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Title: Micro-RNA screening in neuroendocrine lung tumors: Differential expression of miR-29 family members

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Body: miRNAs are a class of small, noncoding, highly conserved single- stranded RNAs with post-transcriptional regulatory features including regulation of cell proliferation, differentiation, survival and apoptosis. They are deregulated in various tumors and show a different expression pattern, e.g. in NSCLC. These profiles can be used as a diagnostic tool. TC, AC, SCLC and LCLC belong to the NELC group, whereas an accurate discrimination of these entities is still difficult. A new and promising method for distinguishing tumor entities may be the alteration of miRNA expression between subtypes. Basis of our analyzed samples was a bio-pool including 201 patient samples with pulmonary tumors showing neuroendocrine features. This dataset is build out of atypical and typical carcinoids of the lung as well as LCLCs and SCLCs. We conducted miRNA screening for 763 known miRNAs involved in different tumorgenetic processes by performing 384 well TaqMan low-density array real-time qPCR. Analysis was done with TaqMan Array Human MicroRNA Card A and TaqMan Array Human MicroRNA Card B v3.0, respectively. In the overall collective comprised out of all four entities we identified 44 significantly different exprimised miRNAs, 11 of them highly significant. 7 miRNAs show an inverse correlation to aggressiveness of the tumor. In addition, we identified 45 micro-RNAs which significantly have an impact on survival in our collective. miRNAs turned out to be potent markers to distinguish between tumor entities. They demonstrate to be a helpful diagnostic tool, especially in discriminating between various entities of NELC. Additionally, some miRNAs are powerful markers to predict patient's clinical outcome.