Comparative microRNA expression profiles in human cervical cancer

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Background:
Cervical cancer is the second leading cause of death among female cancer patients in the world. Clinical manifestation and progression are very diverse and not easily predictable.
Aim:
To identify differentially expressed microRNAs in cervical cancer cases from the Southwestern Transdanubian Region of Hungary in concordance with HPV-positivity, histological and clinical grading.
Objectives and methods:
After HPV-genotyping we analyzed the expression levels of 8 different microRNAs (miR-21, miR-27a, miR-34a, miR-146a, miR-155, miR-196a, miR-203, miR-221) in FFPE primary human cervical cancer samples. Expression profiles were evaluated and statistically analyzed in conjunction to HPV-status, histological and clinical grading.
Results:
The rate of high-risk HPV-positivity in SCC and ACC was 76% and 68,18% respectively. Out of the HR-HPV types HPV-16 and 18 were principally registered, with an overall prevalence for the two combined of 78,95% in SCC and 86,67 % in ACC. HPV-16 was more frequently identified in SCC, than in ACC, and the difference was statistically significant (p=0,041). The overall expression profiles based on the chosen 8 microRNAs were distinctive of the histological characteristics. The magnitude of expression levels of all miRNAs were higher in SCC, than in ACC, but the difference only reached the level of significance in the case of miR-21 (p=0.036), miR-34a (p=0,000) and miR-203 (p=0.023). Further statistical analysis proved, that in SCC the level of miR-34a and miR-196a show significant correlation (p=0.008 and p=0.001 respectively) with clinical grading, while the association between HR-HPV-positivity and miR-155 expression levels was also significant (p=0.048). In ACC none of the studied miRNAs showed significant associations with HR-HPV-positivity, but increased expression of miR-21 was significantly associated with FIGO stage of ACC.
Discussion:
Molecular characterisation of malignant dysfunctions will lead to a better understanding of mechanisms underlying the development of cervical cancer. The alterations we observed in miRNA expressions can be candidate gene targets and might even serve as possible predictive biomarkers in the field of prevention and therapeutic decision support in response to the urging need for an earlier diagnosis, a more precise prognosis and a successful, personalized therapy.