

event in the early stage of hepatocarcinogenesis.^(19,20) Moreover, some studies show that a *p16* deficiency does not fully restore the self-renewal capability of *Bmi-1*. In addition, reduced stem cell frequency occurs in *Bmi-1*-deficient neural stem cells, even when *p16Ink4a* and *p19Arf* are not expressed.^(4,29,30) These studies indicate that there are additional downstream pathways that might mediate the effect of *Bmi-1* on self-renewal and cell proliferation.

From our gene expression analysis, we found that induction of *Bmi-1* in bone marrow cells resulted in an upregulation of *ABCBI*.⁽⁶⁾ *ABCBI* appears to be a consistent feature of mammalian cells displaying resistance to multiple anticancer drugs, and has been postulated to mediate drug resistance.^(31,32) Interestingly, recent findings also show expression of *ABCBI* in various stem cells,^(33–35) which might make them less sensitive to cancer treatment. Increased expression of *ABCBI* was observed in HCC, particularly in early and well differentiated HCC, compared with the surrounding non-cancerous region. *ABCBI* expression decreases with the progression of HCC, suggesting a reflection of tumor dedifferentiation.⁽³⁶⁾ We showed here that *ABCBI* expression was clearly altered in parallel with *Bmi-1* expression. High expression of both *Bmi-1* and *ABCBI* was observed in the early stage of hepatocarcinogenesis, which suggests their collaboration in maintaining the cell's ability for self-renewal, proliferation, and increased resistance from apoptosis.

Although it is possible that *ABCBI* represents a novel downstream target for *Bmi-1*, further analysis is necessary to clarify the mechanism underlying the link between *Bmi-1* and *ABCBI* expression.

In summary, we evaluated the expression and involvement of the "stemness" gene, *Bmi-1*, in HCC, particularly in early stage hepatocarcinogenesis. The strong correlation observed between *Bmi-1* and *ABCBI* expression in HCC indicates a new regulatory pathway for *Bmi-1*, and reveals a potential novel target for enhancing future HCC treatment strategies.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Fig. S1. ATP-binding cassette transporter B1 (*ABCB1*) expression in hepatocellular carcinoma (HCC) cell lines and clinical samples. (a) Quantitative real-time PCR and Western blot of *ABCB1* in HCC cell lines. Expression of *ABCB1* was significantly higher in KIM-1 cells compared with the other cell lines. (b) *ABCB1* mRNA expression levels in HCC clinical cases. The relative mRNA expression levels in tumor tissues (black column, T) and corresponding non-cancerous, background liver tissues (gray column, N) (left panel). High levels of *ABCB1* expression were observed in well differentiated HCC. The average expression levels of *ABCB1* were higher in tumor tissues than in the non-cancerous background liver tissues (2.30 vs 1.23, $P = 0.21$) (right panel). (c) Immunostaining of *ABCB1* in well differentiated HCC. An irregular and thicker form of canalicular pattern with cytoplasmic staining was observed in the tumor region compared with the non-cancerous background region (magnification, $\times 100$). Black arrows outline the border between the non-cancerous background region (N) and the tumor region (T). (d) *ABCB1* expression in moderately differentiated HCC (magnification, $\times 200$). Only an irregular canalicular pattern was observed (a, H&E stain; b, corresponding *ABCB1* staining).

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