

Inclusion of the *ASH1* gene that governs the neuroendocrine differentiation of lung epithelium as an additional prototypic ‘lineage-survival oncogene’

Hirota Osada* and Takashi Takahashi

*Division of Molecular Oncology, Aichi Cancer Center Research Institute, 1-1 Kanokoden, Chikusa-ku, Nagoya, 464-8681, Japan

Division of Molecular Carcinogenesis, Center for Neurological Diseases and Cancer, Nagoya University Graduate School of Medicine, 65 Tsurumai-cho, Showa-ku, Nagoya 466-8550, Japan.

Corresponding to H.O. e-mail: hosada@aichi-cc.jp

We read the insightful review by Garraway and Sellers, which highlighted ‘lineage dependency’ as a new aspect of carcinogenic mechanism¹, with great interest. The authors proposed the ‘lineage-survival oncogene’ concept and described the basic-helix-loop-helix (bHLH) transcription factor MITF as a prototype^{2,3}, and also speculated about other putative candidates. We would like to suggest the addition of another bHLH gene, achaete-scute homologue 1 (*ASH1*), as a prototypic lineage-survival oncogene on the basis of existing experimental evidence. Although pulmonary neuroendocrine cells (PNECs) that reside in the airway epithelium are suggested to have a role as a stem-cell niche for the lung⁴, it has also been reported that gene-targeting of *ASH1* results in the loss of PNECs in the lung⁵, and the *ASH1* transgene promotes the development of lung tumours with a neuroendocrine feature in coordination with SV40 large-T antigen⁶. Further, suppression of *ASH1* expression by RNAi has been shown to induce cell-cycle arrest and apoptosis *in vitro*, as well as the inhibition of tumour growth *in vivo* in an *ASH1*-expression-dependent manner⁷. These findings support the ‘lineage-survival oncogene’ concept proposed by Garraway and Sellers, in that *ASH1* has a decisive role in the differentiation and survival of both normal and malignant cells of neuroendocrine lineage in the lung. Together, *MITF* and *ASH1* seem to constitute what is at present a very limited group of prototypic lineage-survival oncogenes with sufficient supportive evidence. However, we anticipate that the list of lineage-survival oncogenes will expand considerably in the near future with solid evidence from experimental results.

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