

LETTER TO THE EDITOR

Open Access



Loss of heterozygosity related to TMB and TNB may predict PFS for patients with SCLC received the first line setting

Chenyue Zhang^{1†}, Kai Wang^{2†} and Haiyong Wang^{3*}

To the Editor,

Genes have two alleles or copies, with one inherited from each parent. The loss of one of these gene copies, termed as loss of heterozygosity (LOH), is one of the most common genetic alterations in cancer [1]. LOH has been playing a pivotal role in cancer development [2]. For instance, LOH was found to be involved in the relapse of acute lymphoblastic leukemia [3]. LOH of human leukocyte antigen (HLA) alleles hampered the ability of major histocompatibility complex to present neoantigens, thus implicating in resistance to immune checkpoint blockade (ICB) therapy [4]. Therefore, expounding the relationship between LOH and cancer will be very helpful to guide the accurate treatment.

Small cell lung cancer (SCLC) is featured by rapid growth and tendency to metastasize, with grim prognosis and high relapse rate [5]. However, the landscape of LOH and its impact on prognosis and relapse has remained largely unknown in SCLC. Moreover, the association between LOH and immunological features has never been studied in SCLC.

A total of 178 histologically confirmed SCLC patients were collected from Shandong Cancer Hospital and Institute. This study was approved by the Ethics Committee of Shandong Cancer Hospital and Institute. All

included patients in this study offered written informed consent. Whole-exome-sequencing (WES) analyses were performed to detect the of the tumor mutational burden (TMB) and tumor neoantigen burden (TNB) for SCLC patients. We have demonstrated that SCLC patients with higher LOH were associated with lower tumor mutational burden (TMB) (R square = 0.0825, $P = 0.0001$; Fig. 1A). Similarly, LOH was found to be negatively associated with lower tumor neoantigen burden (TNB) (R square = 0.0726, $P = 0.0003$; Fig. 1B). Since CD8 + T cells are the body's main immunological barrier against cancer and PD-L1 expression has reported to be a biomarker for immunotherapy, we next analyzed the association between CD8 + T cell infiltration, PD-L1 expression and LOH in SCLC. CD8 + TIL density and PD-L1 expression was measured using immunohistochemistry. In addition, X-tile software was applied to determine the optimal cutoff of LOH to differentiate progression free survival (PFS) (endup point for PFS: 15th, December, 2020) [6]. LOH was divided low and high in light of the optimal cutoff. The results showed that there was no significant difference in CD8 + T cell infiltration between low-LOH and high-LOH SCLC patients ($P = 0.5796$; Fig. 1C). SCLC patients with low LOH had numerically higher PD-L1 positive expression than those with high LOH (20.69% versus 10.83%; Fig. 1D). Importantly, in the LOH-low cohort, PFS was significantly prolonged compared with that in LOH-high cohort ($P = 0.0305$; Fig. 1E). Moreover, multivariate Cox regression analyses were further conducted to evaluate the prognostic factors on PFS. We have found that LOH remains to

*Correspondence: wanghaiyong6688@126.com

[†]Chenyue Zhang and Kai Wang are first authors and contributed equally to this work

³Department of Internal Medicine Oncology, Shandong Cancer Hospital and Institute, Shandong First Medical University and Shandong Academy of Medical Sciences, Number 440, Ji Yan Road, Jinan 250117, China
Full list of author information is available at the end of the article



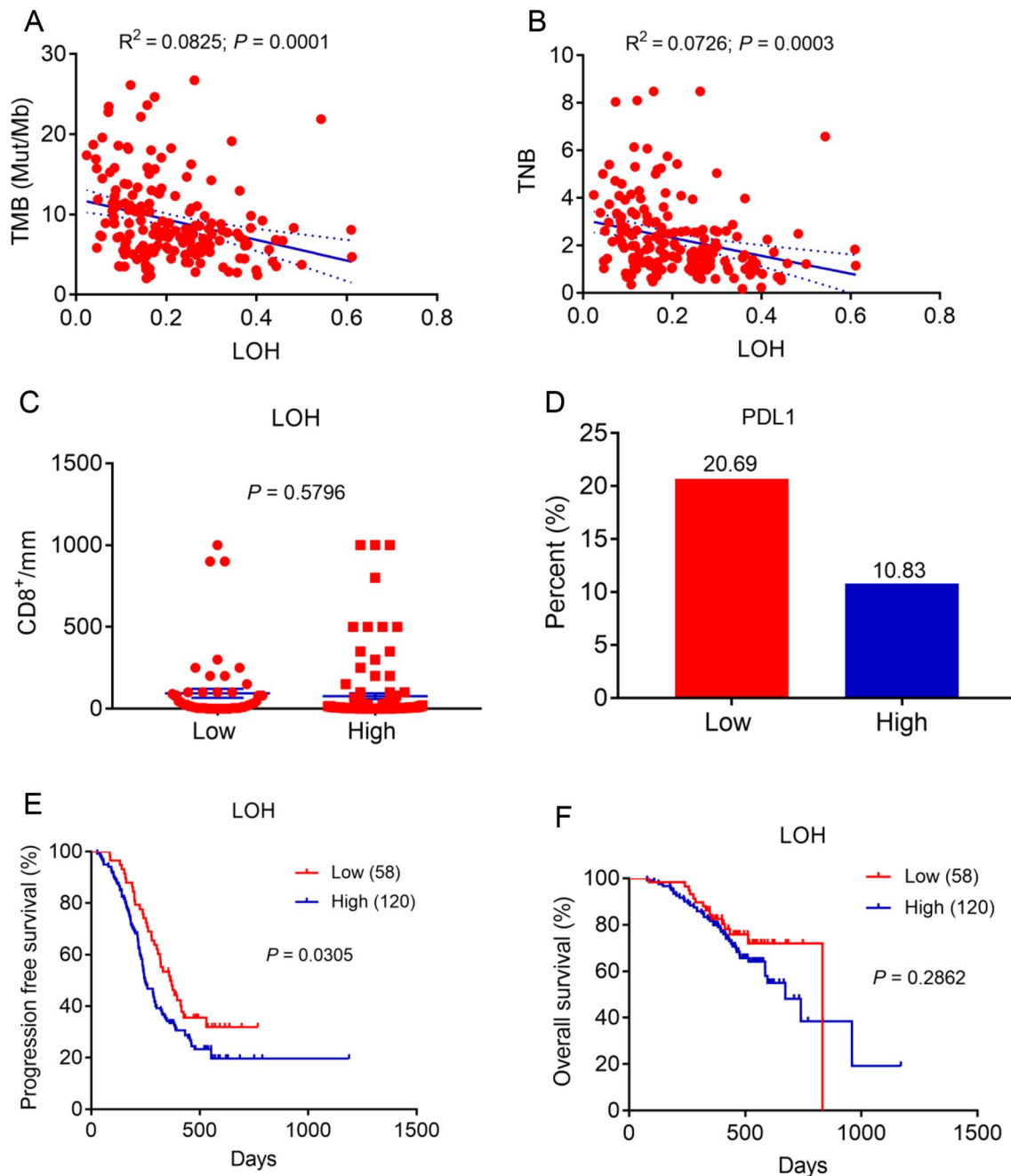


Fig. 1 The association of LOH with immune-related markers and the impact of LOH on survival. **A** The association between LOH and TMB for SCLC patients. **B** The association between LOH and TNB for SCLC patients. **C** The difference in CD8 + TIL infiltration between low-LOH and high-LOH in SCLC patients. **D** The difference in positive PD-L1 expression between low-LOH and high-LOH in SCLC patients. **E** The effect of LOH on PFS in SCLC patients. The cutoff for LOH is determined by X-tile. **F** The effect of LOH on OS in SCLC patients

be an independent factor for predicting PFS even after adjusting for factors including age, sex, smoking, family history and stage (HR, 1.574; 95% CI 1.033–2.398; $P = 0.035$; Additional file 1: Table S1). Additionally, there was no significant difference in overall survival

(OS) (endup point for OS: 26th, November, 2020) between LOH-low and LOH-high cohort ($P = 0.2862$; Fig. 1F).

To the best of our knowledge, we are the first to analyze the association between immune-related markers

including TMB, TNB, CD8 + TIL, PD-L1 and LOH for patients with SCLC. We not only demonstrated the negative association between LOH and TMB, TNB in SCLC, but also revealed that low LOH is associated with prolonged PFS. We concluded that LOH may predict PFS by negatively affecting TMB and TNB in SCLC. Our finding suggests that LOH is a very valuable benchmark that predicts PFS in SCLC. Undeniably, more clinical and translational researches are warranted for confirmation of LOH's role in SCLC.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12967-021-03019-6>.

Additional file 1: Table S1. Multivariate Cox regression analyses to evaluate the prognostic factors for PFS.

Acknowledgements

We thank for the technical support of Chenglong Zhao from Shandong Cancer Hospital for pathological analysis; we also thank for Zhenzhen Li from Berry Oncology Corporation for Bioinformatics technology support.

Authors' contributions

CZ performed data analysis and manuscript preparation. KW re-verified the data and polished the language. HW designed the study and revised the manuscript. All authors read and approved the final manuscript.

Funding

This study was supported jointly by Special funds for Taishan Scholars Project (Grant No. tsqn201812149), Academic promotion program of Shandong First Medical University (2019RC004).

Availability of data and materials

The data are available from the corresponding authors upon reasonable request.

Declarations

Ethics approval and consent to participate

This study was approved by the ethics committee of Shandong Cancer Hospital and Institute. All included patients in this study offered written informed consent.

Consent for publication

All authors give their consent to publish this manuscript.

Competing interests

The authors declare that there is no competing interests.

Author details

¹Department of Integrated Therapy, Fudan University Shanghai Cancer Center, Shanghai Medical College, Shanghai 200032, China. ²Key Laboratory of Epigenetics and Oncology, the Research Center for Preclinical Medicine, Southwest Medical University, Luzhou 646000, China. ³Department of Internal Medicine Oncology, Shandong Cancer Hospital and Institute, Shandong First Medical University and Shandong Academy of Medical Sciences, Number 440, Ji Yan Road, Jinan 250117, China.

Received: 18 May 2021 Accepted: 19 June 2021

Published online: 08 September 2021

References

- Zhang X, Sjöblom T. Targeting loss of heterozygosity: a novel paradigm for cancer therapy. *Pharmaceuticals*. 2021;14(1):57.
- Tapial S, García JL, Corchete L, Holowatyj AN, Pérez J, Rueda D, Urioste M, González-Sarmiento R, Perea J. Copy neutral loss of heterozygosity (cnLOH) patterns in synchronous colorectal cancer. *Eur J Hum Genet*. 2021;29(4):709–13.
- Orlando EJ, Han X, Tribouley C, et al. Genetic mechanisms of target antigen loss in CAR19 therapy of acute lymphoblastic leukemia. *Nat Med*. 2018;24(10):1504–6.
- Rodig SJ, Gusenleitner D, Jackson DG, et al. MHC proteins confer differential sensitivity to CTLA-4 and PD-1 blockade in untreated metastatic melanoma. *Sci Transl Med*. 2018;10(450):eaar3342.
- Dawkins JBN, Webster RM. The small-cell lung cancer drug market. *Nat Rev Drug Discov*. 2020;19(8):507–8.
- Camp RL, Dolled-Filhart M, Rimm DL. X-tile: a new bio-informatics tool for biomarker assessment and outcome-based cut-point optimization. *Clin Cancer Res*. 2004;10(21):7252–9.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

