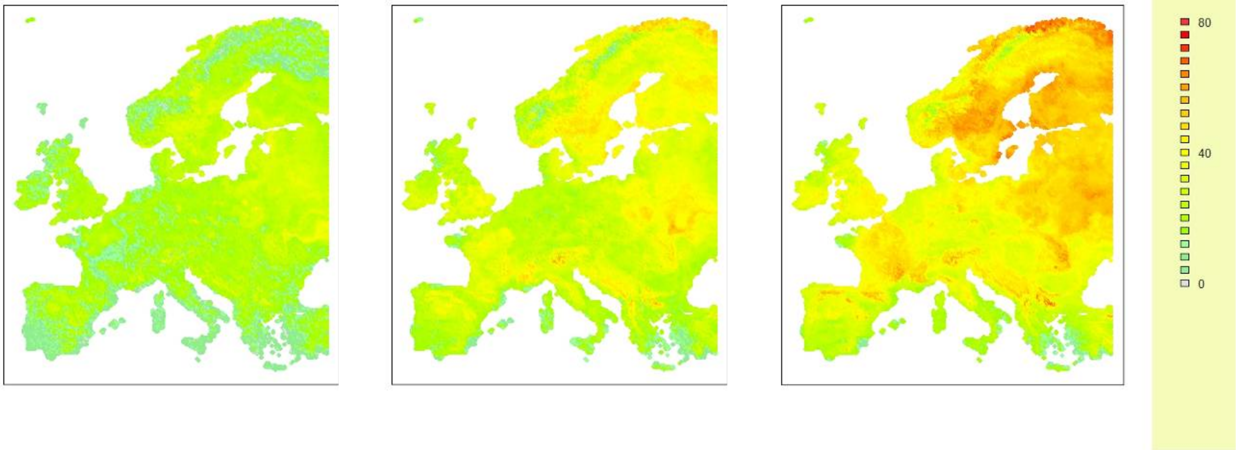
CSIRO2

2020 2050 2080



HadCM3

2020 2050 2080

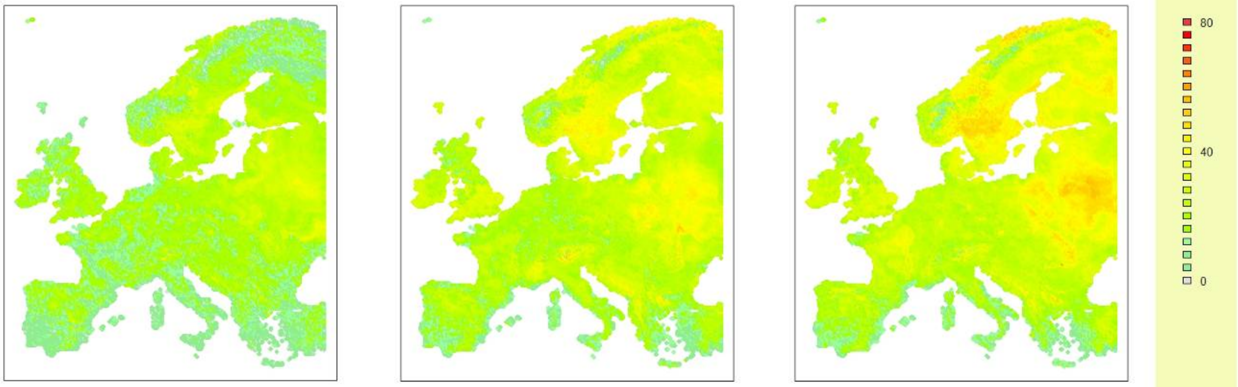


B1

SPECIES TURNOVER IN MAMMAL COMMUNITIES

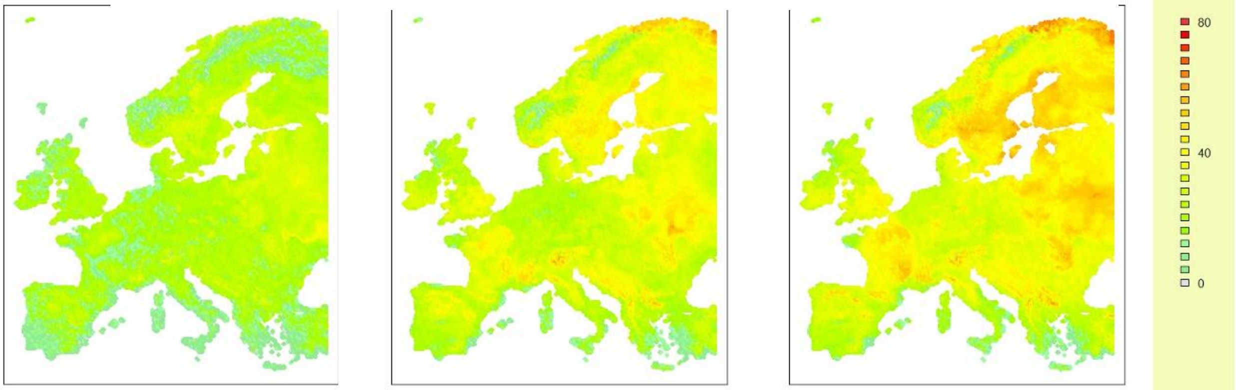
CGCM2

2020 2050 2080



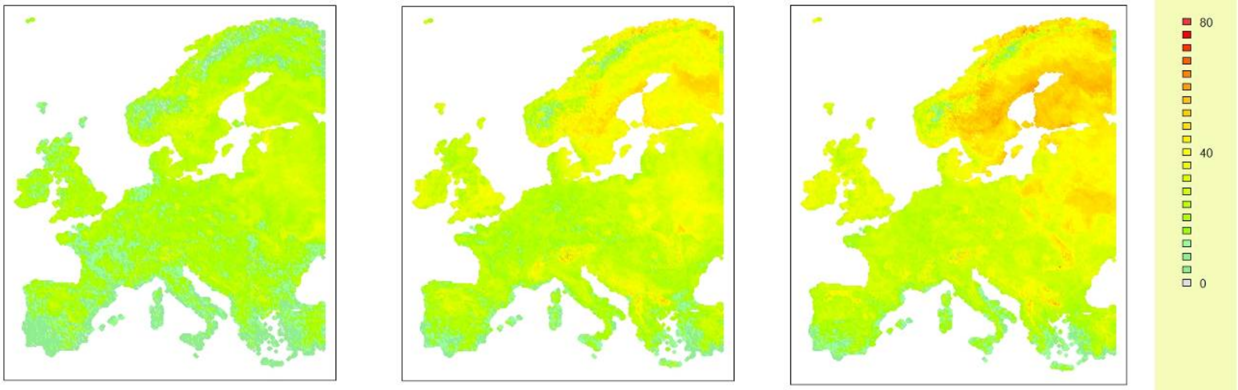
CSIRO2

2020 2050 2080



HadCM3

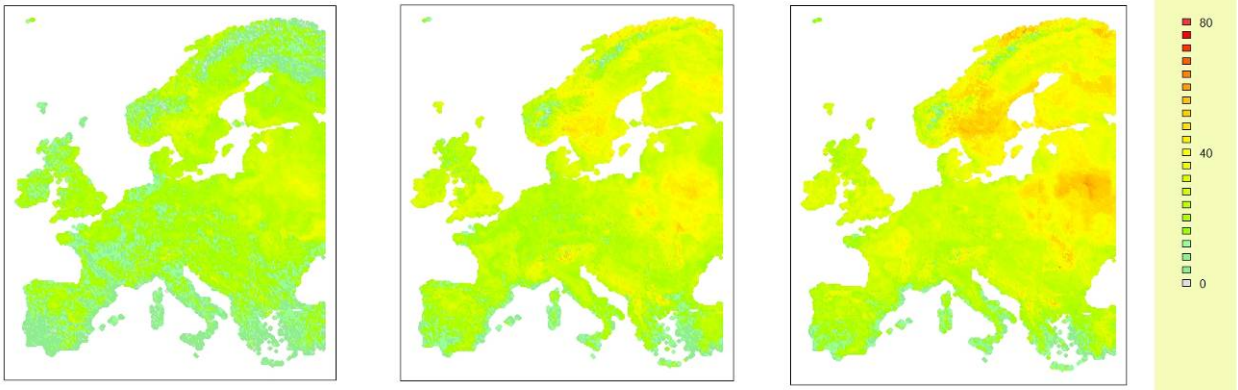
2020 2050 2080



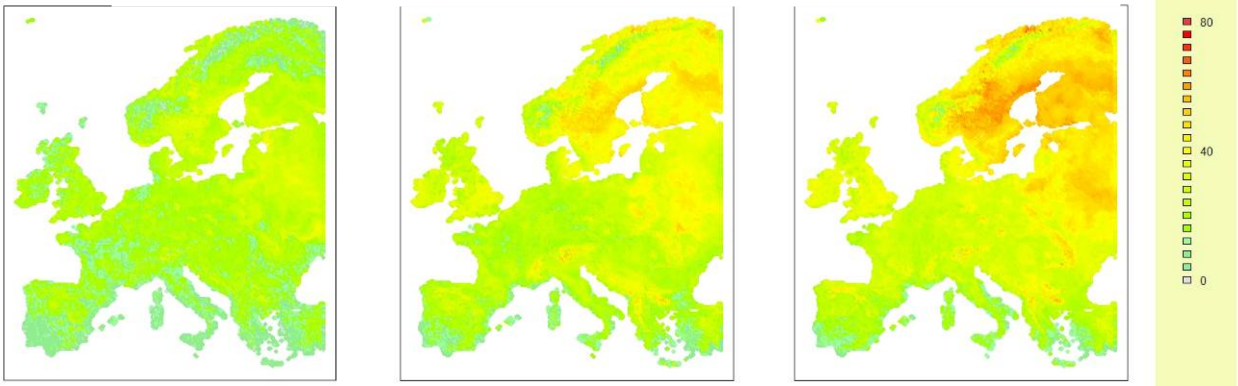
B2

SPECIES TURNOVER IN MAMMAL COMMUNITIES

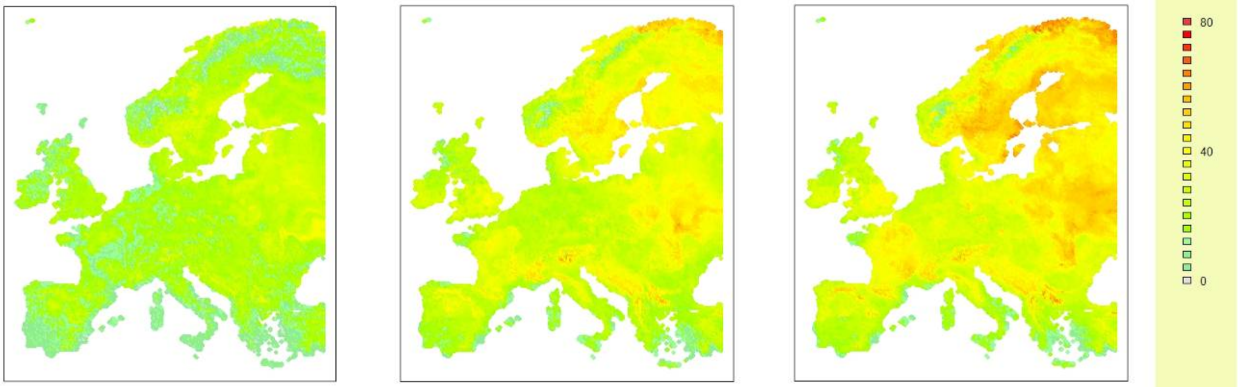
CGCM2


2020 2050 2080

CSIRO2


2020 2050 2080

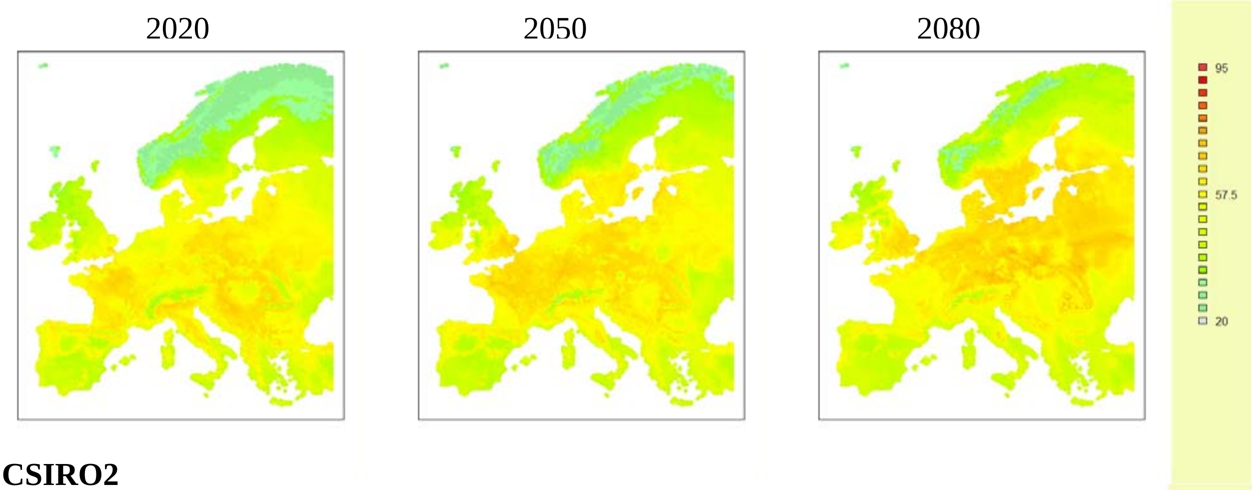
HadCM3


2020 2050 2080

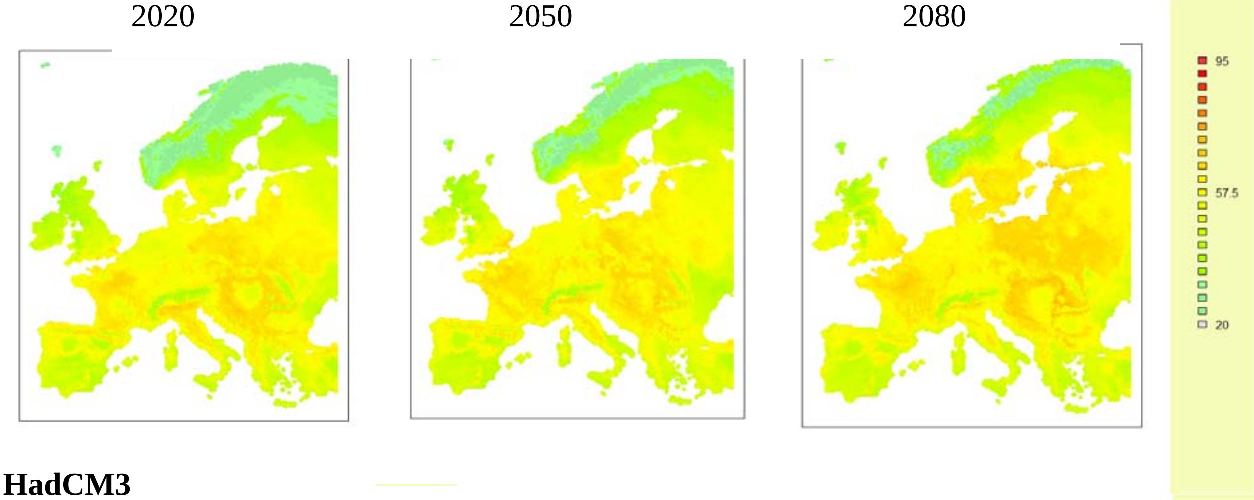
A1

MAMMAL SPECIES RICHNESS

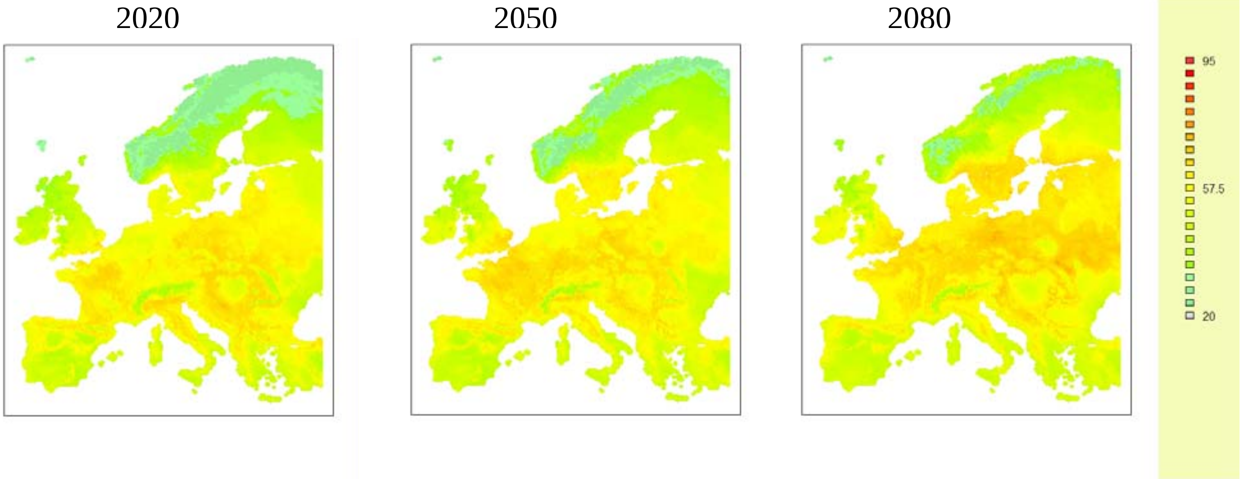
CGCM2



CSIRO2



HadCM3

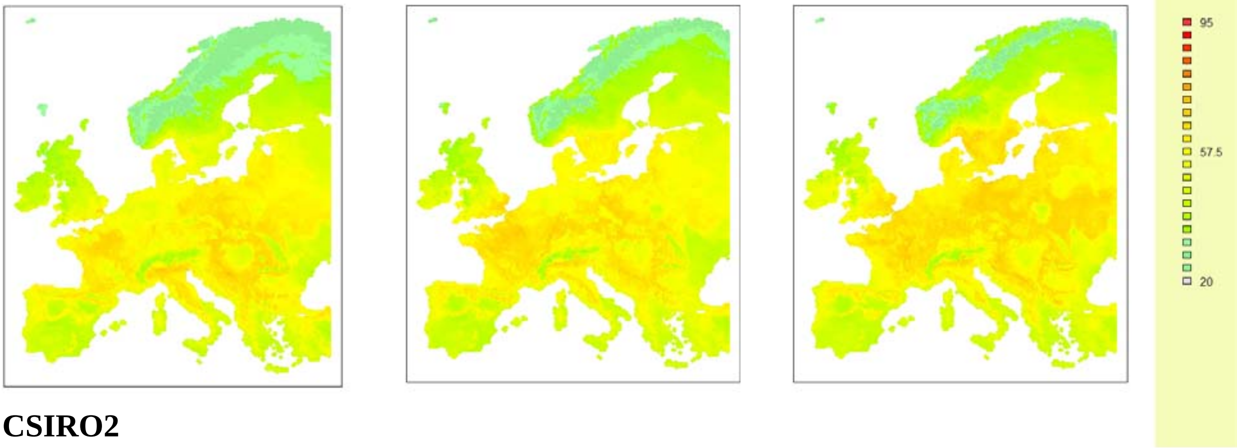


A2

MAMMAL SPECIES RICHNESS

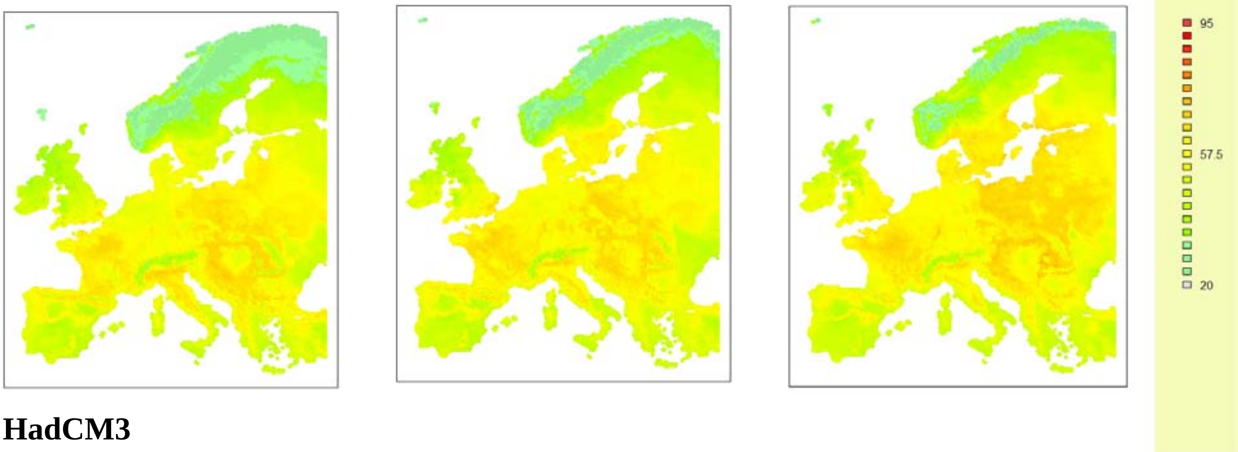
CGCM2

2020 2050 2080



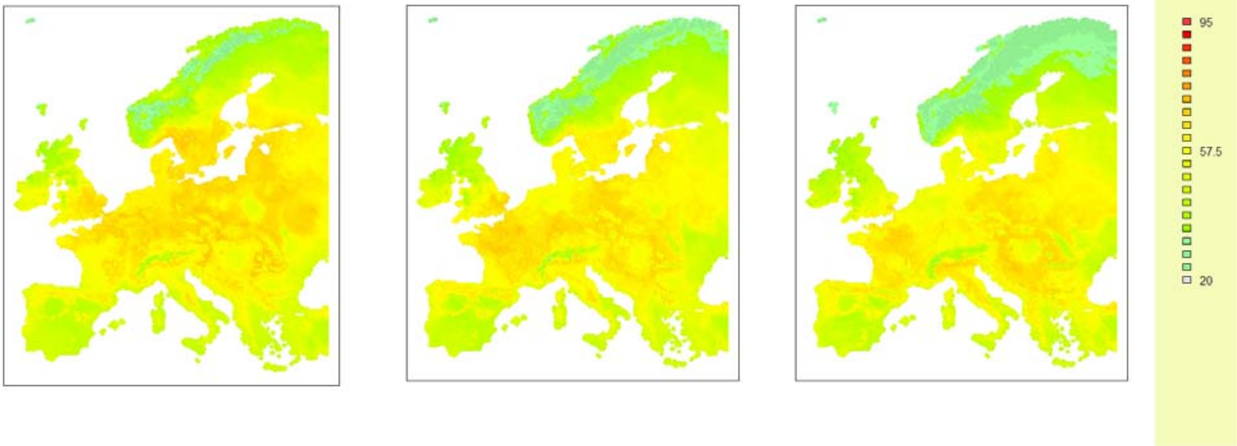
CSIRO2

2020 2050 2080



HadCM3

2020 2050 2080

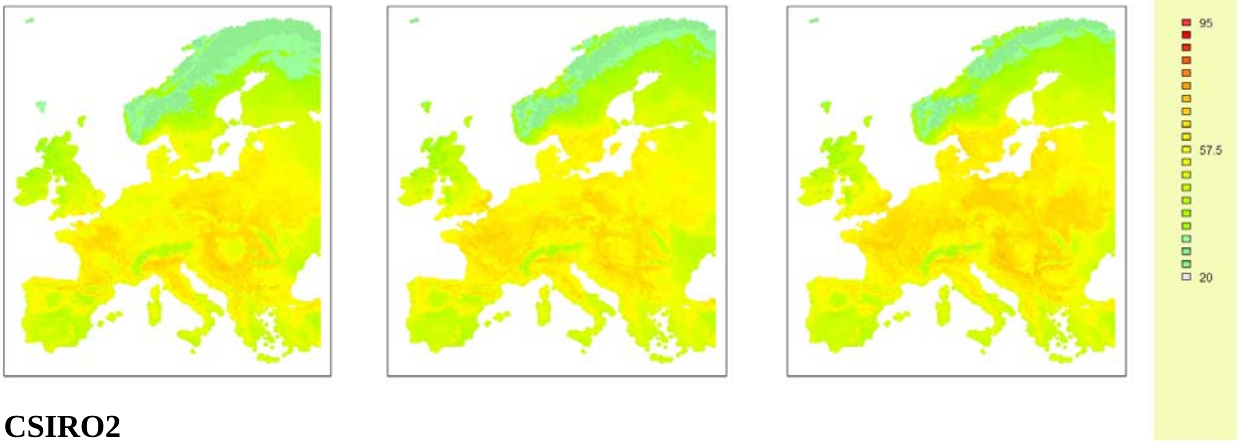


B1

MAMMAL SPECIES RICHNESS

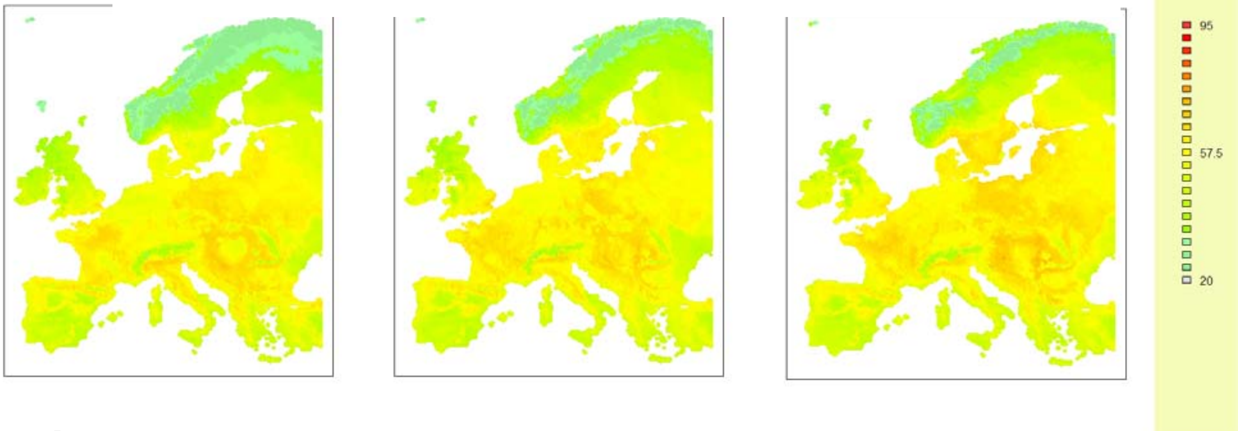
CGCM2

2020 2050 2080



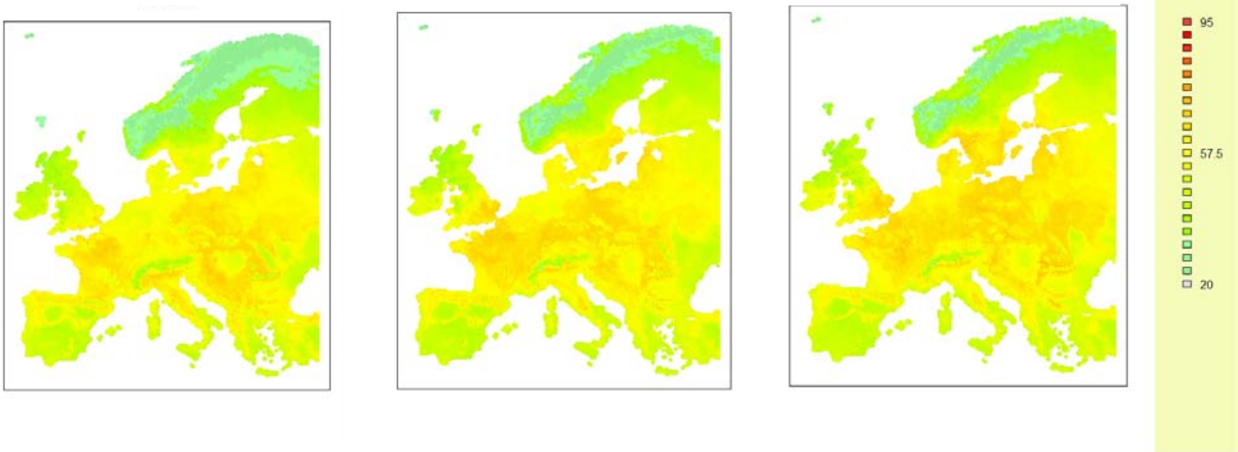
CSIRO2

2020 2050 2080



HadCM3

2020 2050 2080

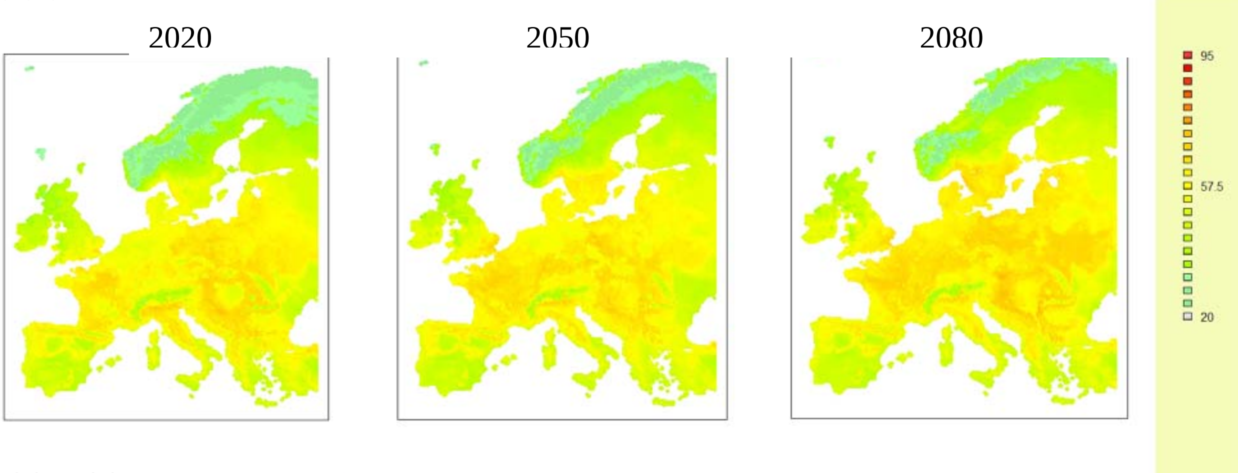


B2

MAMMAL SPECIES RICHNESS

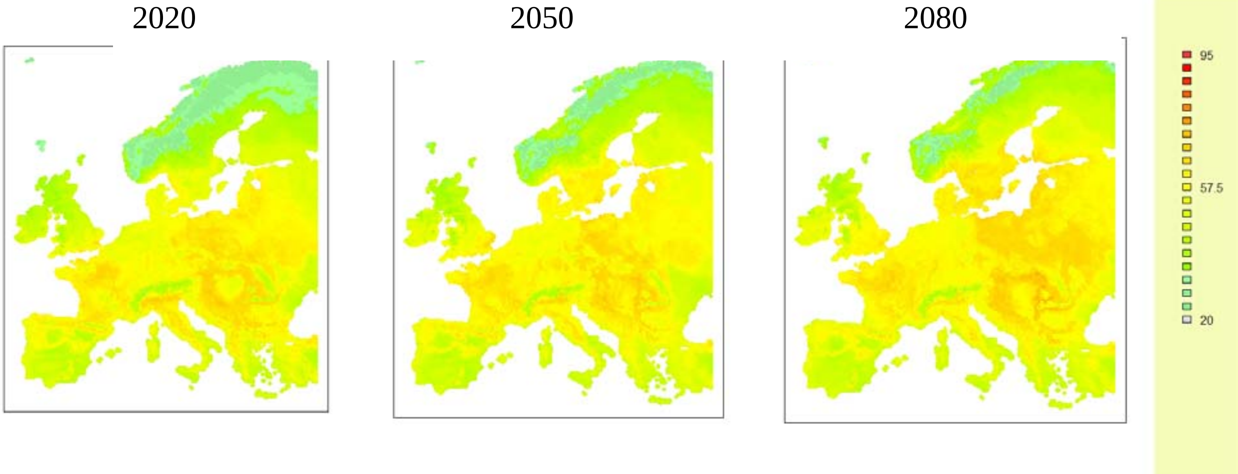
CGCM2

2020 2050 2080



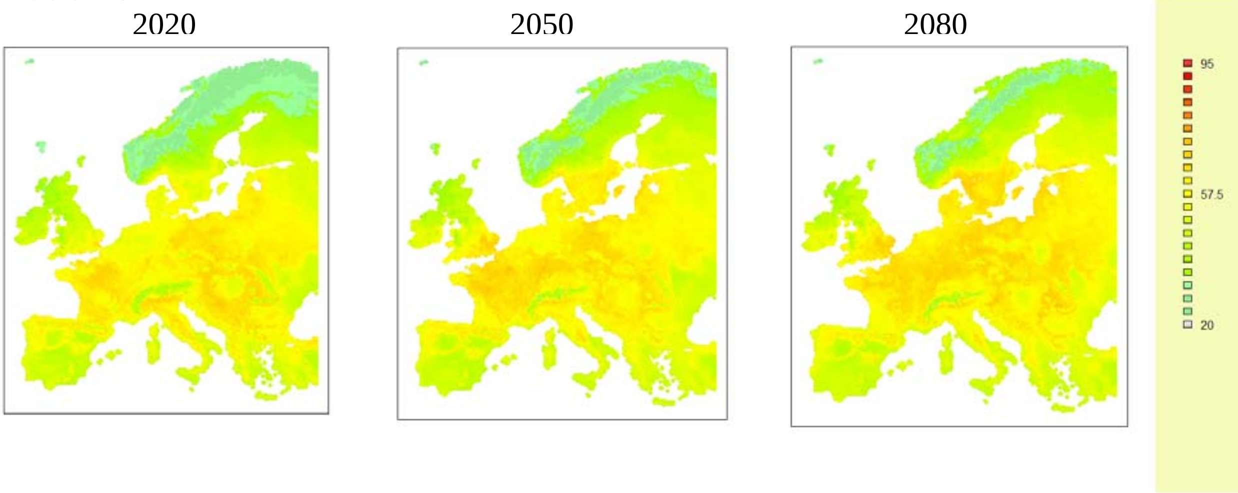
CSIRO2

2020 2050 2080



HadCM3

2020 2050 2080

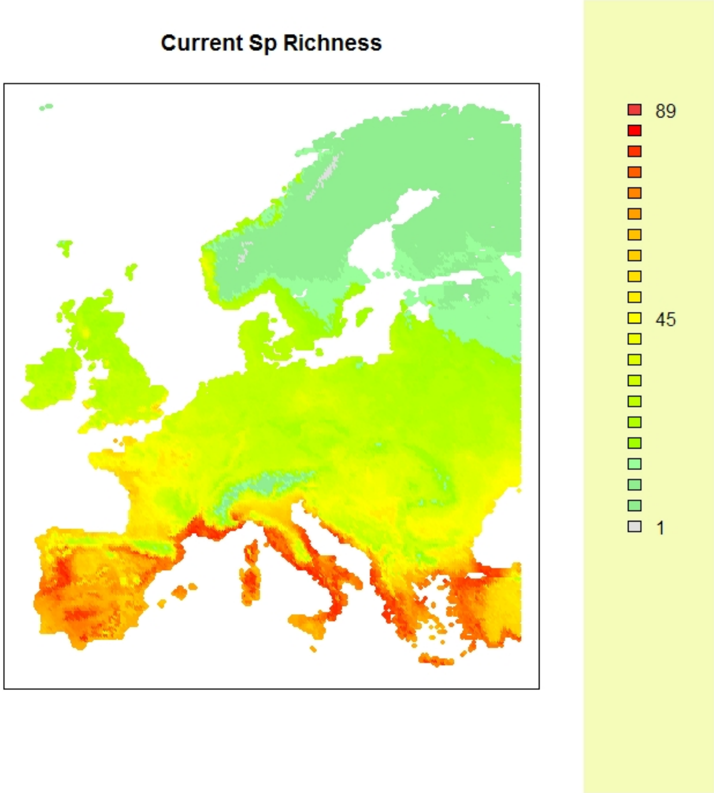


HERPTILES

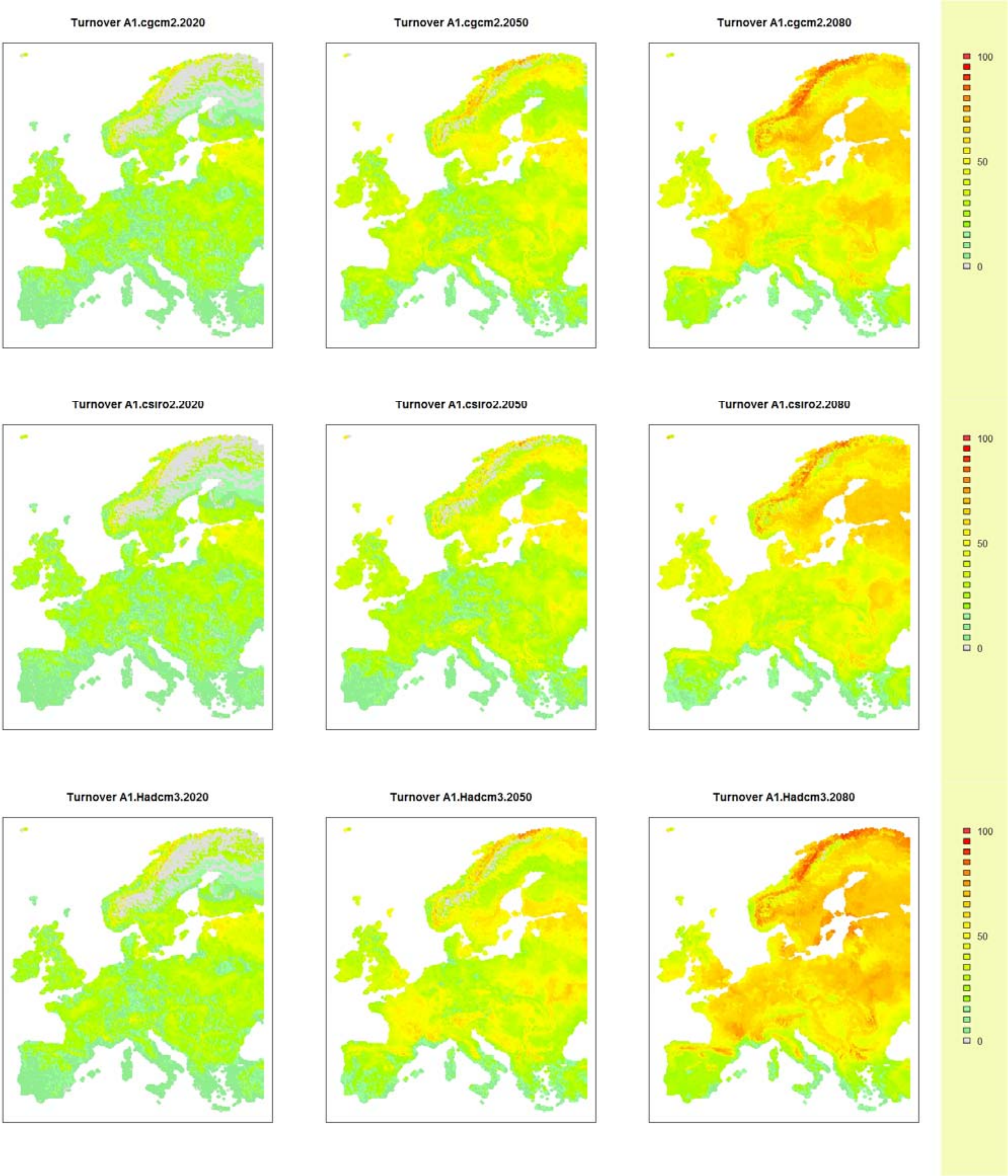
The European herptile community is principally located on the Mediterranean boarder and in the nearby inlands. Across climate change scenarios, the turnover is projected to be strong in the northern part of Europe, where the communities are sparse and less diversified. Because of this, small species changes will have an important impact at the community level.

In the southern part of Europe, however, the projected turnover only reaches a maximum of around 35%. Implying a larger number of species, these changes are thus of greater concern as they will numerously strongly modify the community compositions.

Again, there are only low discrepancies in-between GCM scenarios as for the determination of the turnover importance, spatially or intensively. As for species richness changes, all projections show the following tendency: an increase of inland species diversity going northward, with a clear drift towards the French, Iberian peninsula, southern England and south-eastern Europe territories by 2080.



SPECIES TURNOVER IN HERPTILE COMMUNITIES – A1


Turnover A1.cgcm2.2020

Turnover A1.cgcm2.2050

Turnover A1.cgcm2.2080

Turnover A1.csiro2.2020

Turnover A1.csiro2.2050

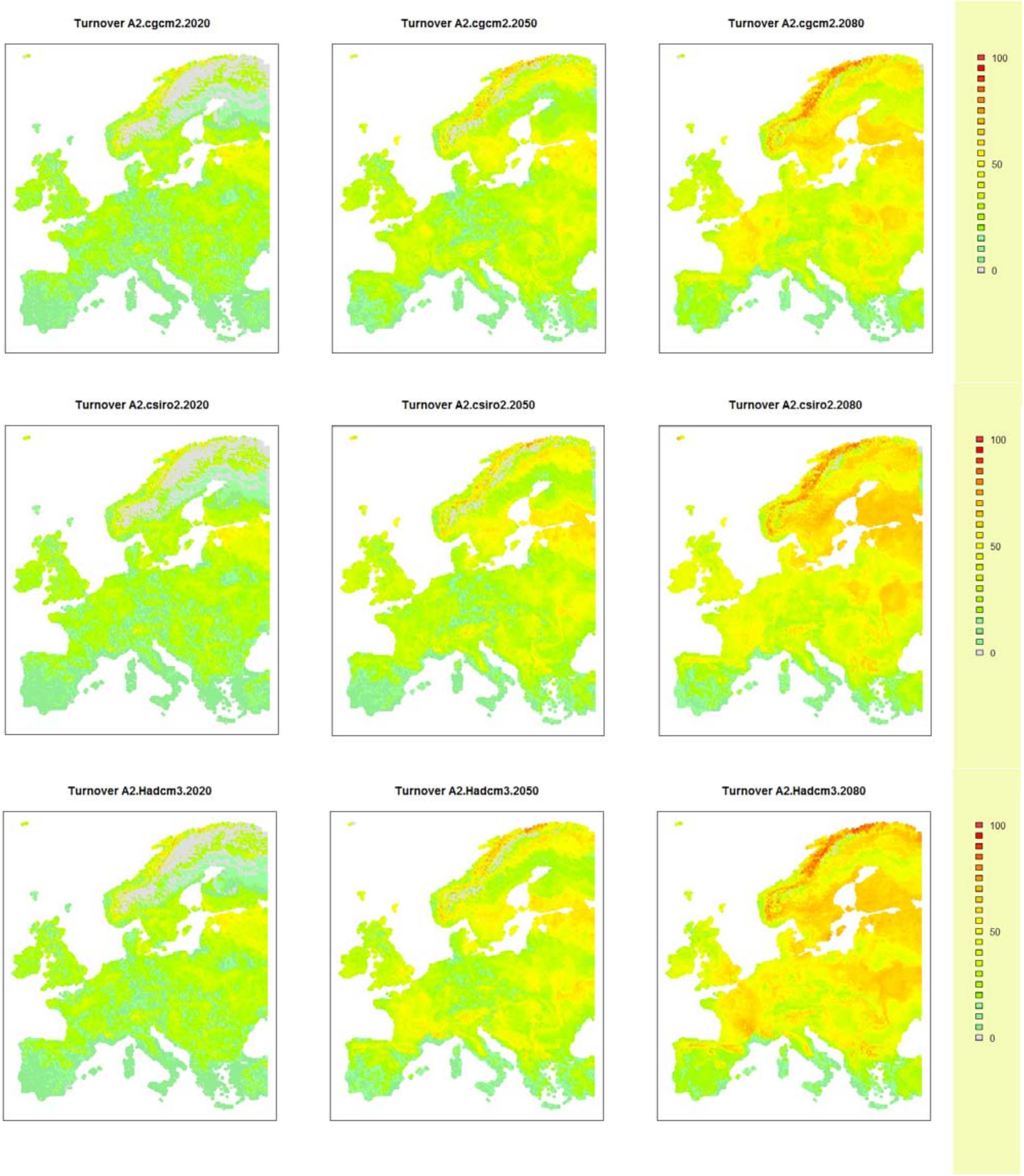
Turnover A1.csiro2.2080

Turnover A1.Hadcm3.2020

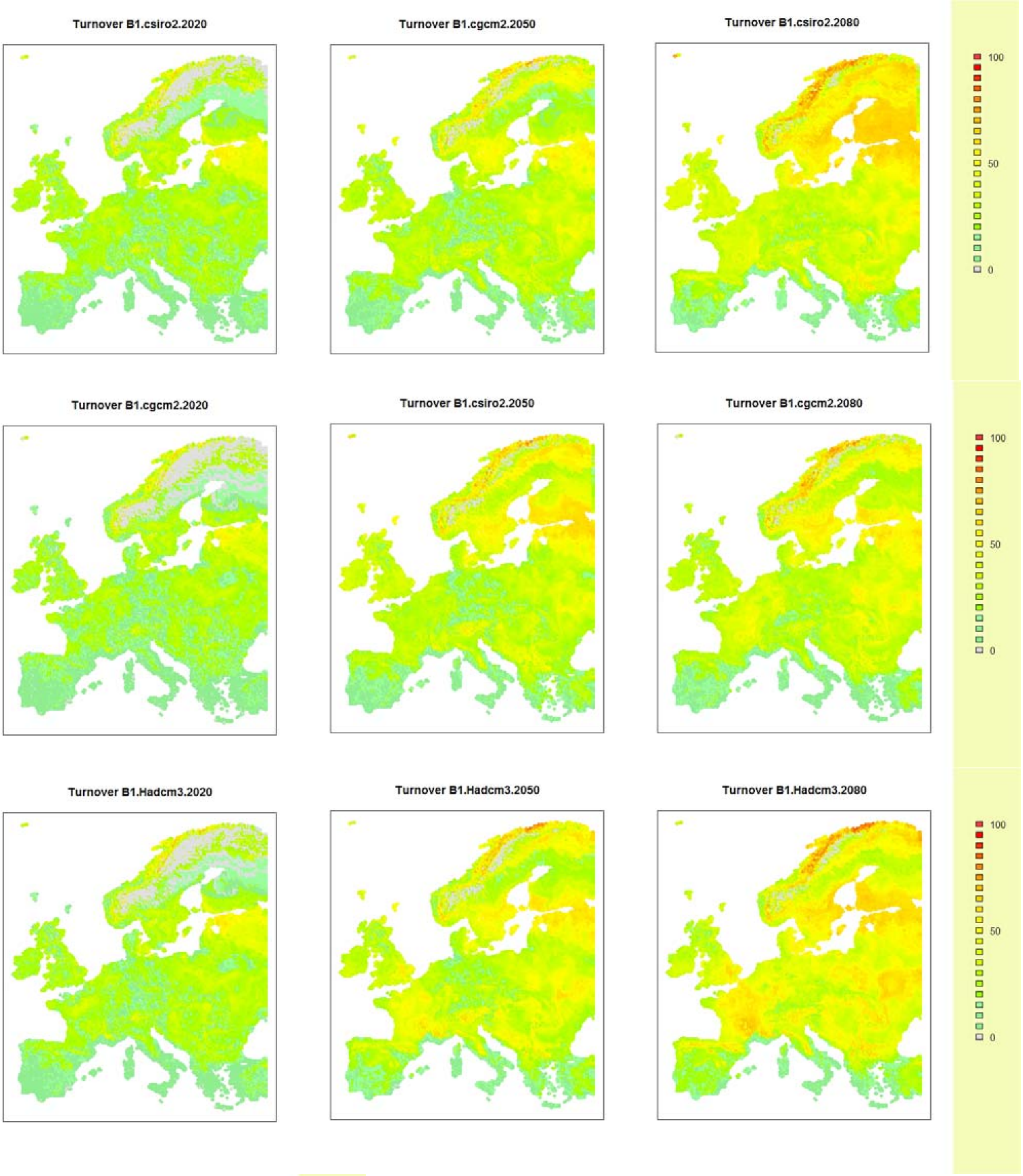
Turnover A1.Hadcm3.2050

Turnover A1.Hadcm3.2080

SPECIES TURNOVER IN HERPTILE COMMUNITIES – A2



SPECIES TURNOVER IN HERPTILE COMMUNITIES – B1



Turnover B1.csiro2.2020

Turnover B1.cgcm2.2050

Turnover B1.csiro2.2080

Turnover B1.cgcm2.2020

Turnover B1.csiro2.2050

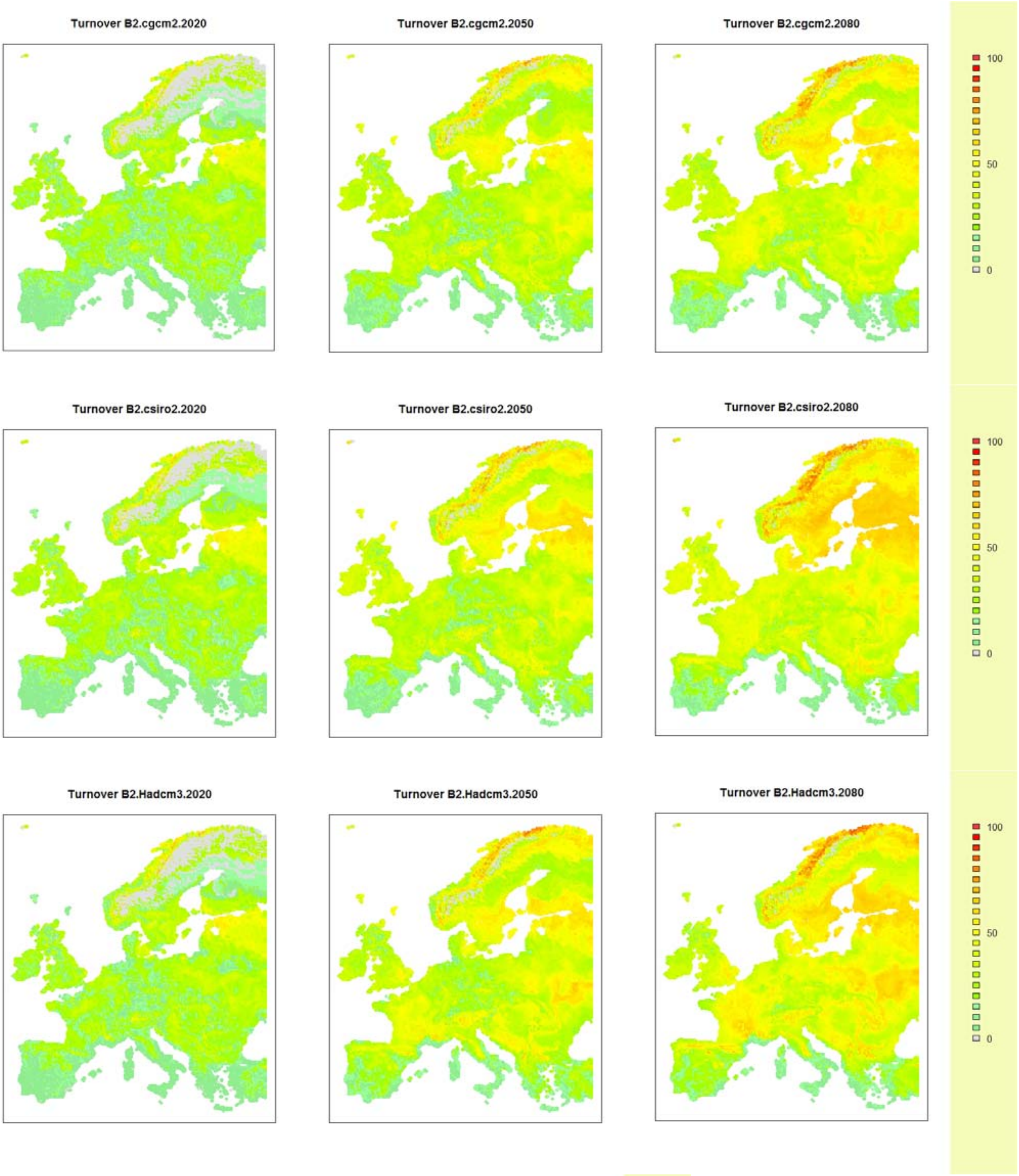
Turnover B1.cgcm2.2080

Turnover B1.Hadcm3.2020

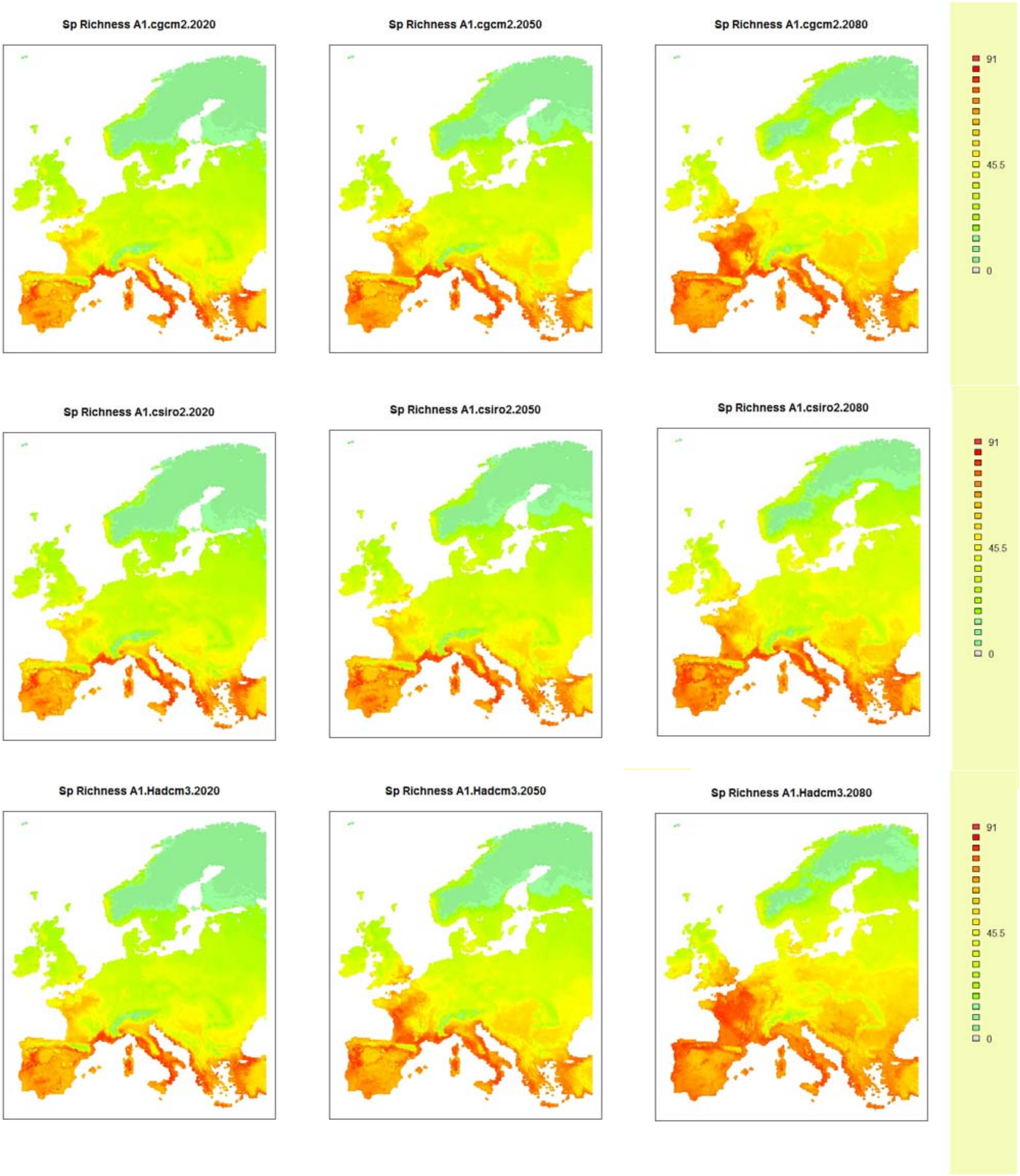
Turnover B1.Hadcm3.2050

Turnover B1.Hadcm3.2080

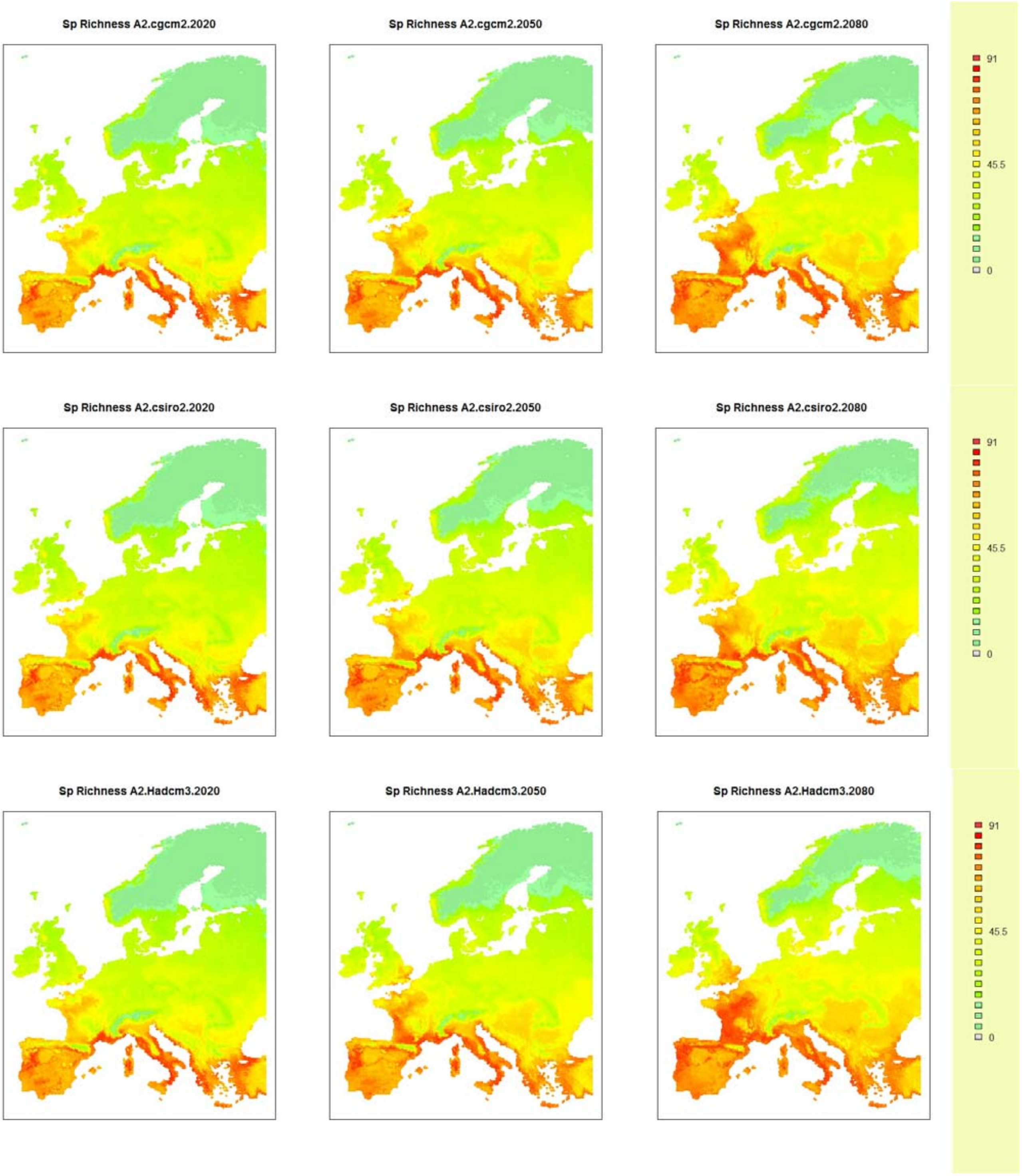
SPECIES TURNOVER IN HERPTILE COMMUNITIES – B2



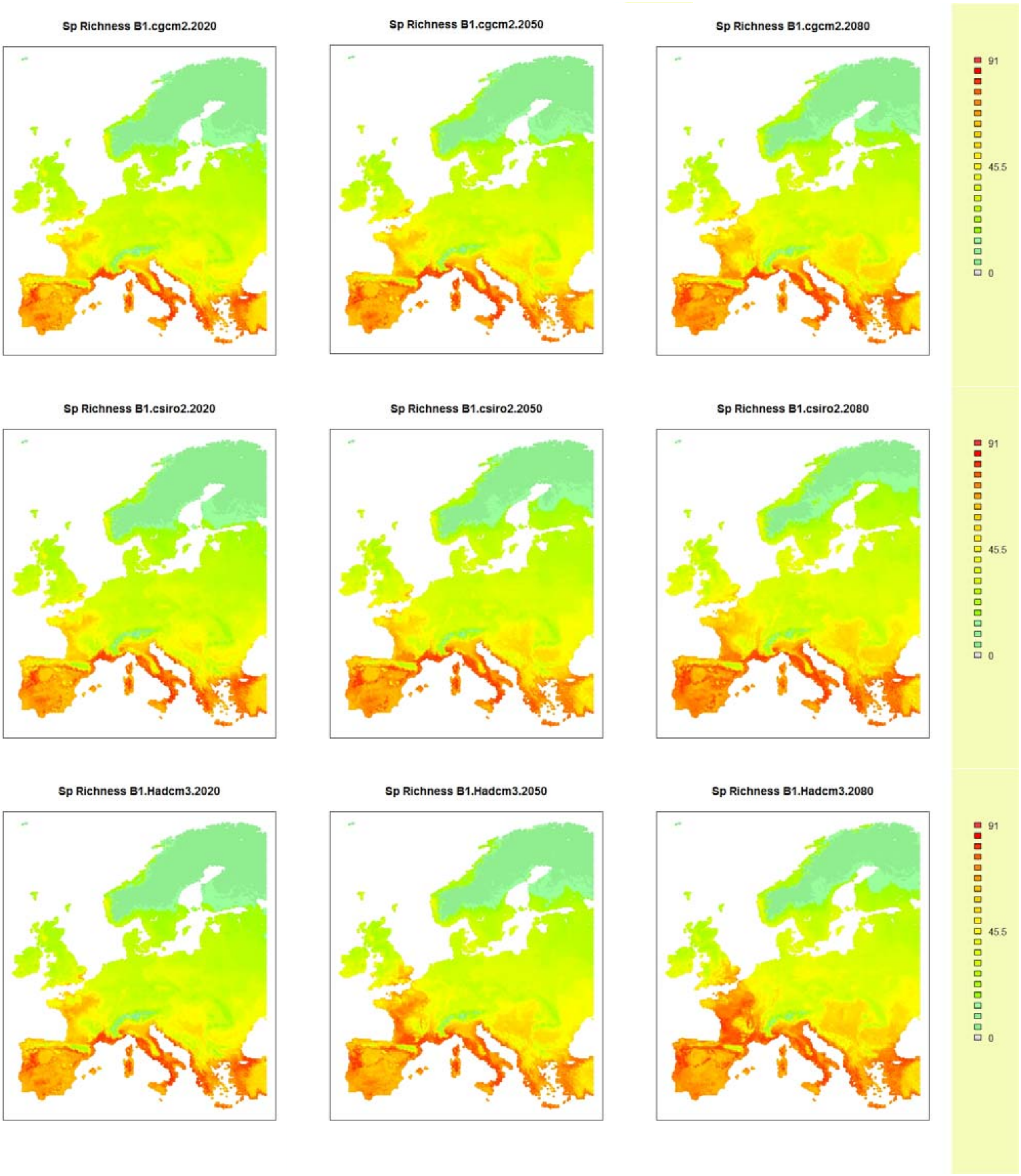
PROJECTED HERPTILE SPECIES RICHNESS – A1



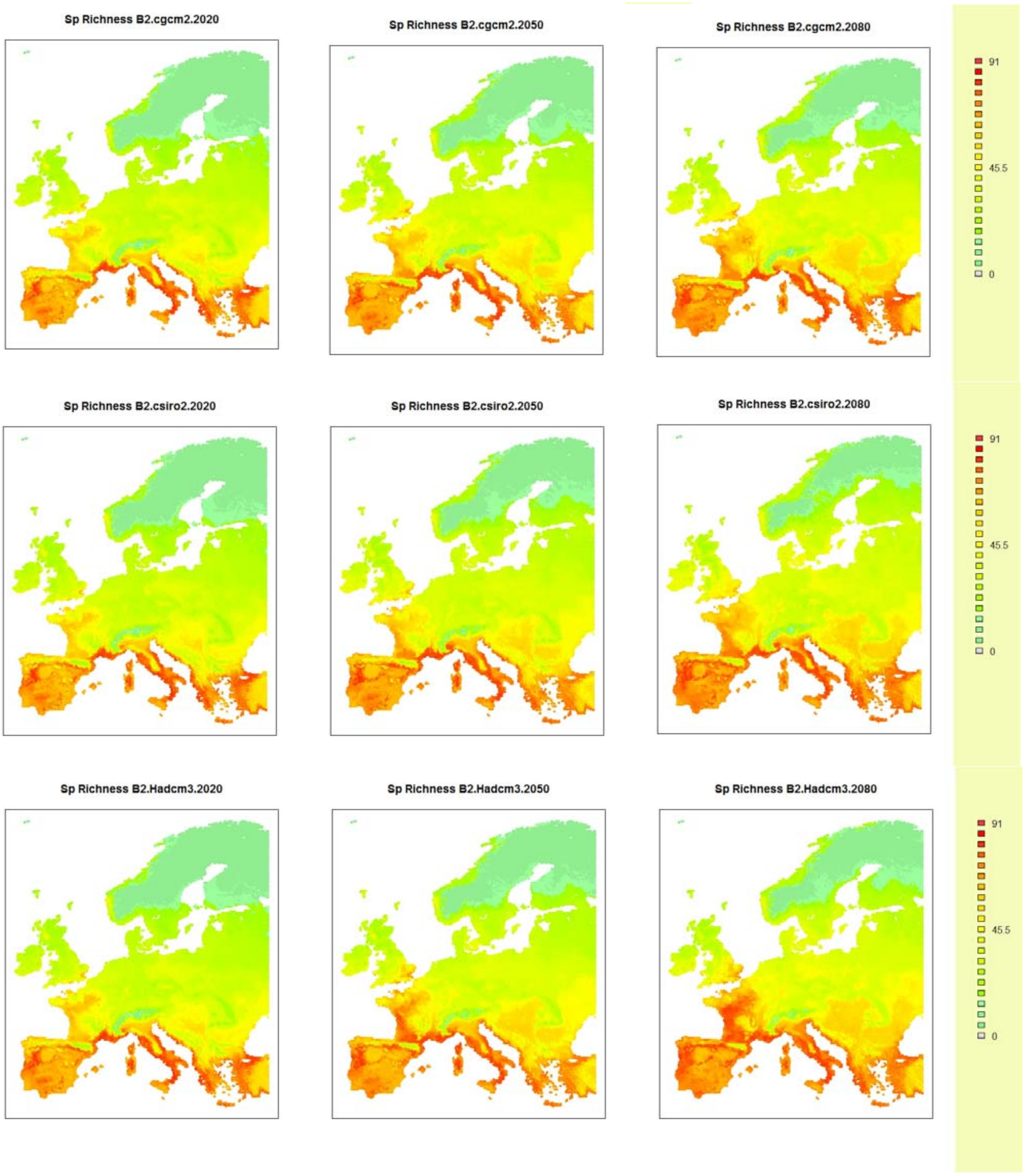
PROJECTED HERPTILE SPECIES RICHNESS – A2



PROJECTED HERPTILE SPECIES RICHNESS – B1



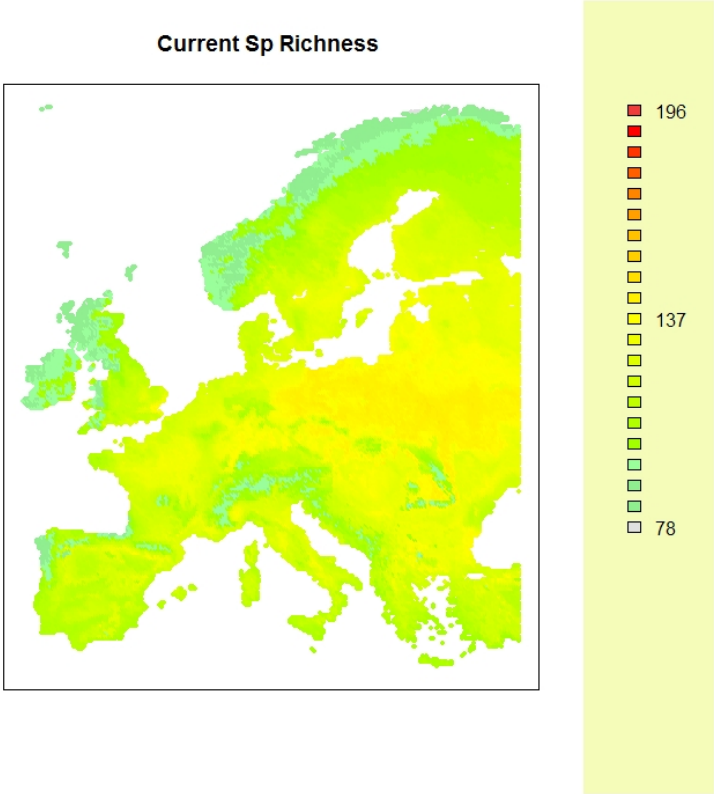
PROJECTED HERPTILE SPECIES RICHNESS – B2



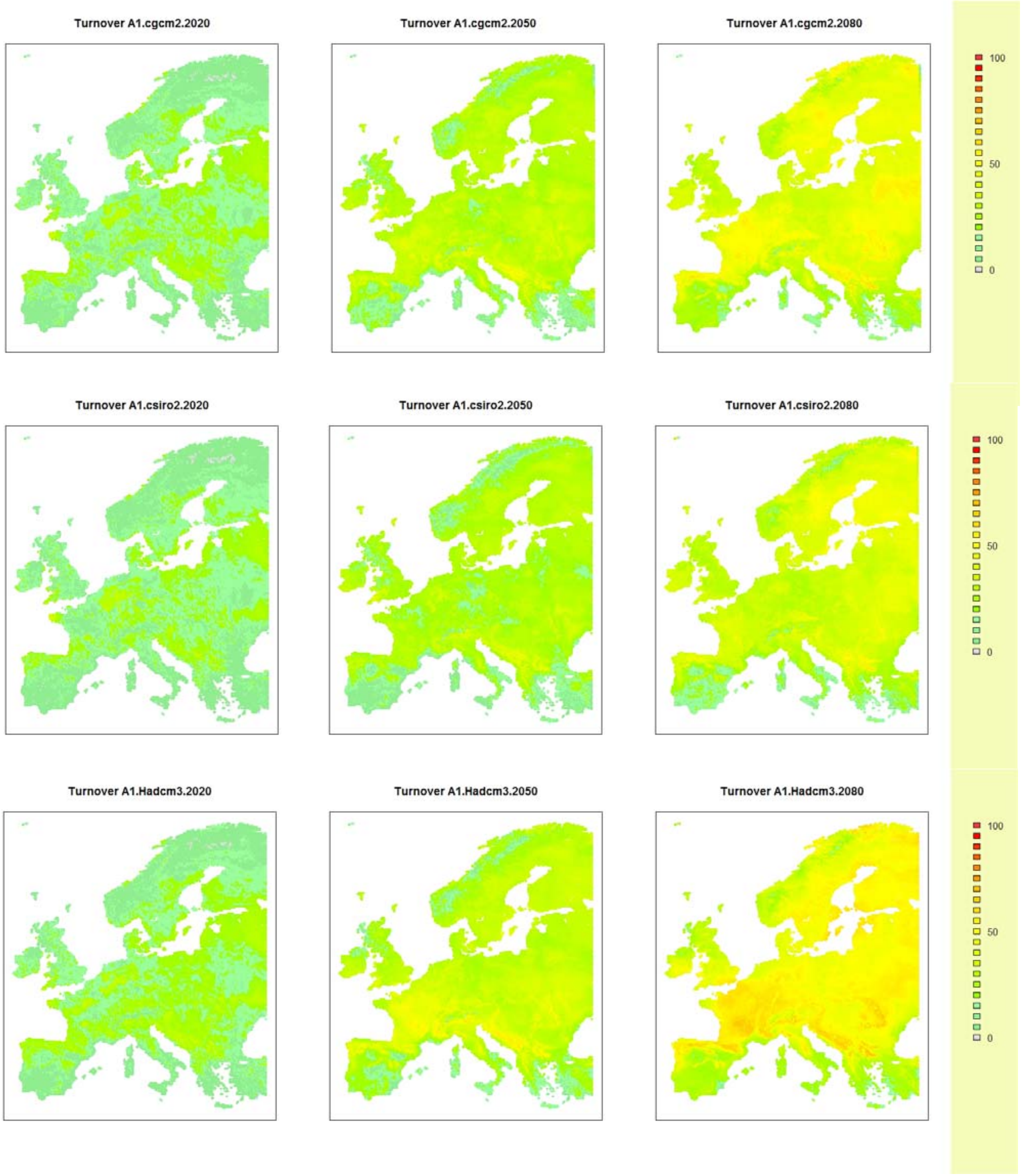
BIRDS

The projections show a moderate expected turnover for bird communities which becomes really significant by 2080 for most GCMs. HadCM3 is again the most harmful scenario. Nevertheless, large community changes can be expected as the turnover hotspots concern well diversified regions like all central Europe and southern Scandinavia.

It results in slow but relevant changes in species richness with a decrease in central Europe and a meanwhile increase in Scandinavia from 2020 to 2080 which is mostly visible in the Cgcm2 scenario. All other parts of Europe seem to remain constant in this time frame as for the overall species richness.


Current Sp Richness

SPECIES TURNOVER IN BIRD COMMUNITIES – A1



Turnover A1.cgcm2.2020

Turnover A1.cgcm2.2050

Turnover A1.cgcm2.2080

Turnover A1.csiro2.2020

Turnover A1.csiro2.2050

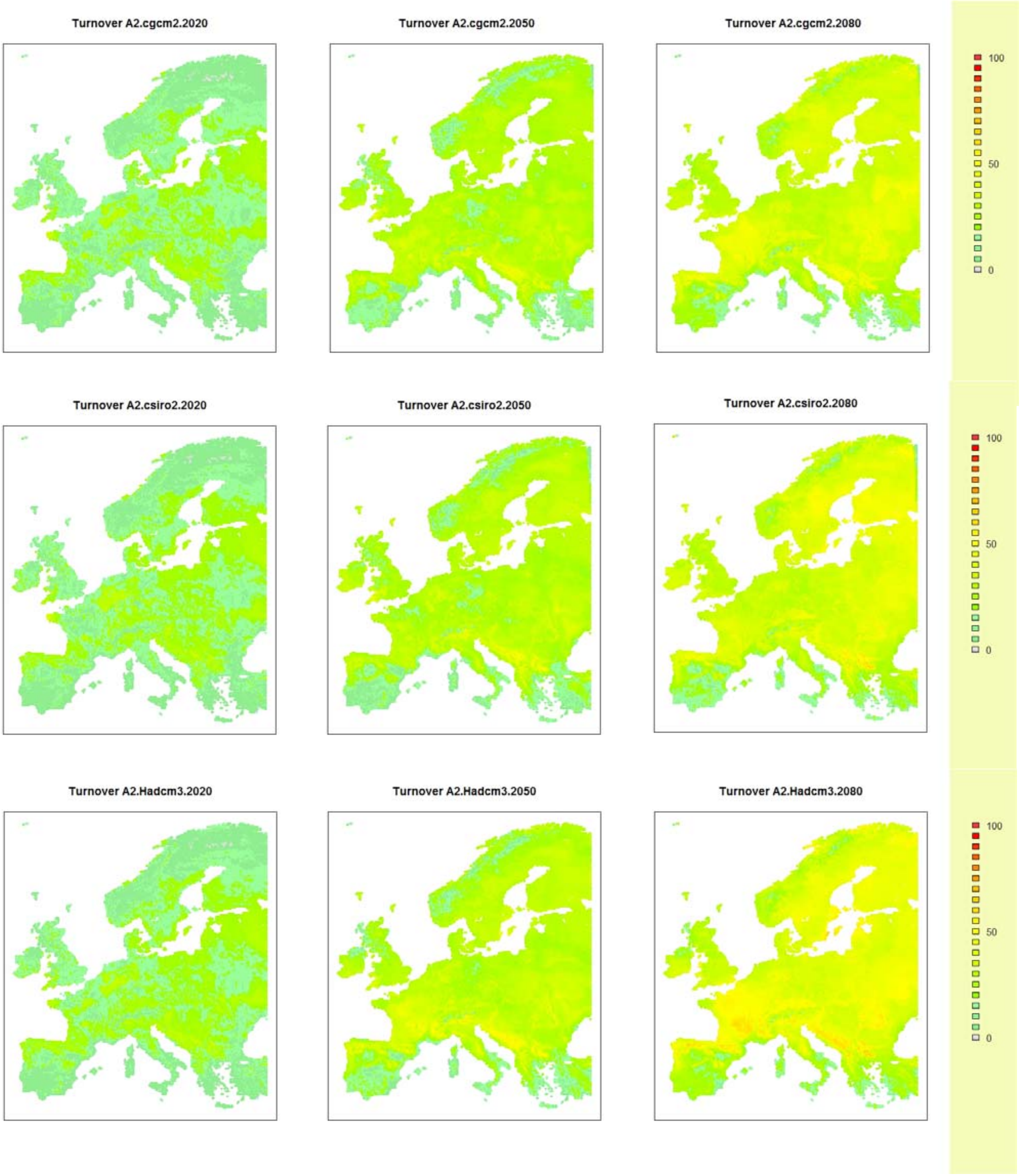
Turnover A1.csiro2.2080

Turnover A1.Hadcm3.2020

Turnover A1.Hadcm3.2050

Turnover A1.Hadcm3.2080

SPECIES TURNOVER IN BIRD COMMUNITIES – A2



SPECIES TURNOVER IN BIRD COMMUNITIES – B1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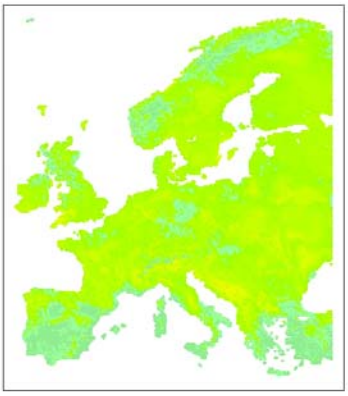
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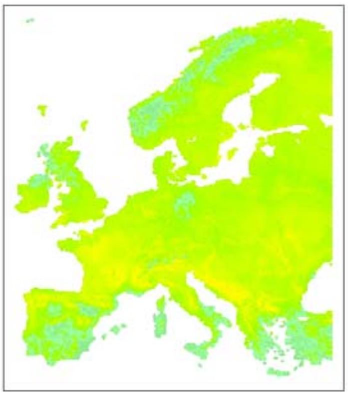
Turnover B1.cgcm2.2080

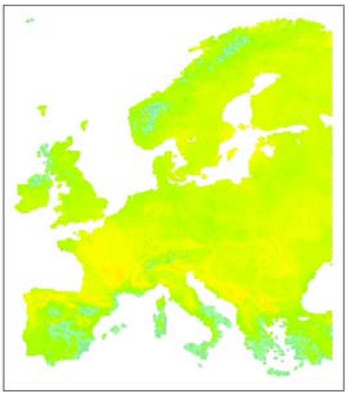

Turnover B1.csiro2.2020


Turnover B1.csiro2.2050

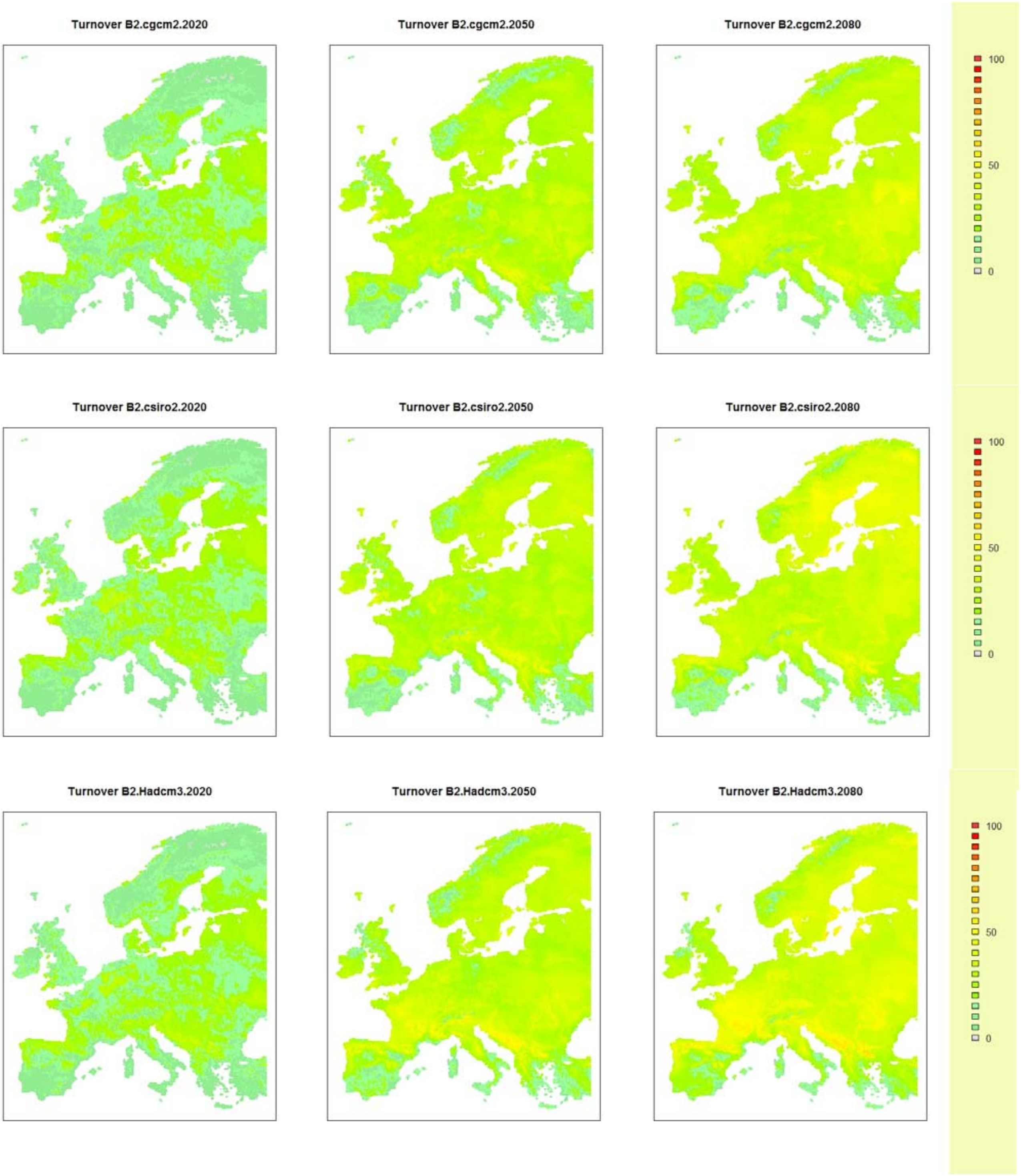

Turnover B1.csiro2.2080


Turnover B1.Hadcm3.2020


Turnover B1.Hadcm3.2050


Turnover B1.Hadcm3.2080

SPECIES TURNOVER IN BIRD COMMUNITIES – B2



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Turnover B2.cgcm2.2050

Turnover B2.cgcm2.2080

Turnover B2.csiro2.2020

Turnover B2.csiro2.2050

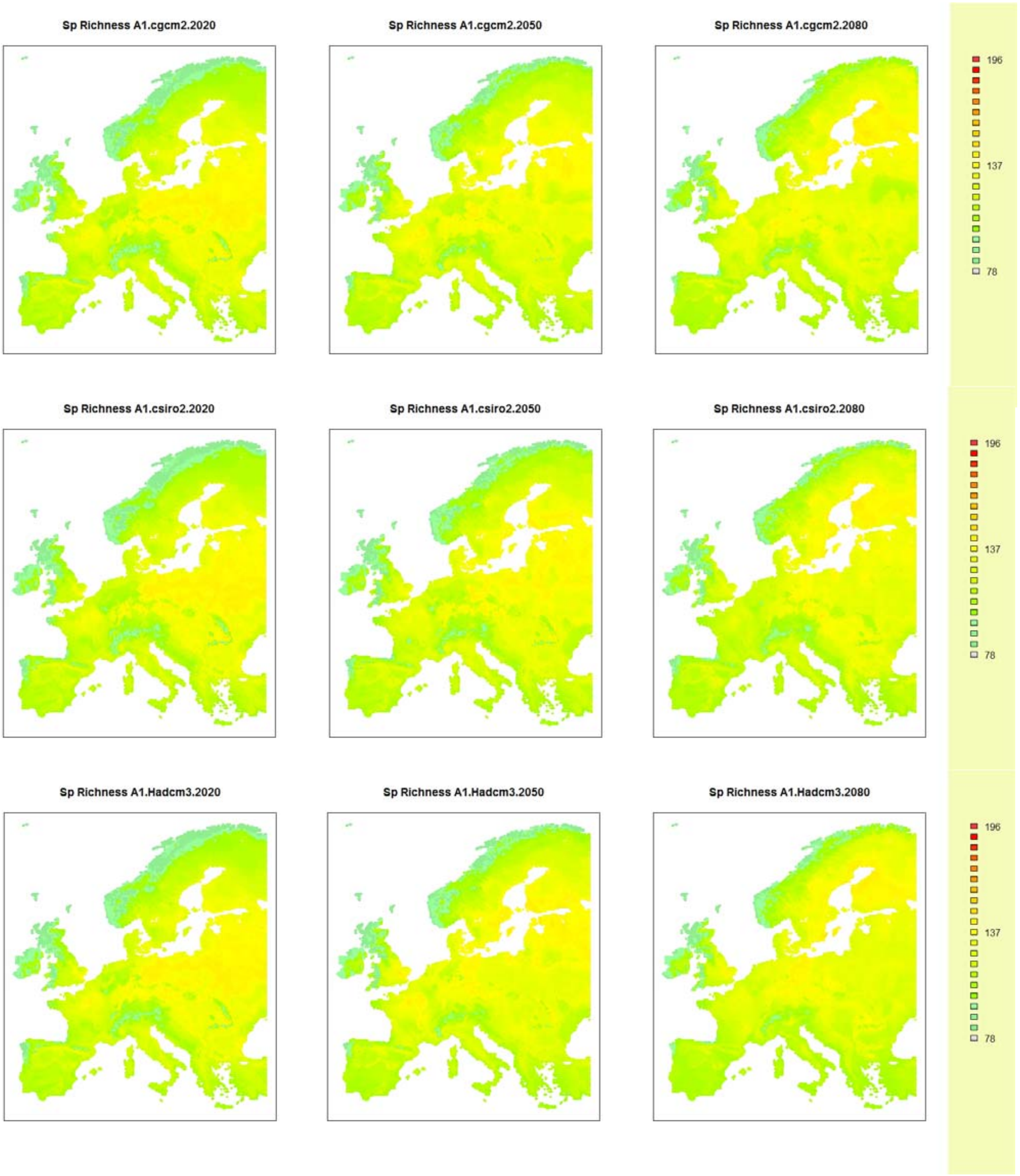
Turnover B2.csiro2.2080

Turnover B2.Hadcm3.2020

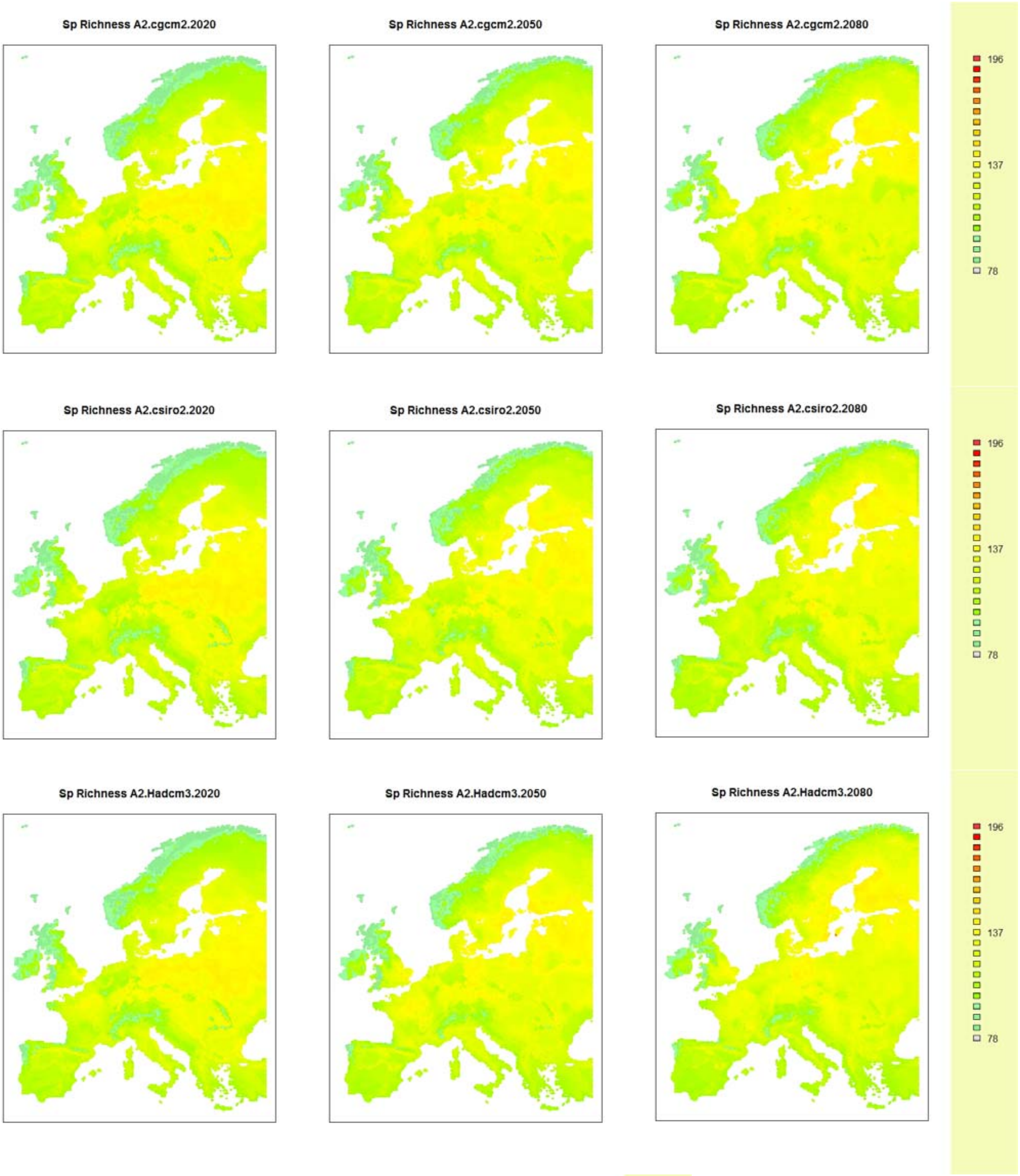
Turnover B2.Hadcm3.2050

Turnover B2.Hadcm3.2080

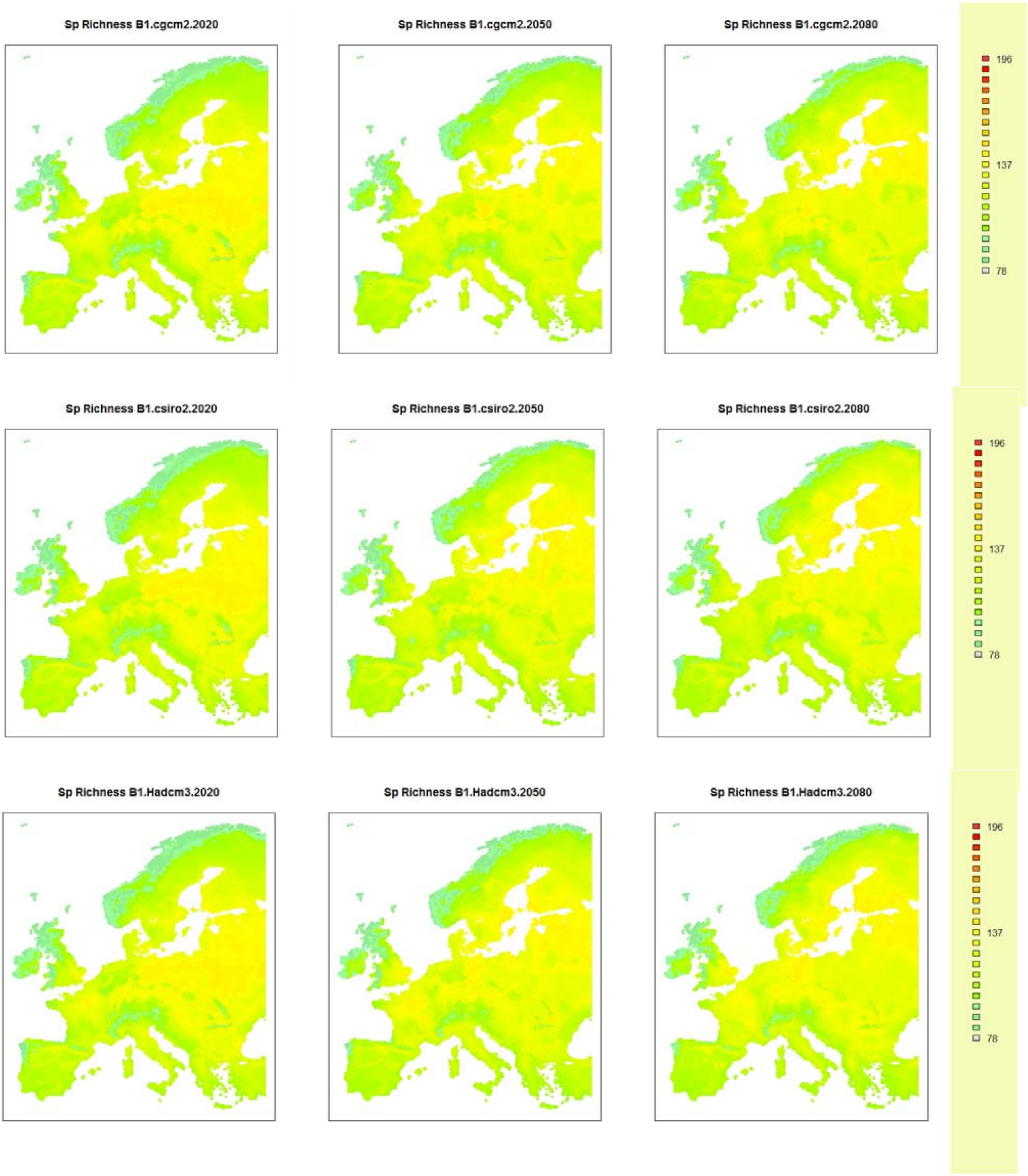
PROJECTED BIRD SPECIES RICHNESS – A1



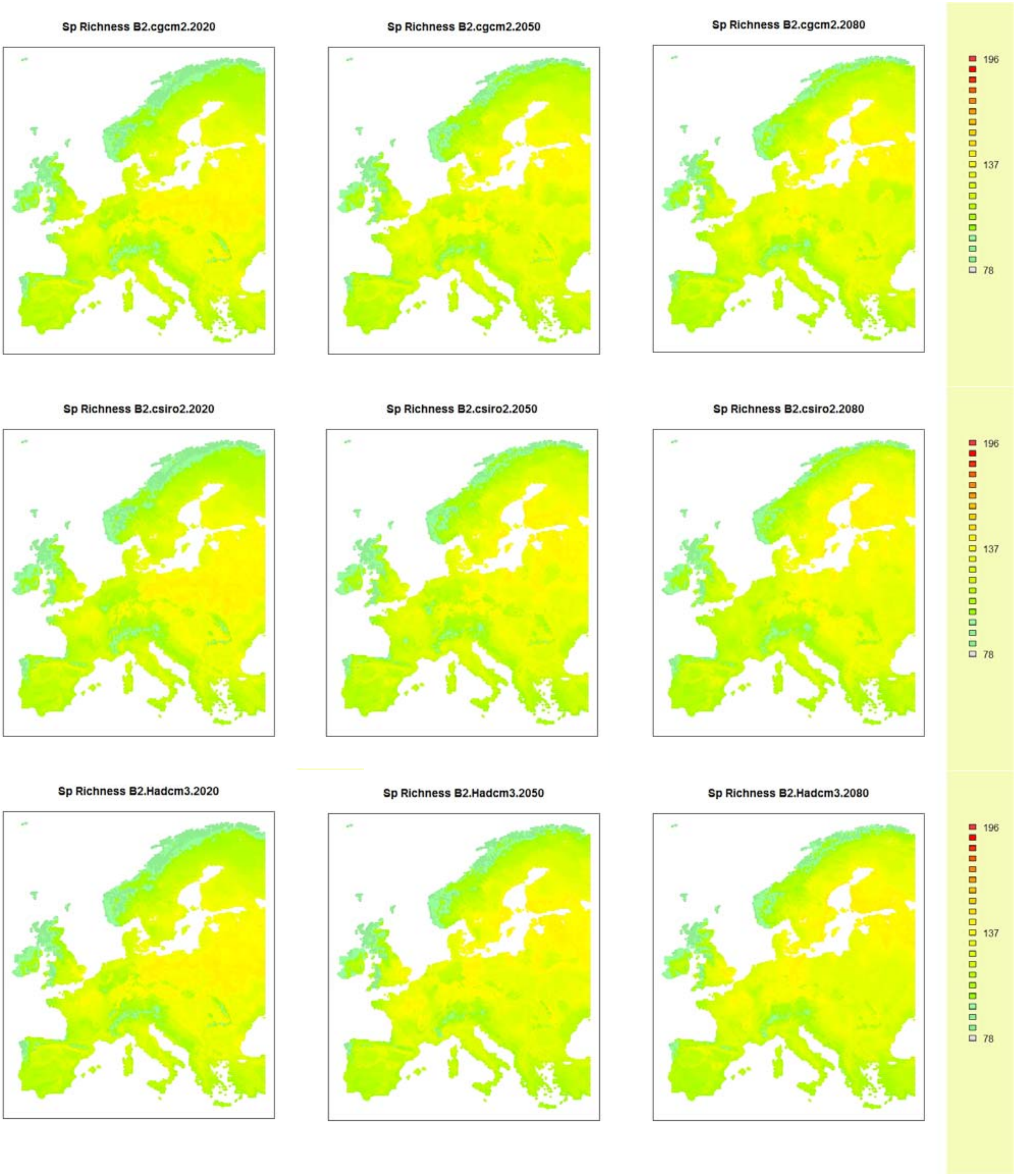
PROJECTED BIRD SPECIES RICHNESS – A2


Sp Richness A2.cgcm2.2020
Sp Richness A2.cgcm2.2050
Sp Richness A2.cgcm2.2080
Sp Richness A2.csiro2.2020
Sp Richness A2.csiro2.2050
Sp Richness A2.csiro2.2080
Sp Richness A2.Hadcm3.2020
Sp Richness A2.Hadcm3.2050
Sp Richness A2.Hadcm3.2080

PROJECTED BIRD SPECIES RICHNESS – B1



PROJECTED BIRD SPECIES RICHNESS – B2



Sp Richness B2.cgcm2.2020

Sp Richness B2.cgcm2.2050

Sp Richness B2.cgcm2.2080

Sp Richness B2.csiro2.2020

Sp Richness B2.csiro2.2050

Sp Richness B2.csiro2.2080

Sp Richness B2.Hadcm3.2020

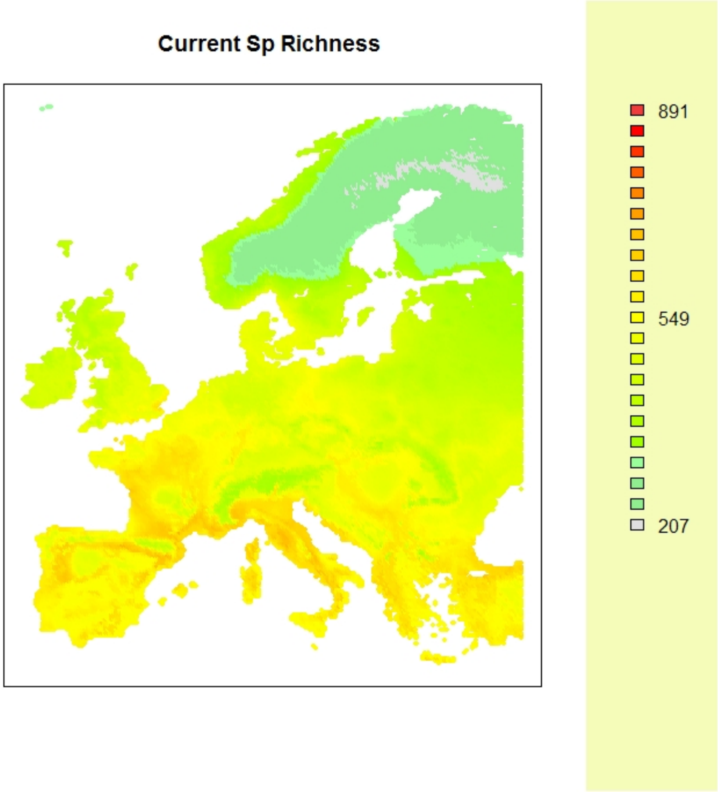
Sp Richness B2.Hadcm3.2050

Sp Richness B2.Hadcm3.2080

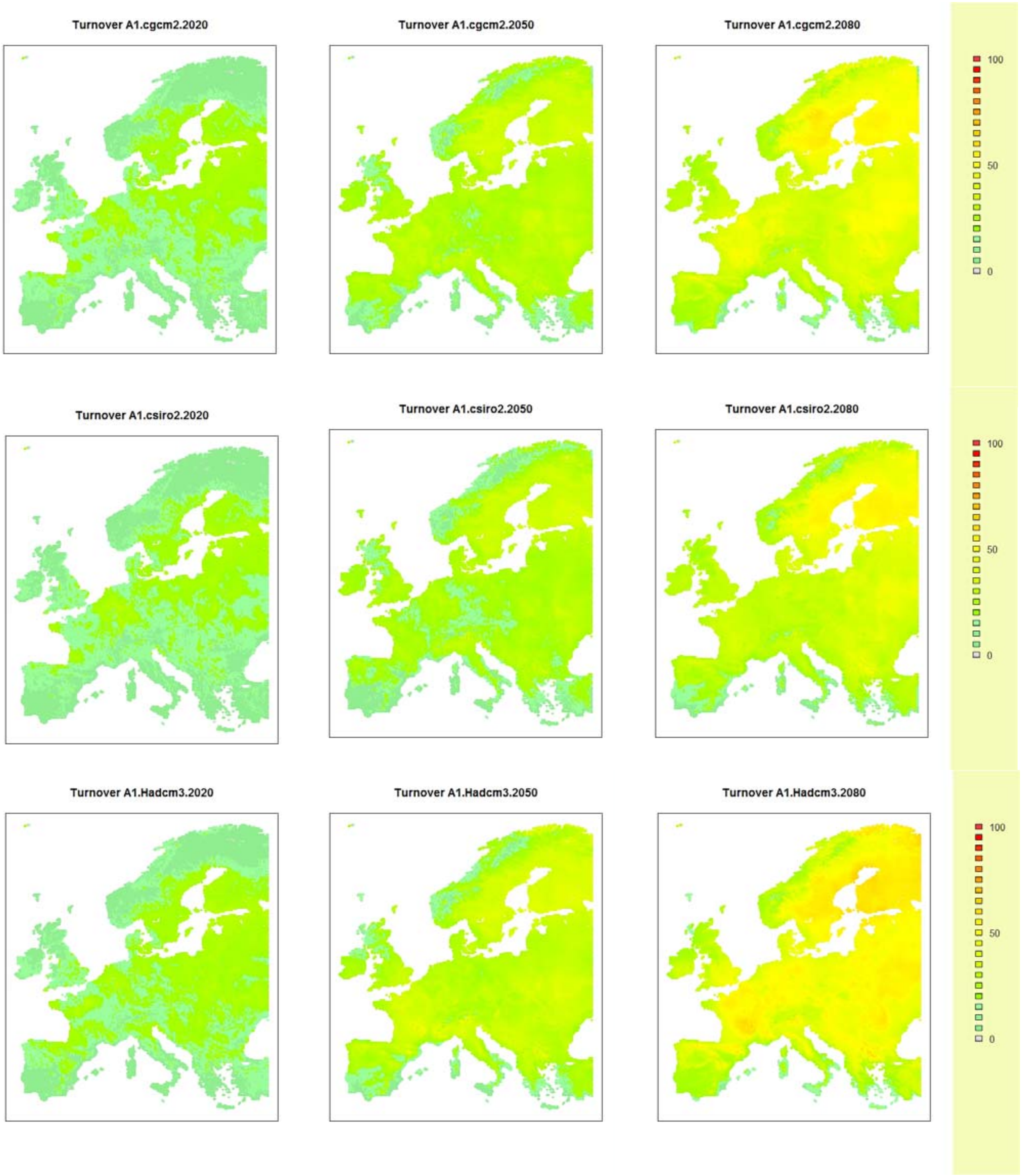
PLANTS

Similarly to Herptile communities, the turnover is projected greatest in the lower diversified regions (minding however that the minimum of diversity is 207 species, which is more important than the maximum of the other taxas), mainly being the Scandinavian and central-eastern territories. The maps show very little differences between GCM scenarios and the turnover stays generally low and most widely under 30%.

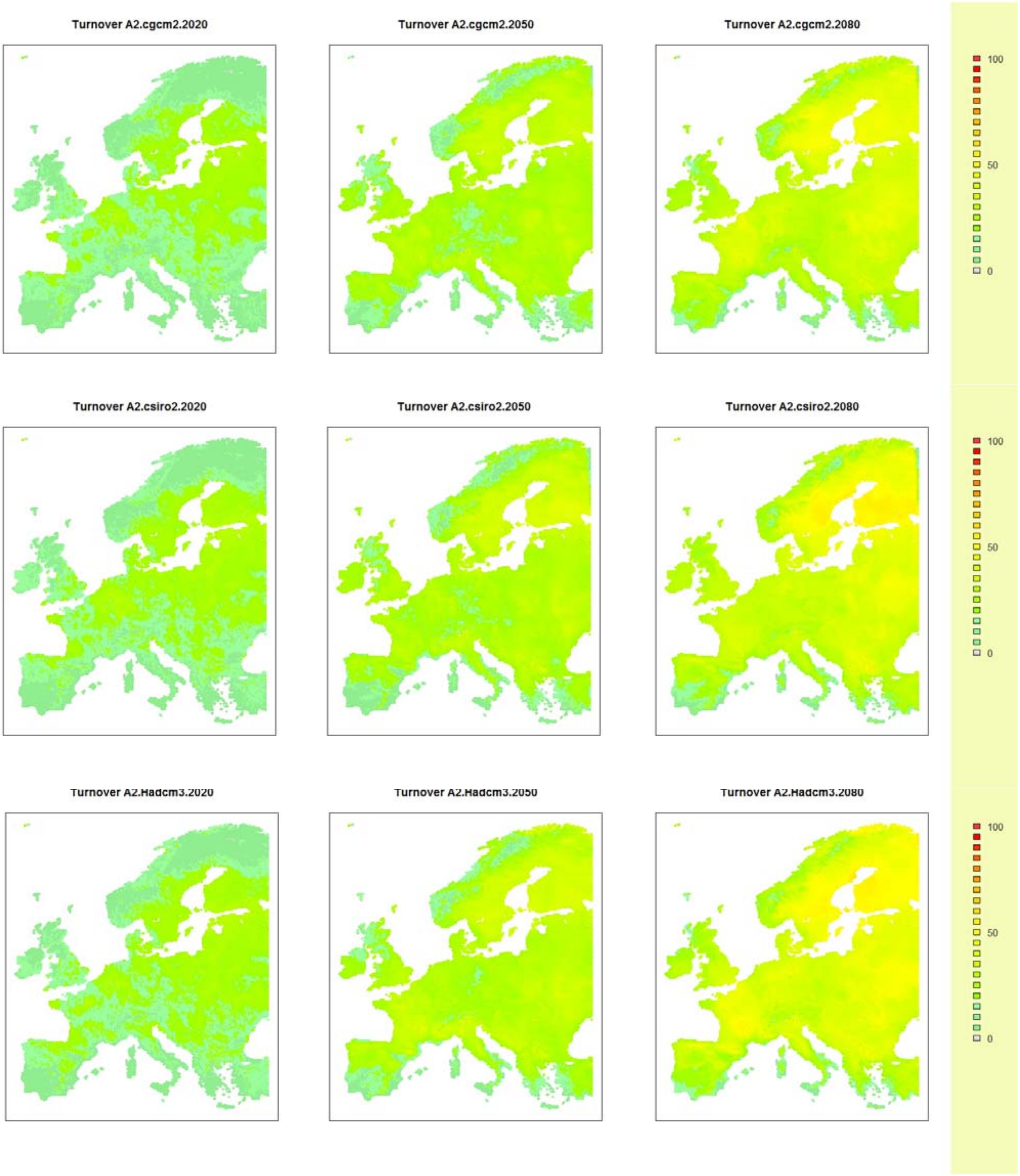
But because plant communities contain a wide amount of species, the consequences are very significantly more important on the community level than for the other taxas. The same pattern is observed than for the Herptiles with shifts of diversity oriented towards eastern and north areas of Europe and with a greater overall diversity. The Cgcm2 shows the fiercest evolutions of the diversity patterns, which HadCM3 and Csiro2 also enable to view.



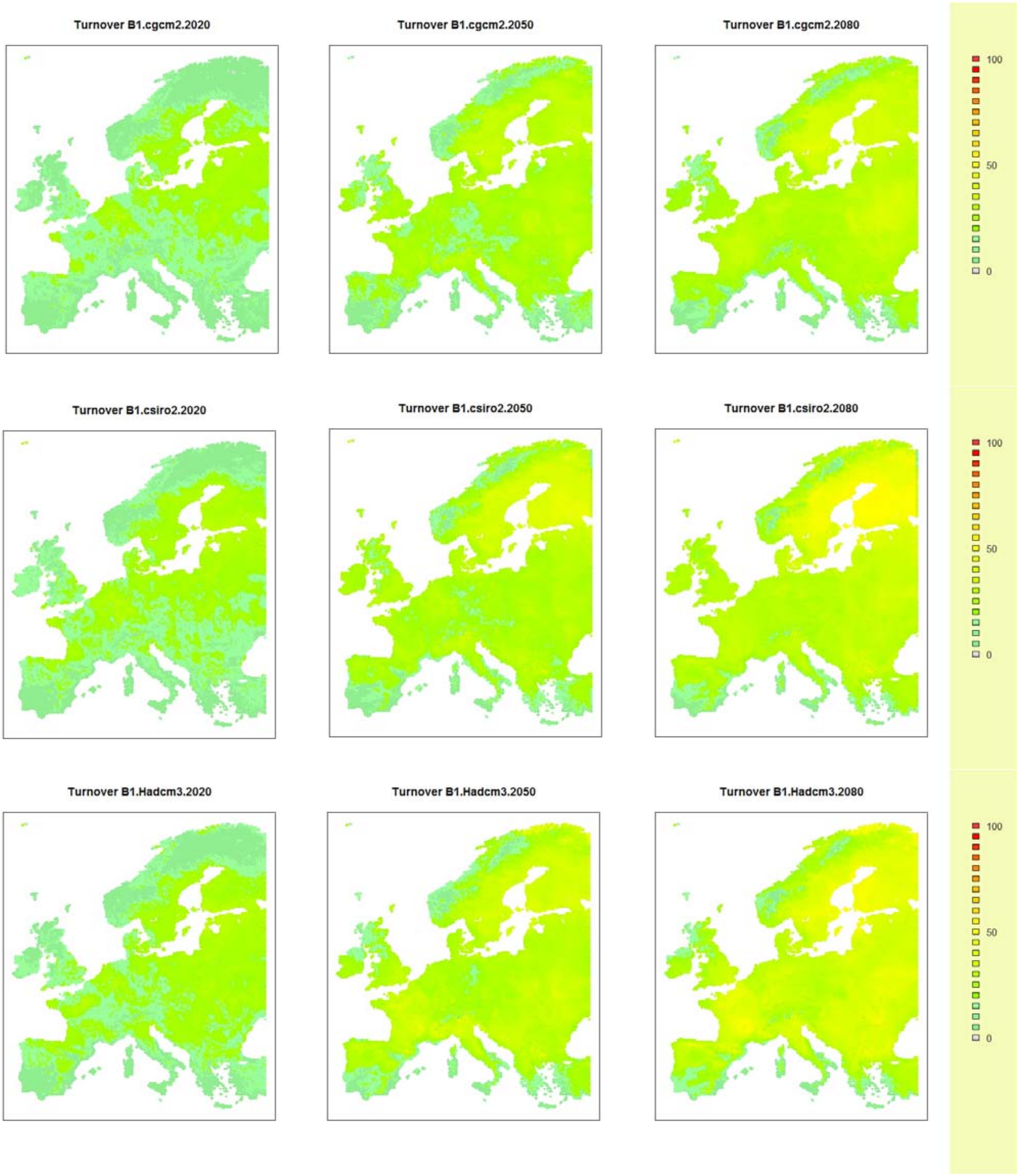
SPECIES TURNOVER IN PLANT COMMUNITIES – A1



SPECIES TURNOVER IN PLANT COMMUNITIES – A2



SPECIES TURNOVER IN PLANT COMMUNITIES – B1



Turnover B1.cgcm2.2020

Turnover B1.cgcm2.2050

Turnover B1.cgcm2.2080

Turnover B1.csiro2.2020

Turnover B1.csiro2.2050

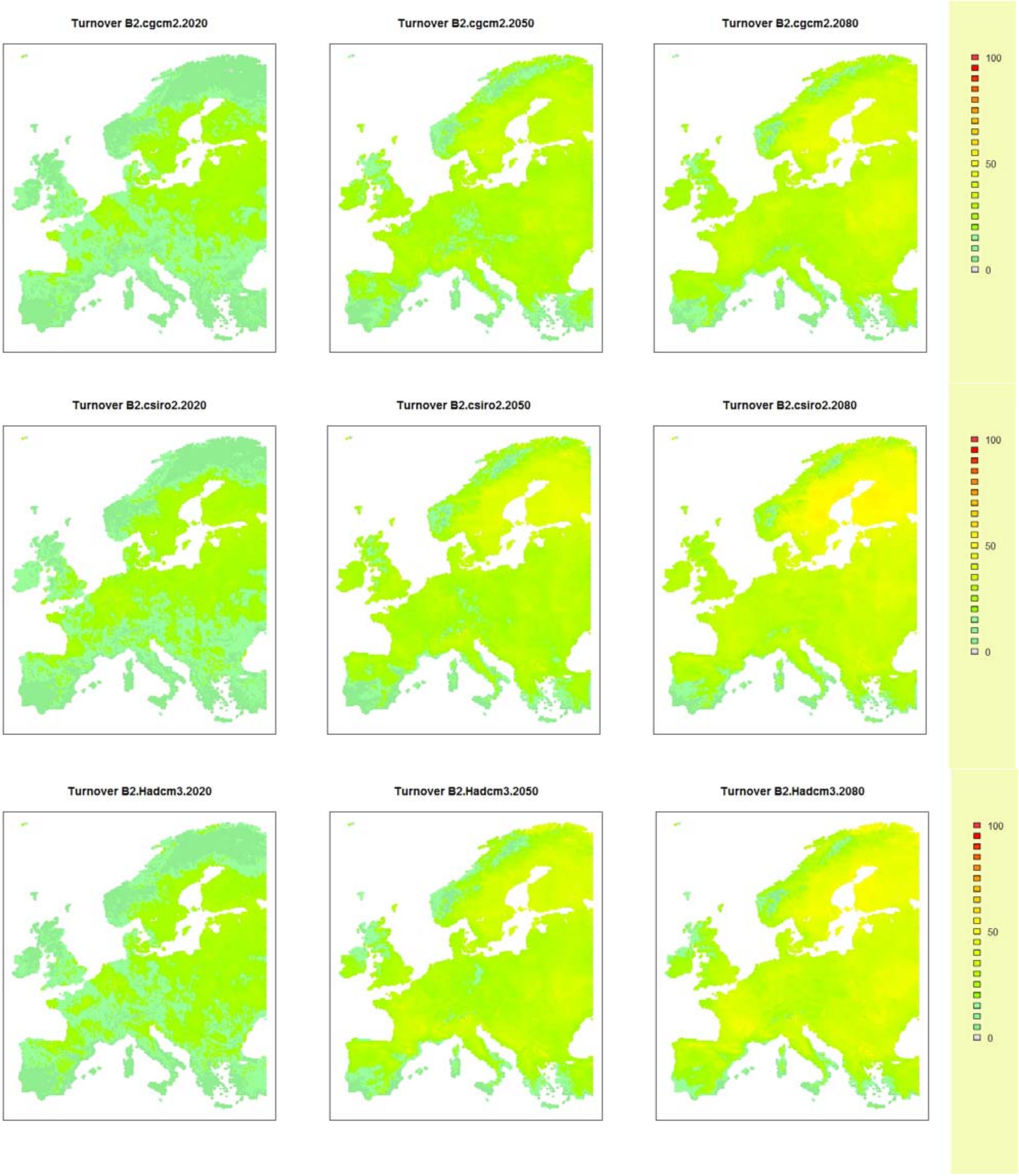
Turnover B1.csiro2.2080

Turnover B1.Hadcm3.2020

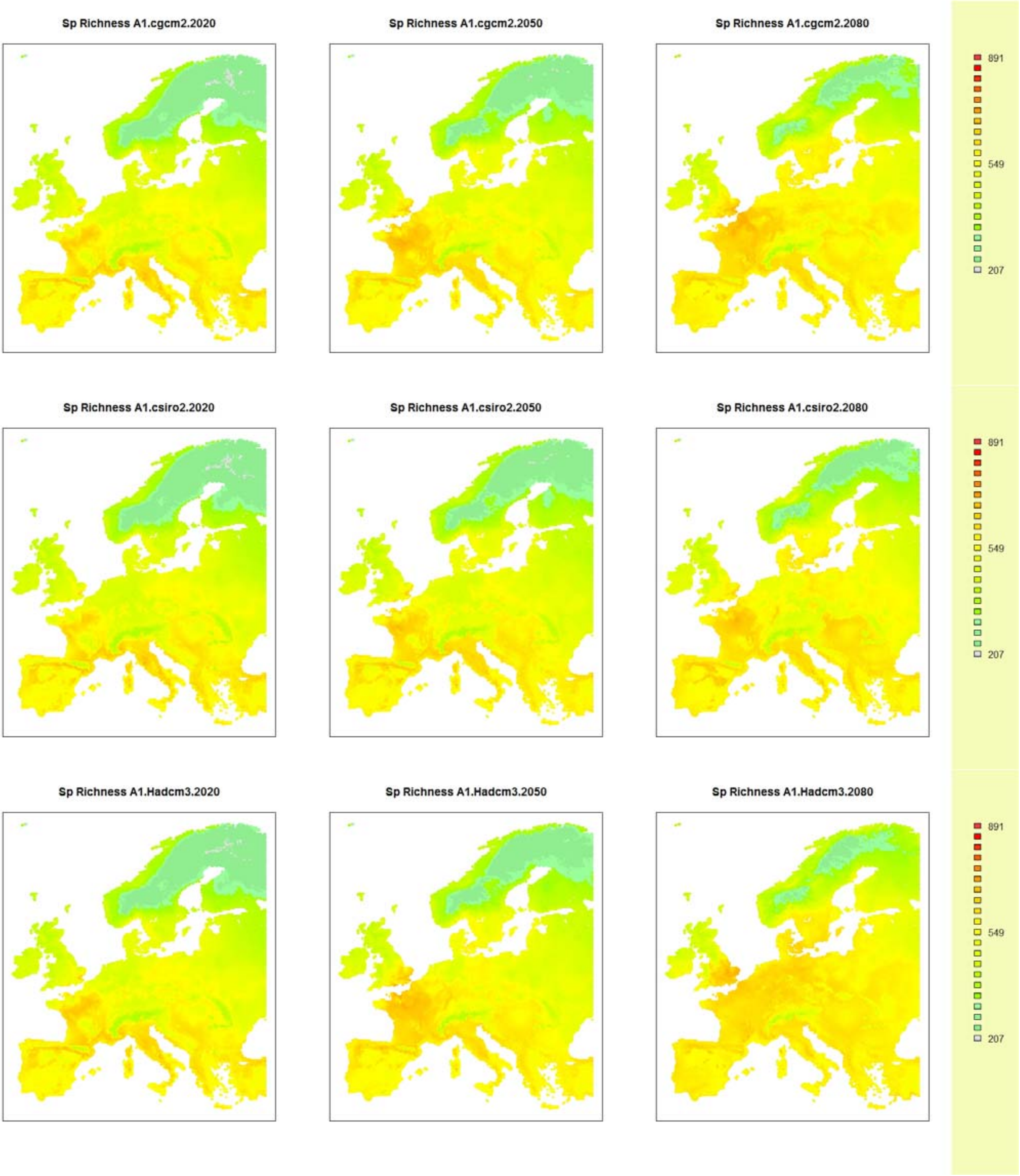
Turnover B1.Hadcm3.2050

Turnover B1.Hadcm3.2080

SPECIES TURNOVER IN PLANT COMMUNITIES – B2



PROJECTED PLANT SPECIES RICHNESS – A1



Sp Richness A1.cgcm2.2020

Sp Richness A1.cgcm2.2050

Sp Richness A1.cgcm2.2080

Sp Richness A1.csiro2.2020

Sp Richness A1.csiro2.2050

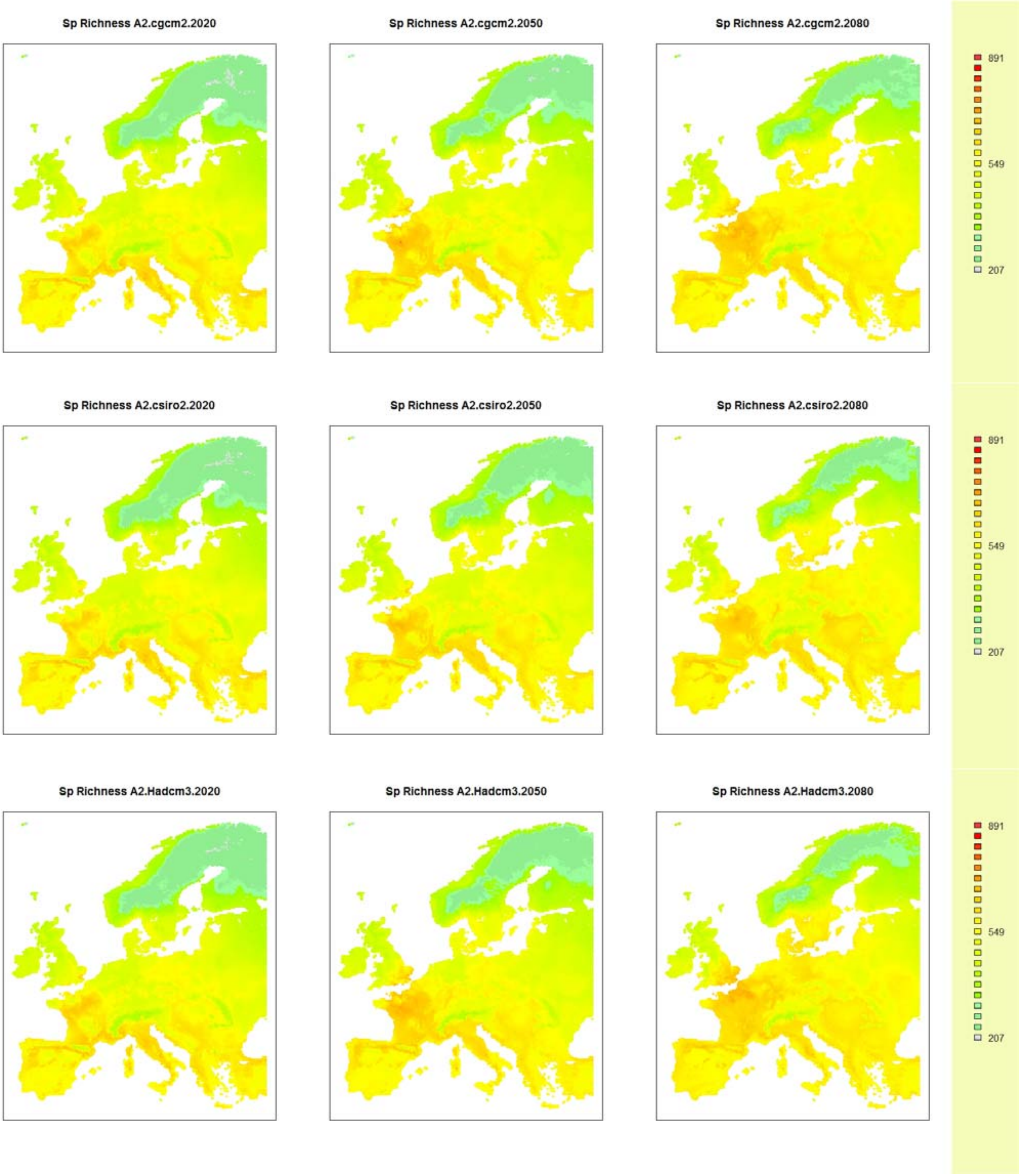
Sp Richness A1.csiro2.2080

Sp Richness A1.Hadcm3.2020

Sp Richness A1.Hadcm3.2050

Sp Richness A1.Hadcm3.2080

PROJECTED PLANT SPECIES RICHNESS – A2



Sp Richness A2.cgcm2.2020

Sp Richness A2.cgcm2.2050

Sp Richness A2.cgcm2.2080

Sp Richness A2.csiro2.2020

Sp Richness A2.csiro2.2050

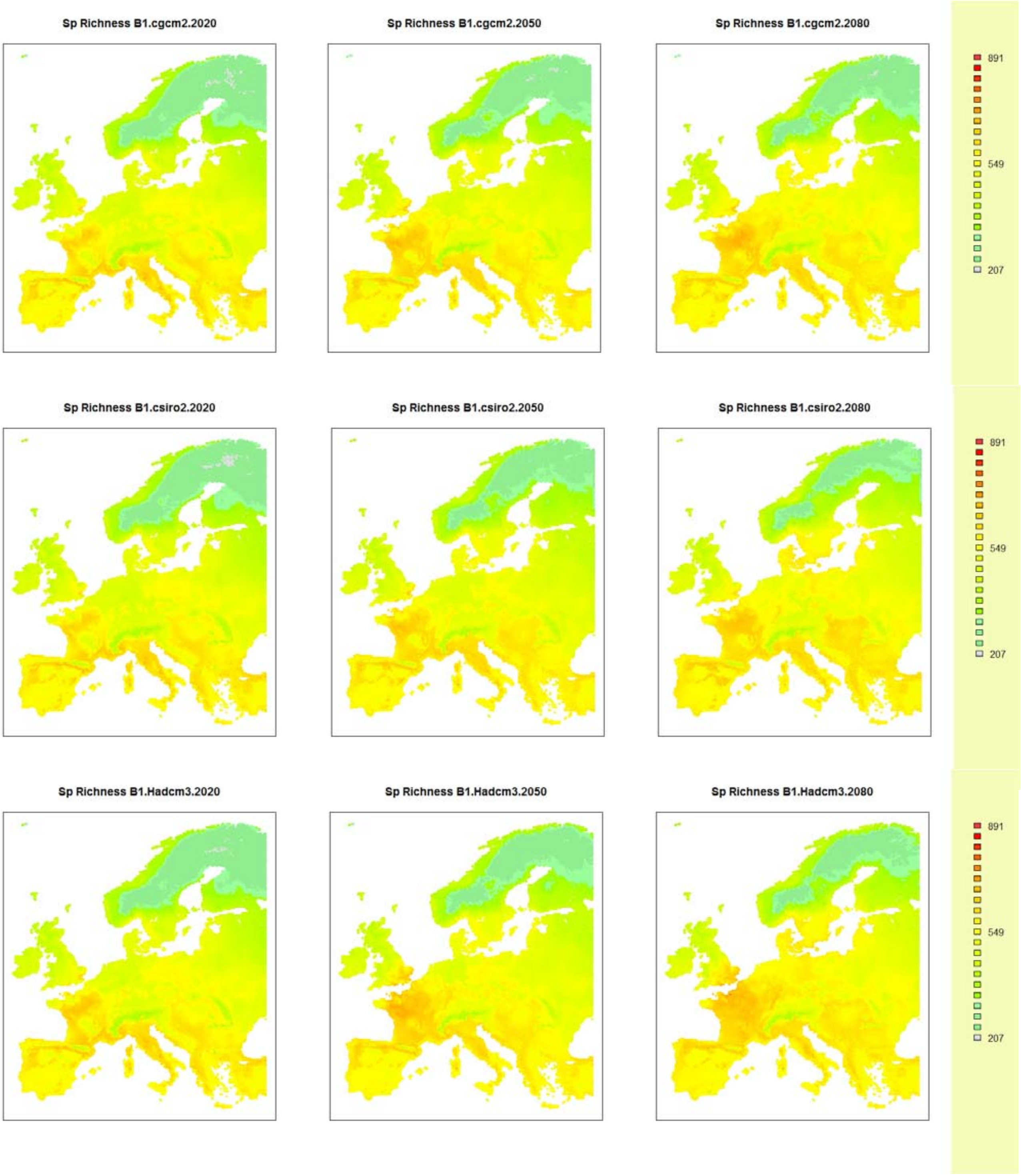
Sp Richness A2.csiro2.2080

Sp Richness A2.Hadcm3.2020

Sp Richness A2.Hadcm3.2050

Sp Richness A2.Hadcm3.2080

PROJECTED PLANT SPECIES RICHNESS – B1



Sp Richness B1.cgcm2.2020

Sp Richness B1.cgcm2.2050

Sp Richness B1.cgcm2.2080

Sp Richness B1.csiro2.2020

Sp Richness B1.csiro2.2050

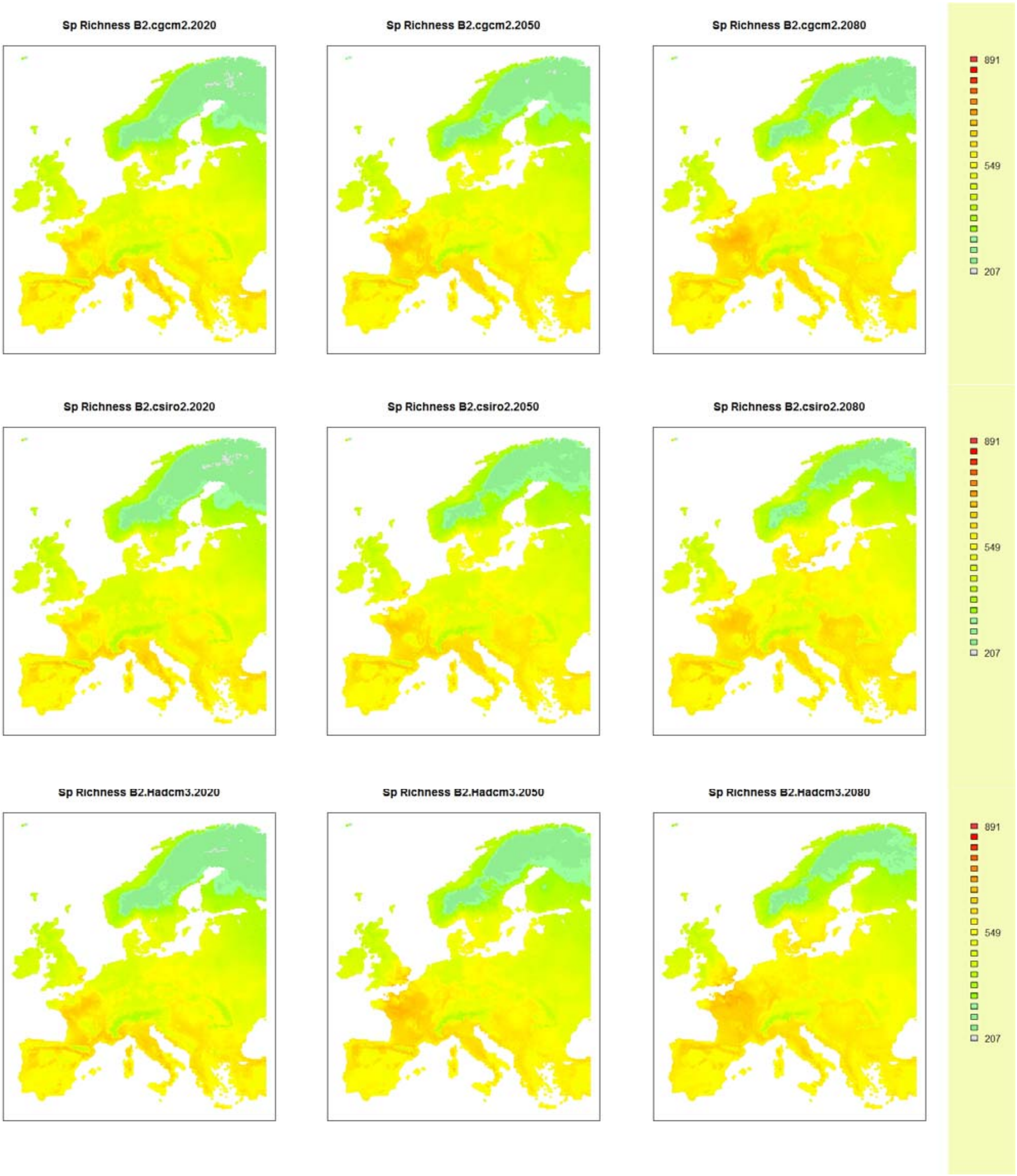
Sp Richness B1.csiro2.2080

Sp Richness B1.Hadcm3.2020

Sp Richness B1.Hadcm3.2050

Sp Richness B1.Hadcm3.2080

PROJECTED PLANT SPECIES RICHNESS – B2



Sp Richness B2.cgcm2.2020

Sp Richness B2.cgcm2.2050

Sp Richness B2.cgcm2.2080

Sp Richness B2.csiro2.2020

Sp Richness B2.csiro2.2050

Sp Richness B2.csiro2.2080

Sp Richness B2.Hadcm3.2020

Sp Richness B2.Hadcm3.2050

Sp Richness B2.Hadcm3.2080