Hepatocellular carcinoma (HCC) has been recognized as a major life-threatening problem and emerged as one of the major cause of cancer death. The molecular mechanism leading to the development of HCC appear to be extremely complex and with recent research efforts, it is beginning to unfold. Several effective therapies are available for patients diagnosed with HCC, but still a majority of individuals are diagnosed at a too advanced stage where no active treatment is feasible. Therefore, understanding the molecular and genetic basis of HCC is likely to facilitate the development of novel molecular strategies for chemoprevention and more efficacious therapies for HCC.

In the present study, we have done the transcriptomic profiling of the differentially expressed genes in X15-\textit{myc} transgenic mouse model for HCC. As this was likely to shed light not only on the cause of pathological changes, but also identify targets for disease detection and intervention. Sequence analysis of the liver cDNA subtraction identified many upregulated genes. Of these, Rps27a exhibited highest frequency of 20 times followed by other genes like COX3, ATP6, COX2 and ND1. Rps27a is an 80 amino acid carboxyl extensive (CEP) ubiquitin hybrid protein belonging to the component of eukaryotic small ribosomal subunit. Functional analysis of this gene revealed its active participation in mitotic cell proliferation. As overexpression of Rps27a strongly promoted the entry of cells from G1 to S phase. Likewise, depletion of endogenous Rps27a resulted in the arrest of cell cycle arrest at G2/M phase. Thus, inhibition of the endogenous Rps27a processing was associated with inhibition of cell proliferation. Noteworthily, changes in cell cycle distribution were less pronounced as expected from the proliferation. Thus, the present data suggested that in addition to a complete cell cycle arrest, the overall cell cycle progression may be affected. The precise nature of this interesting observation needs further investigation.
Rps27a also acts as an early growth response gene like other protooncogenes such as c-jun and c-fos (Wong et al., 1993). So, the regulatory mechanism in controlling early G1 phase gene expression may play a very important role in the pathogenesis of liver cancer. Interestingly another prognostic HCC marker- proliferating cell nuclear antigen (PCNA) is also synthesized in G1/S phase of cell cycle (Irene et al., 1993). In case of Rps27a, the immunohistochemical study revealed that the age adjusted intense nuclear as well as cytoplasm staining were observed in the liver of X15-myc transgenic mice. Notably, the non-tumor liver showed no staining for Rps27a. Thus, our findings suggested that cellular proliferation as defined by Rps27a expression (immunohistochemical study), correlated with the progression of HCC. Besides, the rate or efficiency of ribosome production in the cell could serve as a signal by which cells could negatively or positively regulate cell-cycle progression independent of its effect on protein bio-synthesis. The stratification of HCC cases initially observed in the experimental models needs to be validated in clinical cases. Undoubtedly, Rps27a as a biological marker may provide another criterion to aid in the prognostic grouping of patients with HCC. The molecular mechanism behind the Rps27a during pathogenesis of HCC also need to be elucidated further.

Despite therapeutic advances, the overall survival of patients with HCC has not significantly improved in the last two decades. In view of the side effects of drugs used in the chemotherapy of cancers, traditional herbal medicine and complementary and alternative medicine (CAM) are becoming increasingly popular among cancer patients in the developed countries (Molassiotis et al., 2005 and Yates et al., 2005). Variety of hepatoprotective herbal medicines and plants were reported so far to treat and cure different etiology of liver diseases. However, the anticancer property of Butea monosperma has not been investigated. In the present study, concluded that the aqueous extract (A003) of B. monosperma flower is a potent chemopreventive and anti-angiogenic agent with the ability to delay tumor formation in hepatitis B-related transgenic mouse
model of HCC. The chemopreventive action of fractions, F008 and F009 was less prominent as compared to the aqueous extract A003. Further, its non-toxic characteristics make it an ideal choice for developing herbal formulations for use is hepatitis and HCC. The anti-cancer and anti-proliferative property of *B. monosperma* flower need to be further validated using the new biomarker such as Rps27a, reported for the first time in the present study. In conclusion, these data indicates that the *B. monosperma* flower has the potential for developing new cancer therapeutics and Rps27a may provide use for another efficient biomarker in tumor proliferation.

Our initial findings on the treatment of oncomouse model with aqueous extracts of *B. monosperma* is quite encouraging as not only it showed hepatoprotection but also suppressed the levels of proliferation markers like VEGF (in serum) and Rps27a (in tumor tissue). Thus, the flower extracts of *B. monosperma* has the potential for developing new cancer therapeutics and Rps27a could serve as a good prognostic marker.