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Title: Differential gene expression of two-pore-domain potassium channels in malignant pleural mesothelioma

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Body: Background: The two-pore-domain potassium channels constitute “leaky channels” that are involved in multiple cell functions including cell volume regulation, extracellular pH and mechanical sensing. These function are important in malignancies and recent findings revealed a role for this family of channels in tumorigenesis. No data exist regarding their expression in malignant pleural mesothelioma (MPM). Aims: Our goal was to investigate of the gene expression levels of two-pore-domain potassium channels (KCNK 1-3, 5, 7, 10, 12, 13, 15) in MPM as compared to healthy controls. Methods: We used gene expression data from the Oncomine Cancer Microarray database comparing MPM versus controls in order to investigate the differential expression profile of two-pore-domain potassium channels. Gene expression data were log transformed, median centered per array, and the standard deviation was normalized to one per array. Gene expression was considered over- or under- expressed when $p < 0.05$ in the MPM group compared to controls. Results: In MPM, the gene expression of KCNK-1 was significantly increased compared to healthy tissue ($p = 0.002$). On the contrary, KCNK-3, -7 and -10 were significantly decreased compared to healthy tissue ($p < 0.0001$; $p = 0.0002$; $p = 0.016$ respectively). There was no significant difference in the gene expression of KCNK-2, -5, -12, -13, -15. Conclusions: At the transcriptional level in MPM, members of the two-pore-domain potassium channels are differentially expressed compared to healthy tissue. These results set the basis for the study of the pathophysiological role of KCNK-1, -3, -7 and -10 in MPM.