**Analysis of population and taxonomic structuring of mussel settlements in 2009-2010**

The analysis was conducted in three steps. First, statistical associations between demographic, taxonomic and environmental parameters of mussel settlements were quantified by use of canonical correspondence analysis (CCA, Ter Braak, Verdonschot, 1995). The goals of the CCA were to find out which environmental parameters have a significant influence on the spatial organization of mussel settlements and also to describe characteristic mussel habitats. In initial analysis, the matrix of dependent variables included all demographic and taxonomic parameters while the predictor’s matrix - all environmental parameters ~~of settlements~~ considered. Subsequently the predictor’s set was reduced according to forward selection protocol (Blanchet et al., 2008) allowed constructing the optimal model. The statistical significance of the optimal model and particular constrains was assessed by permutation methods (Legendre, Legendre, 2012).

Second, the permutation multivariate analysis of variance (PERMANOVA, Anderson, 2014) aimed to find out whether the demographic and taxonomic parameters of settlements from various habitats differed significantly. Data preparation for PERMANOVA included the following steps: the matrix of dependent variables (the same as CCA) was transformed (log(x+1)), the Bray-Curtis distance matrix was calculated and equality of within-group variance was checked.

Third, regression analysis was applied to study the association between taxonomic structure of mussel settlements and environmental parameters. We used generalized linear mixed model (GLMM) with beta distribution and a logit link-function. Ptros was the dependent variable, and environmental parameters were predictors. The Transects was included into the model as a random factor influencing the model intercept. The vector values of each quantitative predictor were previously standardized. Before fitting the model, the set of all predictors was checked for variance inflation factors (if vif was >2, such predictors were excluded). The validity of final model was inspected ~~accomplished~~ by visual analysis of residual plots and the assessment of the overdispersion presence.

**Analysis of the temporal dynamics of mussel settlements**

The analysis was performed separately for both the dynamics of the demographic and taxonomic structure because the material was heterogeneous. For the same reason, we analyzed separately changes between I and II observation periods and between other periods. To assess the dynamics of demographic structure and to find out whether it was unidirectional in all mussel habitats, we used PERMANOVA with two factors (Period and Habitat) and the interaction between them. Two analyses were conducted: I vs II observation periods (20 settlements in each) and II vs III vs IV periods (5 settlements in each). ~~The similar percent analysis routine (SIMPER, Clarke, 1993) was performed to evaluate the contribution~~ A similarity percentages procedure (SIMPER) analysis (Clarke 1993 ) was performed to estimate the contribution of each ~~of~~ demographic parameters to temporal dynamics between I and II periods. Data preparation and assumption testing for PERMANOVA and SIMPER were the same as described above.

In addition, we used a correspondence analysis (CA) in order to identify general trends in the temporal dynamics. The matrix of ~~dependent~~ variables consisted of demographic parameters of all settlements accumulated from 2004 to 2018 was used for the CA. The dynamics of the taxonomic structure of settlements (Ptros) was analyzed using the Wilcoxon test. A total of three comparisons were made: I vs II periods (9 settlements), II vs III periods (5 settlements) and III vs IV (5 settlements, the same as in II vs III comparisons).

All statistical analysis were performed with functions of R statistical programming language (R Core Team, 2020). Multidimensional analyses (CA, CCA, PERMANOVA, SIMPER) were performed by “vegan” package (Oksanen et al., 2020), regression analysis was performed by “glmmTMB” package (Brooks et al., 2017).

Получается слишком много demographic parameters/structure, environmental parameters, settlements…Либо надо по-другому формулировать, либо какие-то аббревиатуры давать. Или и так сойдёт?