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Letter to the Editor

Letter to the Editor on "Regulation of HOXA9 activity by predominant expression of DACH1 against C/EBPα and GATA-1 in myeloid leukemia with *MLL-AF9*"

I read with great interest the recent article by Lee et al. [1]. Interestingly, recent data suggests that HOXA9 may be associated with the pathogenesis of a number of systemic malignancies besides leukemias.

For instance, down regulation of HOXA9 expression is seen in most mammary malignancies. In fact, HOXA9 modulates BRCA1 gene expression and thereby modulates and decreases the malignant and metastatic potential of breast malignancies [2]. This is especially true in estrogen and progesterone negative breast malignancies. Similar results are seen in HeLa cell lines. In these cervical cell lines increased HOXA9 expression is seen following knock-down of BMI-1 [3]. Thus targeting BMI-1 may prove to be of significant potential in treating cervical carcinomas.

Similarly, HOXA9 expression when used in conjunction with Smad4 helps in assessing the prognosis in individuals with esophageal squamous cell carcinomas [4]. In fact, increased lymphatic metastasis as well as higher stages are seen following up regulation of HOXA9 expression. Similarly, nearly 80% of lung carcinomas demonstrate hyper-methylation of the HOXA9 gene [5]. Analysis of the induced sputum to identify HOXA9 methylation is thus a very useful way for early diagnosis of pulmonary malignancies. Pyrosequencing of the induced sputum has a specificity of 97.5% in detecting lung cancer. Similarly, assessment of methylation of HOXA9 in the urine helps in early diagnosis of urinary bladder carcinomas [6]. The test has a specificity of 96%.

The above examples clearly illustrate the role of HOXA9 in the etio-pathogenesis of systemic tumors besides leukemias and the need to identify further similar associations.

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