

Peer Review File

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Reviewer A

Kitai et al provide a brief description of the role played by FGFR pathway on cancer progression and when FGFR inhibitors could be used to reduce the activation of the associated signalling pathways. In fact, since the FGFR inhibitors show only a modest response in FGFR1 amplified SQCLC they described a potential novel approach to stratify patients who benefit from FGFR inhibitors. The work is well-written, concise but detailed and interesting.

Reply: We greatly appreciate the reviewers' comments.

Reviewer B

This review deals with the FGFR1 genomic abberations in squamous cell lung carcinoma and some new opportunity for precision oncology by targeting some of these genomic alterations.

Major concerns:

This review should be better structured in different paragraphs and with an introduction and claims the objective.

A brief summary of the different genetic alterations focusing on FGFR (1-4) needs to be described.

Methods of analysis with limitations and advantages for the detection of the genomic alterations should be explained.

Protein expression, mutation, amplification and fusion on FGFR (1-4) have to be well distinguished (and including the different frequencies).

Finally, many recent reviews have been done in the subject, so the authors need to show the add value of this kind of additional work.

A figure and some tables would be useful.

Reply: We believe that the reviewer considers our manuscript as a review and asks us to include an introductory section and broaden the topic to genetic alteration of FGFR2/3/4 as well as FGFR1. However, this manuscript is a solicited editorial commentary of the recent publication at JCI on novel somatic rearrangements of FGFR1. We described current topics and issues in *FGFR1*-amplified NSCLC and the novelty of the paper published in JCI. Although we appreciate the comments from the reviewer, we think that most of the comments from the reviewer are misunderstandings of our manuscript category.

Minor: all names of genes have to be in italics

Reply: As the reviewer suggested, we have revised all gene names in the manuscript to italic.