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PEER-REVIEW REPORT

Name of journal: World Journal of Clinical Oncology

Manuscript NO: 63343

Title: Oncogenic driver mutations in NSCLC: past, present and future.

Reviewer's code: 03853364
Position: Peer Reviewer
Academic degree: MD

Professional title: Doctor

Reviewer's Country/Territory: United States

Author's Country/Territory: Switzerland

Manuscript submission date: 2021-01-27

Reviewer chosen by: AI Technique

Reviewer accepted review: 2021-01-27 23:48

Reviewer performed review: 2021-02-02 01:50

Review time: 5 Days and 2 Hours

Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish
Language quality	[Y] Grade A: Priority publishing [ ] Grade B: Minor language polishing [ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection
Conclusion	[ ] Accept (High priority) [ ] Accept (General priority) [Y] Minor revision [ ] Major revision [ ] Rejection
Re-review	[Y] Yes [ ] No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [ ] Onymous Conflicts-of-Interest: [ ] Yes [Y] No

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SPECIFIC COMMENTS TO AUTHORS

In this review, the authors summarized all driver mutations identified in patients with advanced NSCLC and provided the update about current targeted therapies for NSCLC patients with different mutations. The authors suggest that it is very important to perform oncogene mutation detection before offering therapy for patients with NSCLC. This paper is well written and provides very comprehensive, helpful information to both research and clinical community. However, I have several comments. 1. In this manuscript, the authors mentioned acquired secondary mutation such as EGFR T790M that can lead to resistance to targeted therapy. It is unclear whether the second mutation is pre-exist before targeted therapy or drug treatment generates this secondary mutation. 2. It would be much better for readers to understand if the authors can create a table to summarize current targeted therapies for NSCLC patients based on driver mutation status. 3. Fig.1 is not well presented. For example, KRAS G12C is shown under KRAS section. It is unclear what percentage for KRAS G12C. Additionally, other genes do not show specific point mutations. It should be consistent for all genes. Furthermore, unknown/no mutation is 27%. The word "No mutation" should be removed because we do not know the real answer. 4. Under "RET" section, "RErranged" is one spelling error. 5. How is ALK activated? Please explain.