

MicroRNA Microarray Analysis of Human Adrenocortical Tumors Identifies miR-195 and miR-483-5p as Predictors of Poor Prognosis in Adrenocortical Cancer – Response

We thank Dr. Tömböl and colleagues for their interest in our article and their comments. As with our study, Dr. Tömböl and colleagues also performed microRNA (miRNA) profiling of adrenocortical tumors. There were however only two miRNAs in common between the two studies. This is, of course, usual in these sort of studies. For example, in the gene expression profiling studies differentiating adrenocortical carcinomas (ACC) and adenomas (ACAs; refs. 1–4), only insulin-like growth factor 2 has been found to be common across all the studies.

Dr. Tömböl and colleague' study included 19 ACAs and 7 ACCs, which is a small number of ACCs. No clinical follow-up was provided so the influence of miRNA expression on prognosis could not be assessed. They only included functioning ACCs and question our lack of subdivision of ACCs based on functional status, as this may affect miRNA profiles. We had compared the miRNA expression profile of functioning ACCs ($n = 11$) to nonfunctioning ACCs ($n = 9$) and found no significantly differentially expressed miRNAs between the two groups. We therefore felt that it was justified to group both functioning and nonfunctioning ACCs together. We also found that significantly differentially expressed miRNAs between ACAs and all ACCs, all ACAs and functioning ACCs, and all ACAs and nonfunctioning ACCs, were similar.

In our study, normal adrenal cortices were obtained from adrenalectomy specimens away from the site of the ACA as has been done in several previous studies (1, 5). It is possible, as Dr. Tömböl and colleagues suggest, that this may account for the low number of miRNAs significantly differentially expressed between adrenocortical tumors and normal adrenal cortices, although we think this is unlikely. In any case, the use of normal adrenal cortex as an external control does not, of course, in any way alter the results obtained comparing the miRNA expression of ACCs and ACAs. Nor does it alter our other key finding that aberrant expression of miR-195 and miR-483-5p portends a poor prognosis in ACCs.

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No potential conflicts of interest were disclosed.

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