Reviewer's report

Title: Single Nucleotide Polymorphisms in DNA Repair Genes as Risk Factors Associated to Prostate Cancer Progression

Version: 1 Date: 28 November 2014

Reviewer: Marco Oderda

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MAJOR COMPULSORY REVISIONS

1) Abstract: cT2b is hardly an aggressive tumour. I would focus on T3-4 tumours. The conclusions must not repeat the results of your study. You should rather stress your take-home message.

2) Introduction: in the first paragraph, I would suggest to remove the epidemiological data, which are well known in the urological community. You could use these words to better explain the background of study in terms of genetic findings up-to-date. In the study aim you should stress why you focused on these particular 10 SNPs (one sentence explaining the link between the six genes and tumour aggressiveness would do). I would rephrase the sentence about PSA screening, which is a very complex problem not limited to overdiagnosis and overtreatment. Please revise the manuscript for grammatical errors (i.e. 12 men HAVE to be...).

3) Methods: how was clinical stage assessed? With DRE, with imaging..? I would avoid to report in the M&M section every institution participating in study, as they are already shown in the title page. Rather, you should briefly explain which was the study protocol followed for each patient: baseline infos collection, blood samples, analyses, and so on...

4) Results: you should describe the baseline patient infos! Clinical data of your patients are essential, better if resumed in a table. In my opinion, the whole section should be modified, reporting in a more effective way your results. You speak about two SNPs: what about the others? You say that only 2 SNPs were significantly differently distributed according to clinical variables (only stage and Gleason?): you should better report your findings (all SNPs, all clinical variables). I think that reporting only the distributions is not enough. If you speak about associations between SNPs and clinical variables, you should report crosstabs showing p-values and statistical tests used.

I understand that you focused on rs11615 and rs17503908 as they were the only one to show an association with clinical variables: again, you should better report your results! Did you perform chi-square analysis to calculate an OR? The risk of developing T2b - T4 tumours includes a huge variety of tumours: why you did not focus on T3-T4 (the high risks)? Did you find any associations between SNPs and higher values of PSA? Do not speak of “bigger Gleason scores”! Rather, you
should say “Gleason scores 8-10”. I think that the association with D’Amico groups is not necessary if you perform a thorough analysis on PSA, Gleason score and stage, which are the factors included in the D’Amico classification.

5) Discussion: the discussion should be done according to the previous modification. I would suggest to provide a theory about the biological reasons of your findings on a possible association between certain SNPs and more aggressive cancer features.

6) Conclusions: as for the abstract, the conclusion should not repeat your results. You should rather provide a clear take home message.

**Level of interest:** An article of importance in its field

**Quality of written English:** Needs some language corrections before being published

**Statistical review:** Yes, and I have assessed the statistics in my report.

**Declaration of competing interests:**

I declare that I have no competing interests