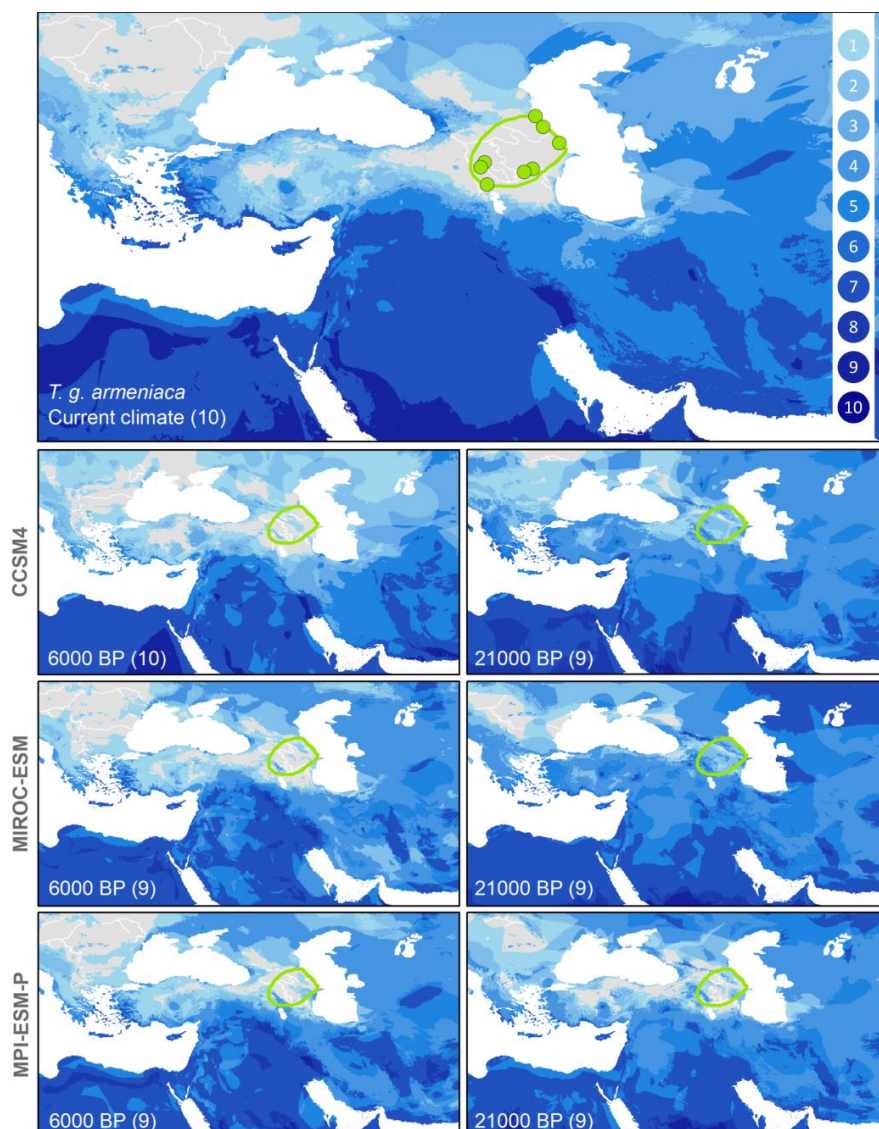
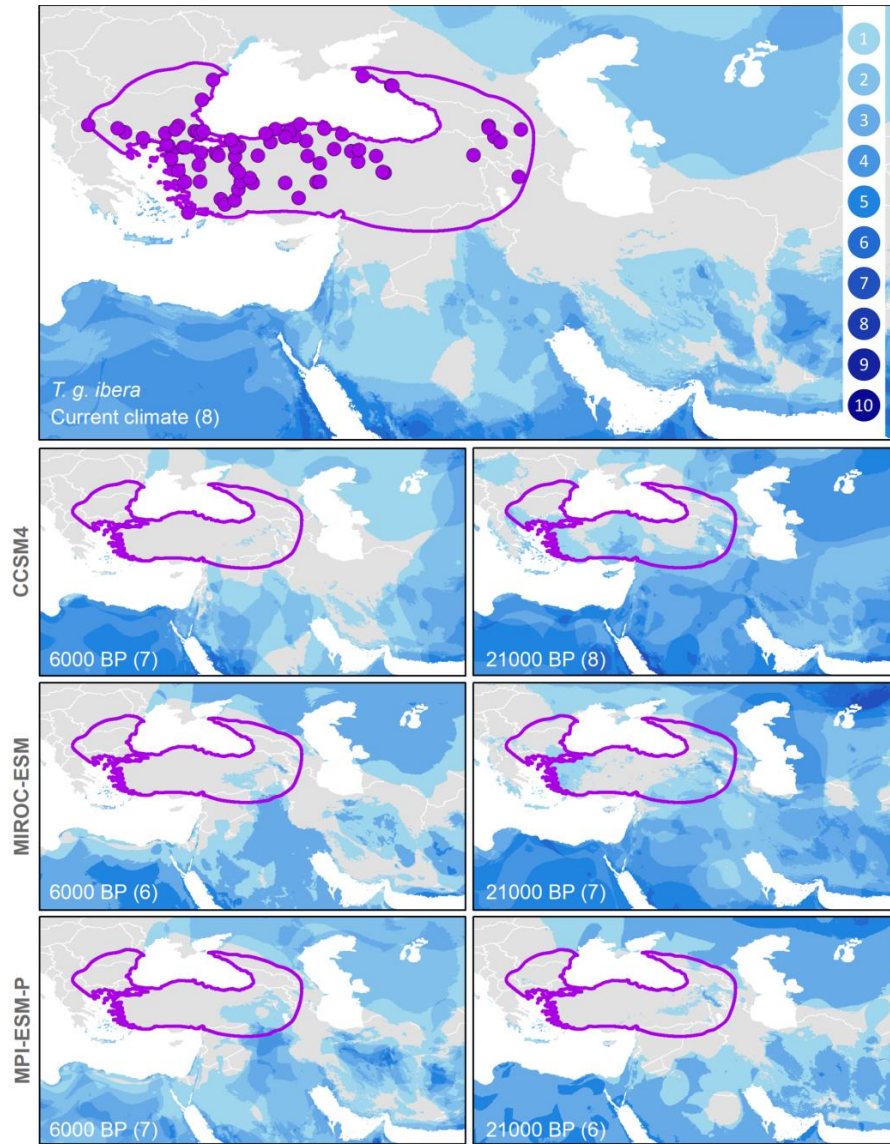


**“Reconstructions of the past distribution of *Testudo graeca* mitochondrial lineages in the Middle East and Transcaucasia support multiple refugia since the Last Glacial Maximum”: A response to Turkozan et al. (2021)**

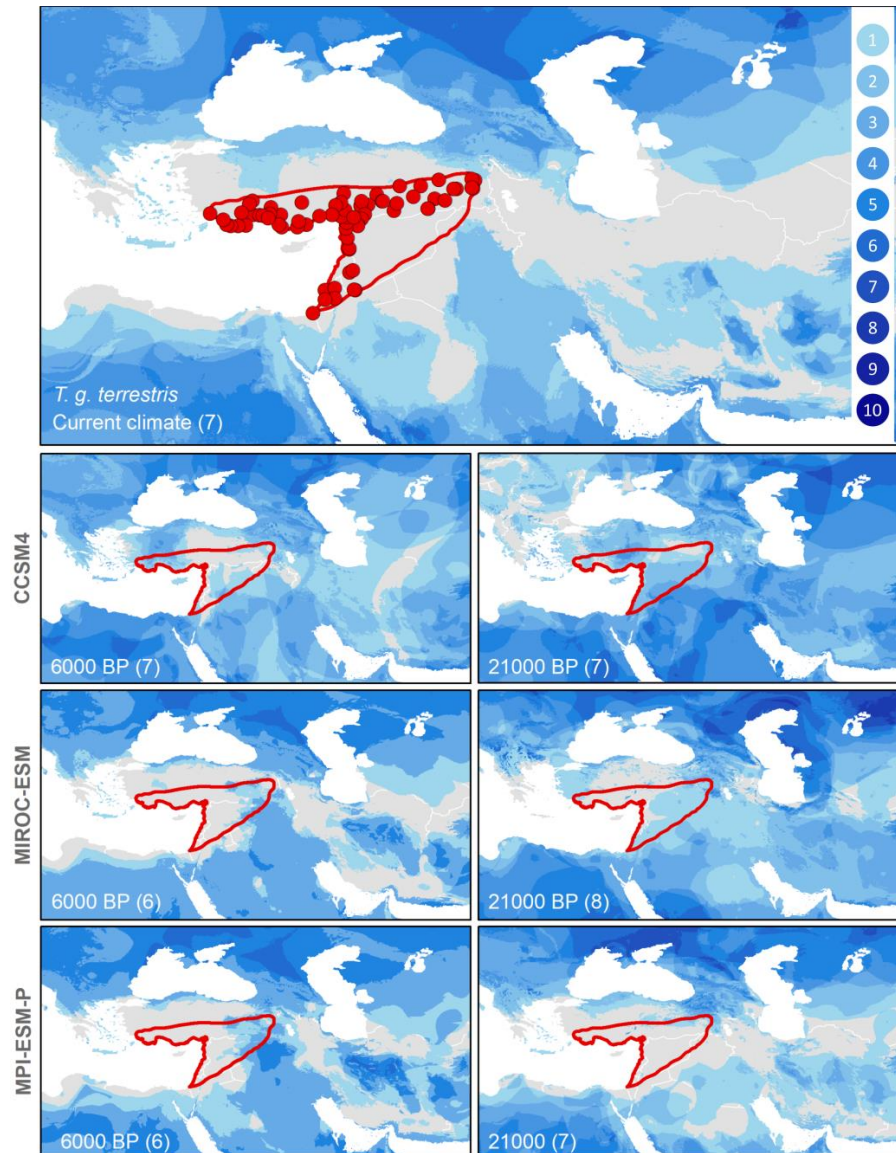
Flora Ihlow, Uwe Fritz, Peter Mikulíček & Dennis Rödder



**Figure S1.** MESS maps for the current and past potential distribution of *Testudo graeca armeniaca* as presented by Turkozan et al. (2021). MCPs and species records were georeferenced from Turkozan et al. (2021). Land surface is displayed as light grey area except for regions where the model is compromised by extrapolation. For compromised regions, various shades of blue indicate the number of predictor variables affected by extrapolation. Accordingly, the lightest blue refers to regions where only a single variable was compromised by extrapolation, whereas the darkest blue represents regions where all 10 predictors were compromised

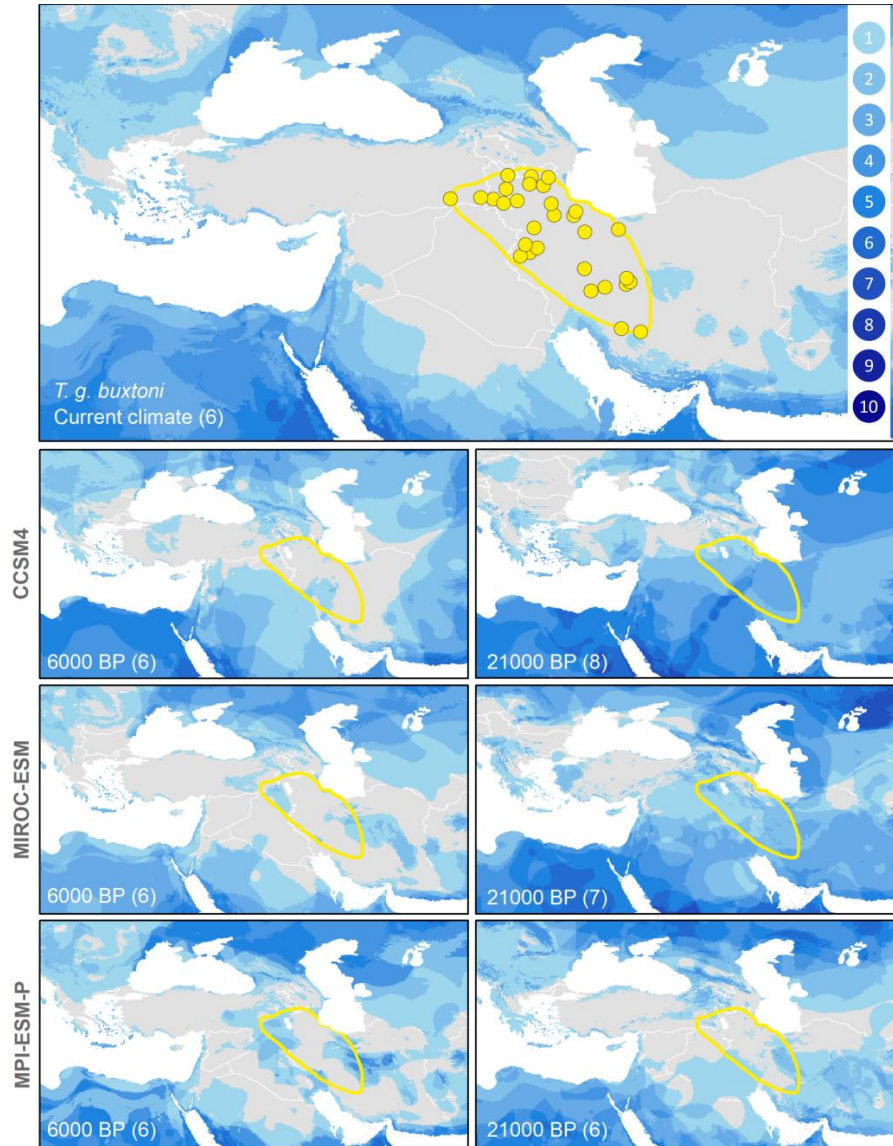


**Figure S2.** MESS maps for the current and past potential distribution of *Testudo graeca iberica* as presented by Turkozan et al. (2021). For further explanation, see Fig. S1

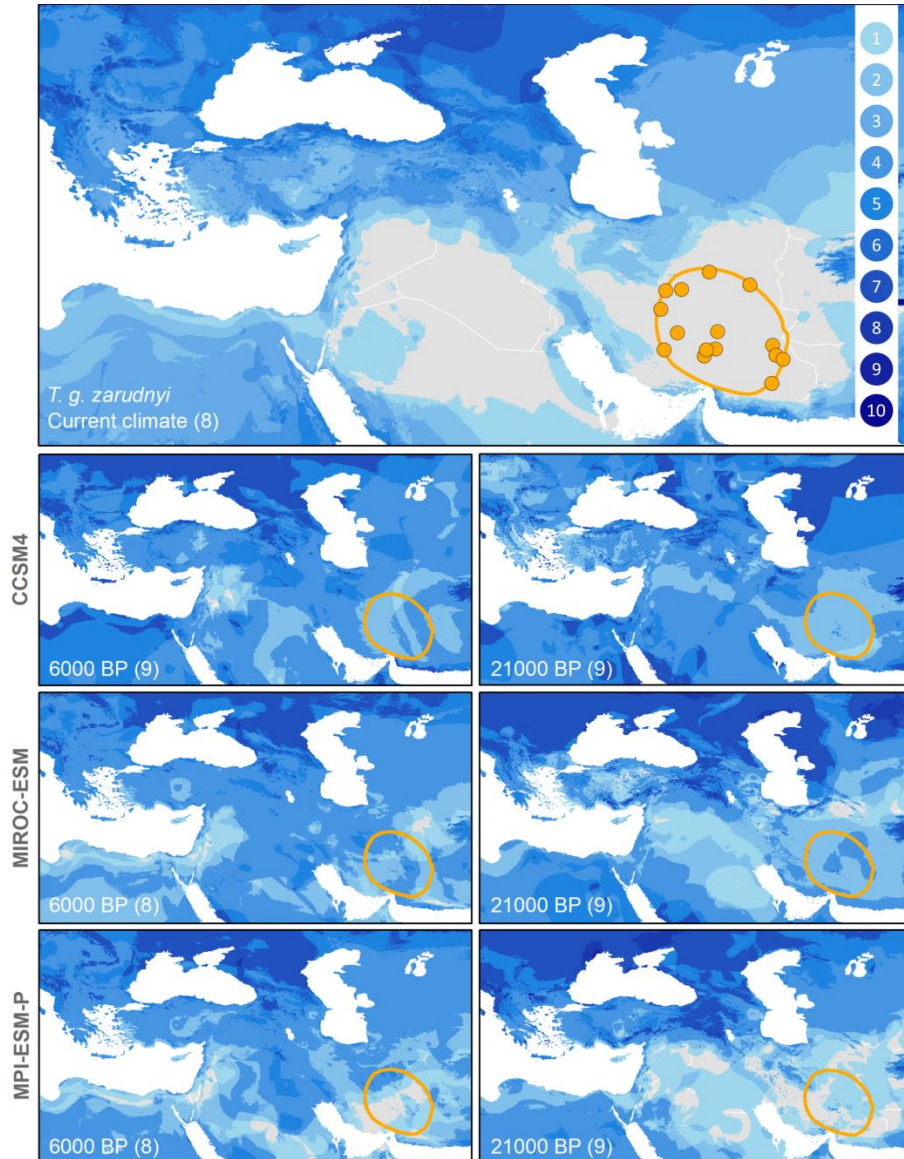


**Figure S3.** MESS maps for the current and past potential distribution of *Testudo graeca terrestris* as presented by Turkozan et al. (2021). For further explanation, see Fig. S1





**Figure S4.** MESS maps for the current and past potential distribution of *Testudo graeca buxtoni* as presented by Turkozan et al. (2021). For further explanation, see Fig. S1



**Figure S5.** MESS maps for the current and past potential distribution of *Testudo graeca zarudnyi* as presented by Turkozan et al. (2021). For further explanation, see Fig. S1

**Supplementary File S6.** R code for computation of multivariate environmental similarity surface (MESS) analyses

```
wd <- "D:/Graeca"

setwd(wd)
library(raster)
library(dismo)

my.masks <- list.files(paste(wd, "/mask", sep=""), ".asc", recursive=T, full.names=T)
current <- list.files(paste(wd, "/Current", sep=""), ".asc", recursive=T, full.names=T)
projs <- list.dirs(paste(wd, "/proj", sep=""), sep="")
names.projs <- list.dirs(paste(wd, "/proj", sep=""), full.names=F)

current <- stack(current)

for (j in 1:length(my.masks)){
  r <- raster(my.masks[j])
  p <- rasterToPoints(r, fun=function(x){x>0.1})
  ref <- extract(current, p[,1:2])

  for (i in 2:length(projs)){
    my.proj <- list.files(projs[i], ".asc", full.names=T)
    ms <- mess(stack(my.proj), ref, full=T)
    rcl <- c(-1000000000000, 0, 1, 0, 100000, 0)
    ms1 <- reclassify(ms[[1:10]], rcl)
    ms1 <- calc(ms1, sum)
    my.name <- paste(names(r), "_", names.projs[i], ".asc", sep="")
    writeRaster(ms1, my.name, overwrite=T)
  }
}

m <- raster("mask.asc")
shp <- readOGR("D:/Graeca/Graeca_mcps/armeniaca_mcp3.shp")
r <- rasterize(m, shp, paste("armeniaca_mcp3.shp", ".asc", sep=""))
```