Author's response to reviews

Title: Single-center study of Lynch syndrome screening in colorectal polyps

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Author's response to reviews:

Reviewer #1:

1) Before analyses of the germline (sequencing), genetic counselling of all patients is mandatory. Materials and methods Patients: DNA extraction and sequencing part add “Patients exhibiting polyps with deficient mismatch repair (dMMR) were referral to genetic counselling and signed informed consent to receive genetic testing”.

2) The conclusion ("The efficiency of performed…is low…") is correct and supports the recommendation for inclusion of patients only meeting the revised Bethesda guidelines in MMR analyses. In this study, all patients in whom a pathogenic MMR mutation could be detected were younger than 50 years.

Detection of LS only performing MMR IHC and/or MSI testing of adenomas in young patients may not be the best strategy. In patients < 40 years-old with colorectal adenoma, MMR IHC and MSI testing found no abnormal results. It may be reasonable to evaluate for LS when a young adenoma patient has a family history of LS-associated cancers, or when a young adenoma patient has high-risk characteristics, such as large size, high-grade dysplasia, and malignant components.

3) The number of the references cited (eleven) appears too low in such a central field of interest. It has been increased to 25 references.
4) The complete manuscript should be revised by an academic native speaker because of the poor quality of English and numerous mistakes.

Manuscripts has been revised by American journal experts.

Reviewer #2:

Introduction:

- All gene names should be in Italics. Revised
- EPCAM is not a causative gene for Lynch; an EPCAM deletion is. Revised
- The last sentence of the paragraph should be changed to: "subsequent genetic testing based on the MMR IHC results will ultimately confirm LS diagnosis". Revised
- Please rephrase the second paragraph and check for errors (e.g. studys). Revised

Materials and Methods:

- Please rephrase the patient selection paragraph. Revised
- It is not clear what you are trying to say in your last sentence of IHC for MMR proteins. Revised
- Multiple grammatical and terminology errors in DNA extraction and sequencing section. What does German Qiagen means? What are the amplified objects? What does mutation style means? Please try to rephrase the paragraph. Revised

Results:

- Please rephrase the sentence: "the mean age…" years should be added and this is the mean age of what? Revised
- Please avoid starting sentences with numbers. Revised
- State in the text what you are presenting in Table 1. Revised
- In tables 1 and 2, please review the legend (pathological information is not an accepted term). Revised
- In table 1, what does caneration means? Revised
- The paragraph following Table 1 is unclear, please rephrase. Revised
- The paragraph following Table 2 is unclear, please rephrase ("one case was not analysis"?) Revised
- Merge information in Tables 3 and 4. When you do that, reconsider your legend. Revised
- When reporting mutations, HGVS nomenclature should be used (reporting in protein and cDNA level), while the RefSeqs used for each gene should be listed (Table 3). Revised
- Please review Table 3; Gene names in italics and phrases such as: not detection vs not detected, sanger sequence vs sequencing, not yet seen vs not detected. Revised
Discussion:

- Please get a native speaker to scan it through.

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