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Response to Letter to Editor "*JAK2* V617F Mutation in Cervical Cancer Related to HPV & STIs" by Stephen E. Langabeer

LETTER TO THE EDITOR

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Dear Editor:

We thank you for the opportunity to reply to the Langabeer's comments [1] on our previous manuscript [2]. The comments could be valuable for improving and clarifying some contents.

Comments:

Firstly, the *JAK2* p.V617F (c.1849 G>T) is located in exon 12 (not exon 14) according to various literatures [3]. The acquired mutation can be presented in those patients with hematologic disorders. It appears that single nucleotide polymorphisms (SNPs) in immune mediators such as *JAK2* could be associated with the risk of cervical cancer. However, these SNPs should be ascertained for justification in different communities and races with various genetic and epigenetic patterns [4].

The second argument raised by Langabeer [1] is that the RFLP method is an inefficient approach for identification of G>T transversion. During the last decades, several PCR-based assays with different analytical sensitivity and specificity parameters have been developed for clinical and diagnostic applications. These include High Resolution Melting analysis, PCR-Amplification Refractory Mutation System, Reverse Transcription-PCR, direct DNA sequencing, Real Time PCR, PCR-RFLP, Allele Specific PCR, etc. However, they have their disadvantages besides advantages. Nowadays, next generation sequencing and other high throughput approaches with high accuracy and performance are applicable in SNPs studies, although they are limited by high cost and interpretations [5]. It seems that PCR-RFLP approach can be reliable in detecting SNPs as well as other methods in developing countries. The current study has been performed in Reference Health laboratory, MOHME, Tehran, Iran. The JAK2 mutation survey is a part of our current projects in SNPs analysis of cervical cancer subjects related to sexually transmitted infections. The PCR-RFLP has been validated and verified by use of approved positive controls. In addition, all of subjects' results have been confirmed by wild type, heterozygous and homozygous controls in each experiment.

We have been trying to decrease any false positive and negative results by utilizing high quality *CE* and *IVD* marked materials and equipment. Nonetheless, the statistical analysis on these subjects would be challenging due to some missing patients' data in that study. For improving and amending the analysis of SNPs survey, another manuscript is being prepared for better understanding of the *JAK2* mutation associated with cervical malignancies as well as other potential polymorphisms in this issue. Obviously, more research is needed to achieve this endeavor for Cancer Care program.

CONFLICTS OF INTEREST

No potential conflicts of interest were disclosed.

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