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Dear Editor,

We read with much interest the paper published in Cancer Lett. 360 (2015) 234–244 [1], which provides relevant data about the effects of the modulation of the store-operated Ca²⁺ entry process (SOCE) by the Latent Membrane Protein 1 (LMP1), the most studied oncogenic product of the Epstein-Barr Virus (EBV). Briefly, the authors reported that the inhibition of the boosting effect of EBV LMP1 on SOCE had a detrimental impact on cell migration, as well as angiogenesis and endothelial permeability in vitro. Furthermore, the mobilization of endothelial cell and vasculature invasion (elegantly assayed in zebrafish model), as well as the formation of distant metastases in Nude/SCID mouse by circulating disseminated LMP1-expressing cells was impaired by SOCE blockage. As a conclusion, the authors claim that LMP1-boosted SOCE contributes for the metastatic potential of nasopharyngeal carcinoma (NPC) cells, taking into account the assumed histogenetic origin of the cell lines used in their experiments.

The reported data strengthen the hypothesis that oncogenic viruses may impact cancer progression, and EBV-associated NPC is a very important model in this regard [2]. Nonetheless, the experiments were conducted with CNE1 and HNE2 cells, which show evidence to be HeLa derivatives [3,4], albeit regarded as EBV-negative NPC cells.

There are obvious shortcomings on drawing conclusions on pathogenesis of EBV-associated NPC based on results from these cell lines, and this issue is not limited to the above-mentioned paper: in a recent study published on another reputed journal, it was reported that the expression of the EBV LMP1 in several epithelial cell lines *in vitro* resulted in enrichment of cells expressing CD_{44}^{high} , a feature commonly associated with the cancer stem-cell phenotype (CSC). Moreover, the LMP1 induction of CSC traits was mediated

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http://dx.doi.org/10.1016/j.canlet.2016.07.031 0304-3835/© 2016 Elsevier Ireland Ltd. All rights reserved. by PI3K/AKT and mIR-21 activity, as well as PTEN suppression. The authors concluded that the results indicate a novel mechanism by which LMP1 expression contributes in the pathogenesis of EBV-associated NPC [5]. However, some of the study experiments were also conducted with the HeLa-contaminated cells, in this case CNE2 and HONE1 [3,4]. Worth to note, the NPC cell lines AdAH, NPC-KT, HONE-1, HNE-1 and HNE-2 were flagged as "potentially misiden-tified" by the International Cell Line Authentication Committee (ICLAC); additional data and biological samples from these cells are currently being requested to the scientific community [6] to determine their inclusion on the ICLAC database of misidentified cell lines [7,8].

Although cell identity issues are reported for some decades now, they continue to be largely neglected. The problem is truly epidemic in some settings: among 380 samples of cell lines from Chinese laboratories, contamination was reported in 1 out of 4, notably by HeLa cells [9]. Cell validation should be an ordinary practice nowadays, but this is not the case, even though accessible and reliable methods to perform it routinely are available. Indeed, costeffective DNA profiling based on short tandem repeats (STRs) can be readily performed in any laboratory with PCR and capillary electrophoresis devices, and third-party services for cell validation are becoming more common everywhere.

Contaminated and misidentified cell lines generate unreliable and misleading data [10], compromise preclinical studies, and ultimately lead to waste incalculable amount of money and other resources. Hence, coordinated actions are vital: researchers must be committed not to generate data without validating each experimental cell lot, whereas funding agencies could increase the awareness by connecting access to grants to disclose quality control procedures for use of cultivated cells. On the publishing side, proof of cell authenticity must be a basic requirement for manuscript consideration. Hitherto, reviewers and editors must require that authors explicitly state how the cells used were validated. Adherence to these measures will minimize the "cell identity" crisis and improve significantly the invaluable role of cell culture for scientific and technological advances.



References

- [1] J. Wei, J. Zhang, Y. Si, M. Kanada, Z. Zhang, S. Terakawa, et al., Blockage of LMP1-modulated store-operated Ca(2+) entry reduces metastatic potential in nasopharyngeal carcinoma cell, Cancer Lett. 360 (2015) 234–244, doi:10.1016/ j.canlet.2015.02.032.
- [2] D. Elgui de Oliveira, B.G. Müller-Coan, J.S. Pagano, Viral carcinogenesis beyond malignant transformation: EBV in the progression of human cancers, Trends Microbiol. 24 (2016) 649–664, doi:10.1016/j.tim.2016.03.008.
- [3] S.Y.-Y. Chan, K.-W. Choy, S.-W. Tsao, Q. Tao, T. Tang, G.T.-Y. Chung, et al., Authentication of nasopharyngeal carcinoma tumor lines, Int. J. Cancer 122 (2008) 2169–2171, doi:10.1002/ijc.23374.
- [4] M.J. Strong, M. Baddoo, A. Nanbo, M. Xu, A. Puetter, Z. Lin, Comprehensive high-throughput RNA sequencing analysis reveals contamination of multiple nasopharyngeal carcinoma cell lines with HeLa cell genomes, J. Virol. 88 (2014) 10696–10704, doi:10.1128/JVI.01457-14.
- [5] C.-F. Yang, G.-D. Yang, T.-J. Huang, R. Li, Q.-Q. Chu, L. Xu, et al., EB-virus latent membrane protein 1 potentiates the stemness of nasopharyngeal carcinoma

via preferential activation of PI3K/AKT pathway by a positive feedback loop, Oncogene (2015) doi:10.1038/onc.2015.402.

- [6] International Cell Line Authentication Committee, More data needed Nasopharyngeal carcinoma (NPC) cell lines, ICLAC. http://iclac.org/can-help/more-data-needed/, 2016 (accessed 20.07.16).
- [7] A. Capes-Davis, G. Theodosopoulos, I. Atkin, H.G. Drexler, A. Kohara, R.A.F. MacLeod, et al., Check your cultures! A list of cross-contaminated or misidentified cell lines, Int. J. Cancer 127 (2010) 1–8, doi:10.1002/ijc.25242.
- [8] International Cell Line Authentication Committee, Database of crosscontaminated or misidentified Cell Lines, ICLAC. http://iclac.org/databases/ cross-contaminations/, 2014 (accessed 20.07.16).
- [9] F. Ye, C. Chen, J. Qin, J. Liu, C. Zheng, Genetic profiling reveals an alarming rate of cross-contamination among human cell lines used in China, FASEB J. 29 (2015) 4268–4272, doi:10.1096/fj.14-266718.
- [10] M. Yu, S.K. Selvaraj, M.M.Y. Liang-Chu, S. Aghajani, M. Busse, J. Yuan, et al., A resource for cell line authentication, annotation and quality control, Nature 520 (2015) 307–311, doi:10.1038/nature14397.