**RESPONSE TO REVIEWER**

**Corrections in concordance with the reviewer remarks.**

Reviewer B comments:

1. Page 2 Ln 59 - Identify the agrotechnology used for breeding and the refs to support this for glucan enhancement.

**Page 2, line 59 - we explained the agrotechnology approach that can be used for increased content of *β*-glucan in oat and barley and we have added references to support that.**

2. Page 3, Ln 66 - What were the selection criteria for the lines selected. Also for effective statistics this needs many more lines than were selected here.

**Page 3, line 78 - we have added the selection criteria for the lines which are** **selected for analysis.**

3. Page 3 Ln74. Only two seasons for growth and one for glucan analysis used. This is insufficient as at least three seasons should be used for the lines that are samples for glucan analysis.

**Number of season for the analysis - the first year served to reject foreign biotypes, the second season we had a homogeneous material, which was confirmed in repeated analyzes considering that we get the same value. The aim of work was not to examine the impact of environmental factors on the content of *β*-glucan, so we do not have results for several years in which the climatic conditions were different. Thanks for the idea - this could be a topic for future work.**

Page 4 ln 117 - Page 6 ln 140. This has far too much detail that can be dealt with by referencing the method. Also stating the absorbance values that are used to generate the glucan values is not necessary. In addition there are no errors values on the glucan values.

**The methods are summarized – line 120. The final formula and abbreviations are left only. We connected the tables for barley and oat (II and III) and now the table shows only the content of beta glucan without absorbance. New table (II) is transferred to the chapter – Results – line 159.**

**Page 5, line 123 – errors values on the *β*-glucan values (± 0.1%).**

Page 6, Ln 142. When comparing the lines for glucan values and creating dendograms for genetic distances this really need the pedigrees of the lines to link this back to genetic relatedness.

**Certainly it makes sense to work on the basis of similarity of genealogy but also it would be another aspect of the research. Genealogy would go beyond the direct parent and differences that could express would be the result of the previous pedigree of male and female parent.**

**Generic distance is presented in the dendrogram that is obtained from the figures as the results obtained in our analysis. Since we used the program Statistica – program that contains complex calculations and formulas to transform the final figures in tree - the resulting tree (dendrogram) reflects the mutual similarities and differences of the investigated genotypes (the genetic distance in our example).**

Sincerely Yours,

**Corresponding author:**

PhD Nevena Djukić, Associate Professor

University of Kragujevac, Faculty of Science

Radoja Domanovića 12, 34 000 Kragujevac, Serbia

E mail: [nevena@kg.ac.rs](mailto:nevena@kg.ac.rs)

Tel. +38134336223

Fax: +38134335040