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Journal Name:	Journal of Agriculture and Ecology Research International
Manuscript Number:	2014_JAERI_21917
Title of the Manuscript:	Selection criteria for high nitrogen use efficiency in wheat (<i>Triticum aestivum</i> L.) parents and their F1 and F2 progenies
Type of the Article	Original Research Article

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This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

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PART 1: Review Comments

	Reviewer's comment	Author's comment <i>(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)</i>
Compulsory REVISION comments	The aim of the study was the identification of selection criteria for improving nitrogen use efficiency (NUE) in wheat, by means of the detection of traits highly correlated with the one of interest. The results allowed the identification of some traits having significant and strong correlation with NUE and representing, such as grain number per spikes or spike number per plants, important yield components. Moreover, they showed high heritability in narrow sense, so that, getting high selection gain, they could be particularly useful to wheat breeders for selection programs. The present work face a problem which deserves to be considered: crop improvement for nitrogen use efficiency is an important target, because not only nitrogen represent a substantial cost for the farmer, but also it has a negative environmental impact. However, the ms has to be drastically improved in order to be published. Frequently, there are discrepancies between the results obtained by different AA, including the AA of the present paper, but there is not any possible interpretation or suggestion on the reason of it. If it is not possible to find a reasonable explanation for these contrasting results, all of them appear to be casual, stochastic events. The abstract is difficult to understand, it is full of acronyms. Really, the entire paper is full of acronyms: the results, particularly of the ANOVA (see for instance page 8) or of the correlations are listed. The AA have to select the relevant, informative findings, and discuss in a clear way just those.	Interpretation of the discrepancies between the results done at some places. The abstract is now Okay after corrections. All your comments were taken into consideration and correction and explanations were added.



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	Finally, when considering the topic of the research, the final, general objectives should be discussed: in order to obtain tools useful for the selection of genotypes able to perform well in low nitrogen regime it is important to understand the physiological and genetic basis of NUE. Only this information could explain the discrepancy between the results obtained by different AA.	
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Minor REVISION comments	Page 1, line 8 – GYP: is it perhaps “GYPP”? Page 1, line 11 – “...is observed that NUPE is strongly correlated with NUE in all studied genotypes...” – NUE has two components: N uptake, and N utilization; in fact, the AA claim (pag.2, line 2) “...cultivars superior in N-use efficiency, either due to enhanced uptake capacity or to more efficient use of absorbed N.” So it is obvious that NUPE is strongly correlated with NUE!!! Page 1, line 13 – “... GYPP is perfectly correlated (1.00) with NUE...” – This result is not possible using biological variables! Page 2, line 14 – “... NUPE accounts for more of the genetic variation in NUE at low-N than at high N supply...”. This may be expected: in the presence of high amount of N, uptake efficiency is not a limiting factor, and the genetic differences are not substantial. Page 2, line 27 – “... consistent improvement in NUTE associated with higher harvest index, e.g. in Mexico ... In contrast, studies in the UK ... found that increases in NUE were explained approximately equally by NUPE and NUTE.” These different findings do not appear to be attributable to environmental effects, but probably to genotypes. The AA should give some information on this point. Page 3, line 6 – “GNC” – The acronym is not explained	Page 1, line 8: It is corrected to GYPP. Page 1, line 11: Okay Page 1, line 13: These are our results. It is expected, because NUE is calculated from GYPP divided by soil nitrogen, which is constant for all genotypes in each environment. However I deleted this sentence from the abstract. Page 2, line 14: These sentences were taken as it is from references. Page 2, line 27: These sentences were taken as it is from references. Page 3, line 6: It is explained now.
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	Page 3, line 12 – What “neutrally associated” does it mean? If the correlation coefficient is not significant, the variables are NOT associated! Page 3, line 16 – “UPE” instead of NUPE? Page 3, line 26 – “To identify ...”: this sentence has to be rewritten Page 4, line 18 – “ ... the half diallel of crosses was again done to increase quantity of F1 seeds...” – Why was the diallelic made in two times? To have a greater amount of seeds it was sufficient to sow a greater number of plants in 2005! Page 8, line 7 – “...the presence of significant heterosis for all studied traits and the presence of inbreeding effects for most studied traits” – What does it mean? Moreover, they vary from one year to the other... This statement have to be rewritten in order to better explain the data. Page 11, line 14 – “On the contrary ...” – How could this discrepancy be interpreted? Page 14, line 14 and 19 – “... high grain yield of high grain protein contents. ... In other studies ... reported negative associations of grain yield with protein content.” – How to explain these findings? Page 15, line 1 and following – It is possible, and perhaps expected, that the role of the two component of NUE,	Page 3, line 12: We took it as it is from references. You can go to references to see it. Page 3, line 16: Corrected to NUPE Page 3, line 26: The sentence was rewritten correctly. Page 4, line 18: We could not obtain good quantity of hybrid seed in the first season; that is why we again re- made the crossing to obtain sufficient quantity of seed for evaluation in two seasons Page 8, line 7: In my opinion this statement is written correctly. Page 11, line 14: A new sentence was added for interpretation. Page 14, line 14 and 19: Most of previous studies mention the negative correlation, but few mentioned positive one. In our study, it showed in some cases a positive relation, but in small magnitude. Page 15, line 1: I agree with you. Some corrections were made.
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	nitrogen uptake and utilization, is different according to the allelic composition of the genes involved in the nitrogen metabolism: inorganic uptake, assimilation, remobilization and partitioning of organic N. For instance, activity or content of glutamine synthetase or glutamate dehydrogenase, enzymes involved in the process, could confer different efficiency to the process, according to the genotype. Page 15, line 28 – “... <i>Both processes</i> ... appear to be governed by different genetic factors...” - <i>The two processes</i>... Page 16, line 16 – It is not possible to observe a value of heritability of 99.9 or 100% for a quantitative trait. How can be interpreted this result? Page 17, comments to the data in Table 3 – Important decrease from broad to narrow heritability is observed, except in the cases of SPP under low N regime and GPS; this indicates that most of the genetic control of the traits is due to non-additive effects, and it is not surprising that the genetic advance is limited. However, can be noted a quite strange result for HI, in particular under high N: H^2_N is only 9.6%, with respect to 87.3% of H^2_B, but GA is 23.9%! This should be commented. Page 18, line 21 and following – Also here, a possible interpretation of the data should be done. See general comments Page 19, Table 4 – The data relating to DTH are unexpected: even though the H^2_N, which is a measure of the heritable genetic variation, is substantial, not very	Page 15, line 28: Corrected Page 16, line 16: ,But results sometimes show such high heritability. It is here for number of grains per spike which might not be a quantitative trait. Page 17. Sometimes happened that h^2_n is low but GA is medium or high. This could be attributed to phenotypic standard deviation or phenotypic variance. Page 18, line 21: Interpretation of the data is present now. Page 19, Table 4: I agree with you, but these are the data we obtained.
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	different from H^2_B, GA is very low. Page 20, line 8 – This sentence has to be better written Page 20, line 23 and following – In this case too (see general comments), the reported discrepancies are not commented Page 22, line 10 – “...are considered selection criteria...” – It has no sense to consider different characters depending on the generation, it should be better choose the ones resulted highly correlated with NUE in every generations.	Page 20, line 8: Correction done. Page 20, line 23: Interpretation and explanation were done. Page 22, line 10: It is here a general conclusion, but it is written in details in the Part of Conclusion.
<u>Optional/General</u> comments		