Response to Reviewer 2 ROUND 1

**Point 1:** The methods, especially the statistical methods are greatly lacking. The reader does not know how statistiacal tests are applied until trying to figure that out by reading the result section. So much more details on sampling and especially statistical analysis are needed.

**Response 1:** The Materials and Methods has been changed and more details on statistics were included in this part

**Point 2** – The authors use really simple statistics for analysing their data. For example using t-test to compare size differences, where (when reading the results) it seems that they were mostly comparing differences between sexes within habitats. For a more detailed information from their size data, giving results on differences between areas and sexes I would strongly suggest the authors to use some kind of linear mixed models for this analysis.

**Response 2:** Authors have icluded the regression models in the analysis of data

**Point 3** – It is impossible to see how the X2 tests were performed. Did the authors considered using Linear Mixed Models for their analysis taking location and sex in to the picture in one, much stronger test.

**Response 3:** The relationship between the frequency of left-sided morph and sex, length and age was already studied and published (Yershov et al. 2022)

**Point 4** – The methods do not discuss how the authors collected information from the published literature. Was this just a random pick of papers or was there a systematic search. Did the authors not consider statistical analysis on this data?

**Response 4:** Authors carried out the systematic search of necessary information from the published literature. Additionally we used data from GBIF (The Global Biodiversity Information Facility) to assess the distribution pattren of flounder in Europe. Regression analysis was applied to these data.

**Point 5** – The discussion is long. It includes quite a lot of speculations regarding the origin of left-right polymorphism in flounder. Often these are highly speculative and the data in the present study does not support those in either way. I would suggest the discussion to be more focused and anchored better in the observed results. Results from other studies on the origin of the polymorphism, could be summarised and combined to a single paragraph.

**Response 5:** The discussion was shortened, revised significantly and some issues not directly related to the topic were removed from the text

**Point 6** – Lines 166 – 179. The discussion in this paragraph is highly speculative and are not supported by the data in any way, which is what large part of the later discussion is indicating. I would suggest this speculations to be taken out of the discussion.

**Response 6:** Thank you for this suggestion. Authors have deleted this paragraph.

**Point 7** – Discussion in lines 225 – 231 is missing references to support the statements of the authors.

**Response 7:** All necessary references were added in the text.

**Point 8** – The final statement is highly speculative. The observed patterns do not have to be adaptive through natural selection, as other factors may play an important role, e.g. plasticity and or change.

**Response 8:** Conclusion was rephrased and more details were provided

Response to Reviewer 2 ROUND 2

**Point 1:** I suggested that the authors used linear models for analysing how sex and size had an effect on the proportion. It looks to me that the authors have removed this data from the analysis, thus no linear models on this, and published in a zoological institute proceedings. I think this data would have been an important contribution here and added value to the paper.

**Response 1:** The main task of our paper was to analyze spatial (local and geographic) variability of the frequency of left-sided flounder morph. Association of probability of the left-sided morph occurrence with predictors (“Sex”, “Size”, “Age”) was analyzed earlier by means of logistic linear model [Yershov et al. 2022].

**Point 2** – Now the authors have included linear models in relation to something else, which I have a hard time understanding what is.  As far as I can understand from the MS the authors are now testing if the proportion of left vs right proportions is related to the distance from the mean of the distribution of the species, either in the European part of the species range or in the Arctic region. It is hard to see the justification of such a test, and the authors need to explain this further.

**Response 2:** Some explanations of the approach were added to the text for better understanding of the material. To analyse the pattern of geographic distribution we constructed two regression models in which the dependent variable was the proportion of left-sided morphs (the value was assumed to follow the beta distribution). The distance from the geometrical center of the European part of the species’ range was used as the first predictor in both models. Longitude was considered as the second predictor, additionally describing the geographic position. Latitude was not included in the models, because it demonstrated collinearity with the other predictors.

**Point 3** – As a follow up on 1. When using data from published literature, the authors need to look in to how meta analysis is performed, reported and analysed. There are special ways of doing so, which the authors have not clearly shown.

**Response 3:** In “Introduction” and “Material and Methods” we thoroughly described how the meta-analysis of published and original data was performed. All references on statistical tools and approaches are provided. We conducted systematical search of published data for analysis of geographical variation in morph proportions in flounder *P.flesus*. No statistically significant and consistent changes in interannual variation in proportion of left-sided individuals were found in flounder populations [Fuks et al. 2021]. This allow us to conduct comparative studies of morph proportions in flounder populations on the base of recent and published data.

**Point 4** – In the reviewed MS it is impossible to see which changes were made in the discussion, as it is now all a track change. However, when reading it through it seems to me to be greatly improved.

**Response 4:** The discussion in the initial version of MS was revised significantly and shortened according to the reviewer’s comments

Response to Reviewer 2 ROUND 3

**Point**. I still have concerns about the proper use of the linear models, but if the authors and the editor believe this to be the right way to analyse the data I will not put my against that.

Я видел этот MS три раза. У меня все еще есть опасения по поводу правильного использования линейных моделей, но если авторы и редактор считают, что это правильный способ анализа данных, я не буду возражать против этого.

**Response**

We conducted a systematic search for published data that provide information on the proportions of morphs in flounder from different populations. Further, using the data of the Global Biodiversity Information Facility, the coordinates of 5992 unique points of flounder occurrence sites in the European part of the range were obtained. Based on these data, the geometric center of the species range was calculated as a point with geographic coordinates equal to the mean latitude and longitude (54.29339N, 8.772293E). Then, the distance from each flounder fishing area indicated in the published studies to the calculated geometric center of its range was estimated. To analyze the pattern of geographic distribution, we built two regression models. The first model was built for the material collected in European part of the flounder range, and the second one for sites located in the Arctic region. We did not combine both data sets (European and Arctic) into one model, as this would lead to the appearance of collinearity between the predictors. The dependent variable in the models was the proportion of left-sided morph (it was assumed that the values of this variable correspond to the beta distribution). The distance from the geometric center of the European part of the species range was used as the first predictor in both models. Longitude was considered as a second predictor, additionally characterizing the geographic location. Latitude was not included in the models because it showed collinearity with other predictors.

Statistical processing was performed using the functions of the statistical programming language R [**20**]. We used the “betareg” package [**21**] to fit the regression model. To check collinearity of predictors in the models the variance inflation factor was estimated using functions from “car” package [**22**]. No collinearity was detected in final versions of the models. Analysis of residuals did not reveal violations of linear models’ assumptions for both models.