

Fig. 2. MAGE-A1 counteracts Notch1-IC transactivation and recruits histone deacetylases

Studies on the transcriptional regulation of cancer-germline genes, such as *MAGE-A1*, showed that DNA methylation is an essential component of their repression in normal somatic tissues (8). The promoters of these genes contain a high density of CpGs, but unlike classical CpG-rich promoters they are heavily methylated in all somatic tissues. In contrast, they are unmethylated in germ cells and in tumors that express these genes. Demethylation and therefore activation of cancer-germline genes in tumors was found to be coincident with overall genome demethylation, a process known to occur in many cancers (9-10). We are currently studying the mechanisms of demethylation of these genes in tumors. This should give insight into the processes leading to genome hypomethylation in cancers. It may also help designing procedures to induce the expression of specific antigens on tumors, thereby facilitating their elimination by the immune system.

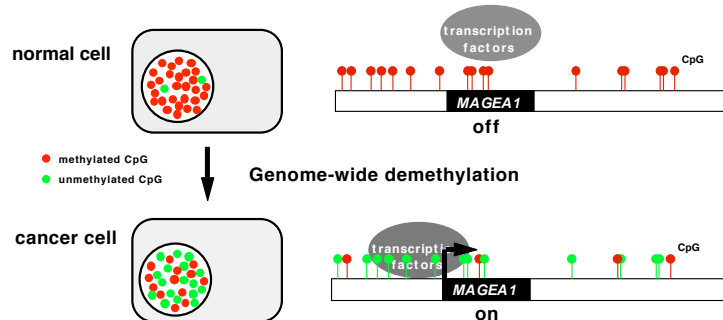


Fig. 3. *MAGEA1* activation as a result of genome demethylation in tumors

Selected publications

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10. De Smet C, Lurquin C, Lethe B, Martelange V, Boon T. *DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.* **Mol Cell Biol** 1999 ;19:7327-35.