The role of microRNA deregulation in the pathogenesis of adrenocortical carcinoma

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Abstract

Adrenocortical carcinoma (ACC) is an aggressive tumor showing frequent metastatic spread and poor survival. Although recent genome-wide studies of ACC have contributed to our understanding of the disease, major challenges remain for both diagnostic and prognostic assessments. The aim of this study was to identify specific microRNAs (miRNAs) associated with malignancy and survival of ACC patients. miRNA expression profiles were determined in a series of ACC, adenoma, and normal cortices using microarray. A subset of miRNAs showed distinct expression patterns in the ACC compared with adrenal cortices and adenomas. Among others, miR-483-3p, miR-483-5p, miR-210, and miR-21 were found overexpressed, while miR-195, miR-497, and miR-1974 were underexpressed in ACC. Inhibition of miR-483-3p or miR-483-5p and overexpression of miR-195 or miR-497 reduced cell proliferation in human NCI-H295R ACC cells. In addition, downregulation of miR-483-3p, but not miR-483-5p, and increased expression of miR-195 or miR-497 led to significant induction of cell death. Protein expression of p53 upregulated modulator of apoptosis (PUMA), a potential target of miR-483-3p, was significantly decreased in ACC, and inversely correlated with miR-483-3p expression. In addition, high expression of miR-503, miR-1202, and miR-1275 were found significantly associated with shorter overall survival among patients with ACC (Pvalues: 0.006, 0.005, and 0.042 respectively). In summary, we identified additional miRNAs associated with ACC, elucidated the functional role of four miRNAs in the pathogenesis of ACC cells, demonstrated the potential involvement of the pro-apoptotic factor PUMA (a miR-483-3p target) in adrenocortical tumors, and found novel miRNAs associated with survival in ACC.

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Introduction

Patients with tumors of the adrenal cortex may present an incidentally detected or hormonally overproducing adrenocortical adenoma, or uncommonly an adrenocortical carcinoma (ACC). ACC is an aggressive tumor associated with poor prognosis in adults (Bertherat et al. 2006). Differential diagnosis between ACC and the more common adenoma is difficult, particularly for the tumors in the marginal category, i.e. Weiss score 2 or 3 vs 4. Moreover, prognostic tools for early recognition of metastatic ACC disease and adverse outcome are presently lacking in routine diagnostics. Profilings of mRNA and microRNA (miRNA) expressions in human cancer have revealed important alterations that do not only have possible diagnostic and prognostic value but also point toward molecular alterations of mechanistic importance for tumor etiology and progression.

In adrenocortical tumors, mRNA expression profilings by several independent groups have revealed significant and reproducible alterations for the
discrimination of adenoma and ACC and for the
determination of ACC prognosis (Giordano et al.
2003, de Fraipont et al. 2005, Velazquez-Fernandez
de Reynies et al. 2009, Soon et al. 2009a). One of
the most striking findings was the significant overexpres-
sion of insulin-like growth factor 2 (IGF2) in ACC,
which was observed in > 80% of cases compared with
adrenal cortices and hormonally active/inactive ade-
nomas (Giordano et al. 2009, Laurell et al. 2009,
de Reynies et al. 2009). In addition, the expression
levels of other genes such as DLG1 and PINK1 have
been associated with the clinical outcome of ACC
de Reynies et al. 2009).

miRNAs are ~22 nucleotide long single-stranded
non-coding RNAs generated by the RNase-III enzyme
Dicer from endogenous hairpin-shaped transcripts
(Iorio & Croce 2009). miRNAs have diverse roles in many biological processes and have
also been shown important for tumor development,
by acting as oncogenic or tumor suppressive species.
Besides, accumulating evidence also supports a role
of miRNAs as diagnostic and prognostic biomarkers
of human cancers (Iorio & Croce 2009, Ferracin
et al. 2010). Profiling of adrenocortical tumors have
identified several deregulated miRNAs in benign
adrenocortical diseases (Iliopoulos et al. 2009,
Bimpaki et al. 2010), as well as ACC (Soon et al.
2009b, Tombol et al. 2009, Doghman et al. 2010,
Patterson et al. 2011). Several deregulated miRNAs
have been reported in ACC, including overexpression
of miR-483-3p and miR-483-5p, which are tran-
scribed from an intronic sequence of the IGF2
gene (Soon et al. 2009b, Doghman et al. 2010).
miR-483-3p has recently been shown to target the
pro-apoptotic gene BCL-2-binding component 3/p53
upregulated modulator of apoptosis (BBC3/PUMA)
in cancers of the colon, liver, and breast (Veronese
et al. 2010), suggesting its anti-apoptotic role in a
variety of tumor types.

In this study, we characterized miRNA expression
patterns of ACC compared with adenomas and normal
adrenal cortices, and related the findings to outcome
at follow-up. The functional consequences of
miR-483-3p, miR-483-5p, miR-195, and miR-497
deregulations were studied in vitro concerning cell
proliferation and apoptosis. We further explored the
involvement of PUMA, a potential target of miR-483-3p,
in clinical samples. Our findings may contribute to
further understanding of ACC development, and
suggest a role for selected miRNAs as diagnostic
and prognostic biomarkers in ACC.

Materials and methods
Tumors and normal tissues
A total of 68 snap-frozen primary sporadic adrenocor-
tical tumors collected at the Karolinska University
Hospital were included in this study. In addition,
histopathologically verified normal adrenal cortical
samples were obtained from ten patients undergoing
nephrectomy for other reasons and used as non-
neoplastic reference tissues. All samples were obtained
with informed consent and the study of the tissue
materials was approved by the Local Ethics Committee.
Tumors were diagnosed following the WHO classifi-
cation (DeLellis et al. 2004) as adrenocortical adenoma
(Ad 1–43) or ACC (Ca 1–25). Clinical details have been
partly published for subsets of the cases in previous
studies (Laurell et al. 2009). All 25 carcinoma cases
were followed-up until May 2011 or until their death,
and the follow-up data is detailed together with clinical
and histopathological information in Supplementary
Table 1, see section on supplementary data given at the
end of this article. Thirteen of the 43 adenoma cases
were cortisol-producing tumors (Cushing) from one
male and 12 female patients with a mean age of
diagnosis at 56 years (range 27–81) and a mean tumor
size of 3.8 cm (range 1.5–6.5). Sixteen adenomas were
aldosteronomas (five male and 11 female patients) with
a mean age of 46 years (range 16–79) and a mean tumor
size of 2.0 cm (range 0.9–4.7). The last 14 adenomas
were classified as incidentalomas (six male and eight
female patients) with a mean age of 59 years (range
42–65) and a mean size of 3.9 cm (range 2.5–5.3). The
median follow-up time for adenomas was 39 months
(range 12–258). At the end of the follow-up, no
adenoma patient had disease progression or metastasis.

Cell line
The ACC cell line NCI-H295R was purchased from
the American Type Culture Collection (ATCC# CRL-2128; LGC Standards, Middlesex, UK). Cells
were maintained in DMEM:F12 medium containing
2.5% of NuSerum (cat. no. 355500; BD Biosciences,
Bedford, MA, USA), 1% penicillin/streptomycin and
1% insulin-transferin-sodium selenite (ITS+1) liquid
media supplement (cat. no. I2521; Sigma–Aldrich
Logistik GmbH) at 37 °C and 5% CO2. Authentication
of the cell line was evaluated and verified by Bio-
Synthesis, Inc. (Lewisville, TX, USA) employing
genotyping of 15 short tandem repeat (STR) loci and
the amelogenin gene (AMEL), and comparison with
genotype information at the ATCC (Supplementary
Table 2, see section on supplementary data given at the
end of this article).
RNA extraction

Total RNA isolation was performed by mirVana miRNA Isolation Kit (Applied Biosystems/Ambion, Austin, TX, USA). Measurement of RNA concentrations was done using a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA).

Microarray-based miRNA profiling

Global miRNA expression profiling of adrenocortical tumors and normal cortices was performed by the Human Agilent’s miRNA microarray system (Agilent, Santa Clara, CA, USA) with probes matching 903 human miRNAs (miRBase release 14). Array hybridizations and data analyses were performed essentially as described previously (Caramuta et al. 2010). In brief, samples of 120 ng total RNA were labeled with Cyanine 3-pCp, hybridized onto arrays 2010). In brief, samples of 120 ng total RNA were labeled with Cyanine 3-pCp, hybridized onto arrays 18–20 h at 55°C, followed by washing. Slides were scanned in an Agilent microarray scanner G2565BA and images were processed with Feature Extraction Software v10.7.3.1 (Agilent). Cluster 3.0 Software (http://bonsai.hgc.jp/~mdehoon/software/cluster/) was used for normalization and median centering (de Hoon et al. 2004). Normalized miRNAs with <50% missing values were included in subsequent analyses for hierarchical clustering and significance analysis of microarrays (SAM). The data from microarray analysis have been deposited at NCBI Gene Expression Omnibus (GEO accession number, GSE22816).

QRT-PCR analysis of individual miRNAs

Selected mature miRNAs were quantified using commercially available TaqMan qRT-PCR assays (Applied Biosystems) and a 7900HT Real-Time PCR System (Applied Biosystems). cDNA was synthesized from 25 ng total RNA using TaqMan mRNA RT Kit (Applied Biosystems) and used for quantification of miR-483-3p (ID 002339), miR-483-5p (ID 002338), miR-497 (ID 001043), miR-195 (ID 000494), miR-1974 (ID 121209_mat), miR-210 (ID 000512), miR-21 (ID 000397), miR-503 (ID 001048), miR-1202 (ID 002858), miR-1275 (ID 002840), miR-638 (ID 001582), miR-1915 (ID 121111_mat), and miR-572 (ID 001614) with normalization against RNU6B (ID 001093). All reactions were performed in triplicate, and relative expression levels were determined with the ΔC_T method and reported as 2-ΔΔC_T.

miRNA inhibition and overexpression in NCI-H295R cells

NCI-H295R ACC cells were transfected using Nucleofector Technology (Amaxes Systems, Gaithersburg, MD, USA). In brief, 3 × 10⁶ cells were resuspended in 100 µl Nucleofector solution R, and mixed with 100 pmol of miRNA inhibitors (anti-miR-483-3p or anti-miR-483-5p; Applied Biosystems/Ambion) or miRNA precursors (pre-miR-195 or pre-miR-497; Applied Biosystems/Ambion). Anti-miR-negative control #1 or pre-miR-negative control #1 (Applied Biosystems/Ambion) containing a non-targeting sequence molecule was used as a negative control. Cells were then electroporated using the program T-20, allowed to recover in DMEM:F12 media for 15 min at 37°C and seeded in T-25 flasks with 5 ml DMEM:F12 media. Culture media was replaced after 24 h and cells were cultured for additional 72 h. All transfection experiments were repeated at least three times and used for proliferation and apoptosis assays. Transfection efficiency was determined by measuring the endogenous miR-483-3p, miR-483-5p, miR-195, or miR-497 expression levels by qRT-PCR (Supplementary Figure 1, see section on supplementary data given at the end of this article). To demonstrate that the transfected miRNAs achieved physiologically relevant expression levels, we compared the expression fold change differences between the experimental cell culture systems (anti-miRNA/pre-miR versus control) and the clinical materials (carcinomas versus normal cortices) for miR-483-3p, miR-483-5p, miR-195, and miR-497. In the transfected cells expressing specific miRNA assayed, we observed a reduction of ~12-fold for miR-483-3p and approximately ninefold for miR-483-5p while we noticed ~15- and 30-fold increase for miR-195 and miR-497, respectively, compared with the negative control. The effect of transfections had a similar magnitude of miRNA expression levels as for the comparison between carcinomas and normal adrenal cortices. In carcinomas, we observed an average increased expression of 166-fold (range 0.1–1330) and 73-fold (range 0.1–400) for miR-483-3p and miR-483-5p, respectively; but a reduced expression of sixfold (range 0.6–26) and 18-fold (range 0.3–170) for miR-195 and miR-497 respectively.

Cell proliferation WST-1 colorimetric assay

WST-1 (4-(3-(4-iodophenyl)-2-(4-nitrophenyl)-2H-5-tetrazolio)-1,3-benzene disulfonate; cat. no. 11644807001; Roche Applied Science) colorimetric assay was carried out to determine the effects of
miR-483-3p and miR-483-5p inhibition or miR-195 and miR-497 overexpression on cell proliferation. The assay was performed by 96-well plates, with seeding of ~20,000 cells in each well. After 72 h of transfection, 20 µl of the WST-1 solution were added to the culture medium and incubated for 2.5 h at 37 °C. Absorbance was subsequently determined using a microplate ELISA reader (VERSAmax; Molecular Devices, Sunnyvale, CA, USA) and analyzed with SoftMax Pro 5 Software (Molecular Devices) applying the wavelengths 450 nm for measurements and 650 nm as reference. All experiments were conducted in eight wells for each condition, and replicated at least three times. Cell proliferation was calculated by comparing the absorbance values of the samples after background subtraction. The fraction of surviving cells was calculated by defining the anti-miR- (or pre-miR)-negative control #1-treated cells as one.

Apoptosis caspase-3 colorimetric assay

The caspase-3 colorimetric assay (cat. no. L00289; Genscript, Piscataway, NJ, USA) was used to evaluate the effects of miR-483-3p and miR-483-5p inhibition or miR-195 and miR-497 overexpression on apoptosis; 3×10^5 cells were transfected and seeded in T-25 flasks. After 72 h of transfection, proteins were isolated and quantified by Bio-Rad Protein Assay (Bio-Rad). Fifty microliters of lysate containing 50 µg protein was mixed with 50 µl of 2× reaction buffer and 5 µl of caspase-3 substrate and incubated for 4 h at 37 °C. Absorbance was subsequently determined using a microplate ELISA reader (VERSAmax; Molecular Devices) and analyzed with SoftMax Pro 5 Software (Molecular Devices) applying the wavelengths 405 nm for measurement. Apoptosis was calculated by comparing the absorbance values of the anti-miR/pre-miR treated cells with the respective negative control-treated cells. All the experiments were replicated three times.

Western blot analysis

Whole cell lysates were prepared from normal and tumor tissue samples by homogenization in NP-40 lysis buffer (cat. no. FNN0021; Invitrogen), with addition of protease inhibitor (complete protease inhibitor cocktail; Roche Diagnostics Corporation) and 1 mM of phenyl-methanesulfonyl fluoride (Sigma–Aldrich). After quantification by Bio-Rad Protein Assay (Bio-Rad), 60 µg of lysate was separated in Novex 10% Tricine gels (Invitrogen) and transferred to nitrocellulose membranes (LC2001; Invitrogen). Filters were blocked with 5% non-fat milk diluted in TBS/0.05% Tween 20, and incubated with rabbit polyclonal anti-PUMA antibody (#4976, Cell Signaling Technology, Danvers, MA, USA) at 1:1000 dilution, followed by an anti-rabbit IgG–HRP (1:3000; #170-6515; Bio-Rad Laboratories) used as secondary antibody. Detection was carried out with Novex ECL HRP chemiluminescent substrate reagent (#WP20005; Invitrogen). Novex Sharp Pre-stained protein standards (#57318; Invitrogen) and MagicMark XP (#LC5602; Invitrogen) markers were used to determine relative molecular weights. Protein levels were quantified on X-ray films from immunoblots using ImageJ Software (http://rsb.info.nih.gov/ij/). Subsequent incubation of the filters with an anti-GAPDH antibody (sc-47724; Santa Cruz Biotechnology, Inc, Santa Cruz, CA, USA) diluted at 1:5000 was performed for normalization purposes.

Statistical analysis

All analyses were performed by Statistica 8.0 (StatSoft, Inc., Tulsa, OK, USA) or MS Office Excel 2007, unless otherwise specified. Unpaired Student’s t-test was conducted to compare miRNA expressions in different groups, while paired Student’s t-test was performed to analyze transfection experiments. Correlations between miR-195 and miR-497, and miR-483-3p and PUMA expression levels were assessed by Pearson’s correlation analyses and P values were estimated by permuting the samples. SAM survival analysis was used to identify miRNAs associated with survival. P values were obtained for the Cox score statistics using the χ²-distribution. For survival analysis, all patients who died of unknown causes or causes unrelated to ACC (i.e. Ca 3, Ca 7, Ca 12, and Ca 14) during follow-up were considered as ‘censored’. Selected miRNAs potentially associated with survival were analyzed by TaqMan qRT-PCR and carcinoma patients were classified into different groups with high or low expression of each miRNA according to median level. The inter-relationship of miRNAs with survival was studied using Kaplan–Meier plots, and the curves for each group were compared by log-rank test. All the analyses were two-tailed and P values <0.05 were considered significant.

Results

Deregulated miRNAs in ACC

In this study, we characterized miRNA expression patterns in a cohort of 48 adrenocortical tumors (26 adenomas and 22 carcinomas) and four normal adrenal cortices using a microarray-based approach. Unsupervised clustering analysis classified the samples in different subgroups based on the similarity of their miRNA expression profiles. In Fig. 1, clustering based
on 213 miRNAs revealed four main clusters: cluster A consisted of the majority of carcinoma samples (16 of the 22 ACC; 72%) and cluster B comprised 19 adenomas and the remaining six carcinomas. Five of the six ACC patients in cluster B are still alive at the end of follow-up and one died of unrelated causes with ACC after 65 months. All four normal adrenal cortices were grouped in cluster C, and the remaining seven adenomas were included in cluster D.

We also performed SAM analysis to identify the most significant deregulated miRNAs that could distinguish carcinomas from adenomas and adrenal cortices. The analysis identified 72 differentially expressed miRNAs with a false discovery rate (FDR) of 0% (Supplementary Table 3, see section on supplementary data given at the end of this article). Several of these miRNAs were also found to have significantly differential expression in the comparisons between carcinomas and adenomas or normal adrenal cortices (Supplementary Tables 4 and 5, see section on supplementary data given at the end of this article). To verify the significance of the results obtained by microarray analysis, we evaluated the expression levels of seven miRNAs (miR-483-3p, miR-483-5p, miR-210, miR-21, miR-1974, miR-195, and miR-497) by qRT-PCR in a series of 68 adrenocortical tumors.

**Figure 1** Unsupervised clustering analysis of microarray-based miRNA expression data for four normal adrenal cortices (N), 26 adenomas (Ad), and 22 carcinomas (Ca). Samples were clustered using the Spearman rank correlation and complete linkage. The four main clusters obtained (A–D) are indicated above the heatmap. Red and green colors indicate relatively high and low expression respectively. Missing values are indicated in gray. *Alive; †dead of disease; ‡dead of unrelated or unknown causes.
We found that the expression of miR-195 belongs to the same miRNA cluster and are likely to be co-expressed, suggesting that miR-497 upstream of miR-195 is located at a distance of 200 bases and is correlated with the P value (see section on supplementary data given at the end of this article). Interestingly, two of these miRNAs, miR-483-3p and miR-483-5p, were also significantly differential expressed between the carcinomas in cluster B and cluster A observed in unsupervised clustering (Supplementary Table 6, see section on supplementary data given at the end of this article). The precursor of miR-497 is located at a distance of ~200 bases upstream of miR-195 at chromosomal region 17p13.1, suggesting that miR-497 and miR-195 belong to the same miRNA cluster and are likely to be co-expressed. We found that the expression of miR-195 was strongly correlated with the miR-497 expression (corr = 0.9, P < 0.00001; Supplementary Figure 3, see section on supplementary data given at the end of this article).

Effect of altered miR-483, miR-195, and miR-497 expression on cell proliferation and apoptosis in NCI-H295R cells

We further evaluated the functional consequences from dysregulation of four miRNAs in human NCI-H295R ACC cells. These miRNAs were chosen because of their associations with malignancy in adrenal cortical tumors. In Fig. 3A, inhibition of miR-483-3p or miR-483-5p expression resulted in significant reduction (20 and 30% respectively), of cell proliferation compared with negative control cells (treated with anti-miR-negative control #1). In addition, cells transfected with anti-miR-483-3p, but not with anti-miR-483-5p, showed a significant increase (approximately twofold) in apoptosis compared with cells transfected with negative control (Fig. 3A).

We also explored the functional consequences of miR-497 and miR-195 overexpression, which were found significantly downregulated in ACC compared with adenomas. In line with the effects observed for miR-483-3p, overexpression of miR-195 or miR-497 led to a significant decrease in cell growth (30 and 40% respectively), and a concomitant induction of cell death (40 and 30% respectively), compared with negative control (Fig. 3B).

**Figure 2** Relative expression levels of miR-483-3p, miR-483-5p, miR-210, miR-21, miR-195, miR-497, and miR-1974 in the different sample groups. Box plots show miRNA expression levels determined by qRT-PCR in adrenocortical carcinomas, adenomas, and adrenal cortices. Statistical significances between the groups were determined with two-tailed unpaired t-test and P < 0.05 were considered significant.
Relationship between miR-483-3p and PUMA expression in adrenocortical tumors

Recent findings of the pro-apoptotic gene BBC3/PUMA as a direct target of miR-483-3p (Veronese et al. 2010), in combination with our observations of the pro-apoptotic and anti-proliferative effects of miR-483-3p silencing, prompted us to investigate a possible connection between PUMA and miR-483-3p expression in adrenocortical tumors.

We measured the PUMA protein expression levels by western blot analysis in three normal adrenal cortical samples, 26 adenomas, and 22 carcinomas, and compared with the expression of miR-483-3p. In Fig. 4, high levels of PUMA expression were detected in almost all adenomas and adrenal cortices, but only in a small proportion of carcinomas. The PUMA protein expression was inversely correlated with the miR-483-3p expression (corr = −0.31, P = 0.025). Notably, those carcinomas expressing low levels of miR-483-3p had a higher PUMA protein expression (e.g. Ca 20), and vice versa (e.g. Ca 6; Fig. 4).

miRNAs associated with survival of ACC patients

In an attempt to identify specific miRNAs associated with survival, we performed SAM survival analysis on the carcinoma cases. The analysis identified 11 miRNAs that could predict the disease outcome with a SAM survival score >2.6 (FDR: 0%; Fig. 5A). Specifically high expression of miR-638, miR-1246, miR-1915, miR-1275, miR-503, miR-671-5p, miR-1268, miR-762, miR-331-3p, miR-1202, and miR-572 were found associated with short survival (Fig. 5A). Although two of the carcinoma cases (Ca 23 and Ca 24) had a shorter follow-up (25 and 20 months respectively), exclusion of these cases from the survival analyses did not affect the significance of our results. Using the miRNA set selected by SAM survival analysis, we performed a hierarchical
clustering analysis and observed that the samples were classified into three clusters. As shown in Fig. 5A, the survival analysis revealed a significant difference between cluster 3 and the other two clusters ($P=0.03$, log-rank test). Furthermore, using Kaplan–Meier survival and log-rank analyses, we evaluated the association with survival for each individual miRNA detected by SAM. The analysis revealed six of these 11 miRNAs as significantly associated with survival (Supplementary Figure 4, see section on supplementary data given at the end of this article). High expression of $miR-503$ ($P<0.001$; log-rank test), $miR-1202$ ($P=0.009$), $miR-1915$ ($P=0.013$), $miR-638$ ($P=0.018$), $miR-572$ ($P=0.024$), and $miR-1275$ ($P=0.035$) were significantly associated with shorter overall survival (Supplementary Figure 4).

To validate the significance of these prognostic miRNAs, we evaluated the expression of six miRNAs in the cohort of 25 ACC by qRT-PCR. Using Kaplan–Meier survival curves and log-rank analysis, we confirmed the significant association of $miR-503$ ($P=0.006$), $miR-1202$ ($P=0.005$), and $miR-1275$ ($P=0.042$) with overall survival (Fig. 5B), which is in concordance with the array-based results. However, $miR-572$, $miR-1915$, and $miR-638$ were not found statistically significant (data not shown).

**Discussion**

In this study, we identified a set of miRNAs that is differentially expressed between malignant and non-malignant samples, and a small number of miRNAs associated with survival in ACC patients.

**miRNA deregulation in ACC**

Using a microarray approach, we identified distinct miRNA expression patterns between carcinoma and non-carcinoma samples. The consistency of the findings was supported by the validation of seven of the most significant differentially expressed miRNAs in an extended series of adrenocortical tumors by TaqMan qRT-PCR methodology. Taken together, the observations indicate the significant importance of these miRNAs in the pathogenesis of ACC.

We showed that $miR-497$ expression is significantly reduced in ACC compared with adenomas. In concordance with our results, $miR-497$ was reported underepressed in childhood adrenocortical tumors (Doghman et al. 2010). Decreased expression of $miR-497$ has also been observed in peritoneal carcinoma (Flavin et al. 2009) and male breast cancer (Lehmann et al. 2010). Downregulation of $miR-195$ was recently reported in adult ACC (Soon et al. 2009b), which is consistent with our results. The precursors of $miR-497$ and $miR-195$ are likely generated from the same miRNA cluster because of their close proximity in genomic location. A strong positive correlation between $miR-497$ and $miR-195$ expressions also indicates that these two miRNAs were co-expressed. The co-expression of the $miR-497$–$195$ cluster suggests that these miRNAs could be co-regulated by common transcriptional factor(s) and they may have some common functions. Although the factor(s) regulating the transcription of this miRNA cluster are yet unknown, a common deletion within this chromosomal region (17p13) has been reported in ACC (Kjellman et al. 1996, Soon et al. 2008), but not in benign adrenocortical conditions (Almeida et al. 2011). This may, at least in
part, explain the reduced expression of the miR-497–195 cluster in ACC.

Despite the expression association, functional roles of miRNAs in ACC cells remain uncharacterized. In this study, we demonstrate the functional role of deregulated miRNAs in ACC cells using experimental cell culture systems. Overexpression of miR-195 or miR-497 in the NCI-H295R human ACC cell line could significantly reduce cell proliferation in combination with a pro-apoptotic effect. Consistent with our findings, miR-497 was previously shown to promote neural death by negatively regulating expression of anti-apoptotic proteins, bcl-2 and bcl-w (Yin et al. 2010). Moreover, overexpression of miR-195 could induce cell cycle arrest in hepatocellular carcinoma cells (Xu et al. 2009) and promote cell apoptosis in human colorectal cancer cells (Liu et al. 2010). Taken together, these findings revealed the potential tumor suppressive role and pro-apoptotic activity of this miRNA cluster in ACC and other cell types. Further investigation is certainly warranted to identify their potential targets and elucidate their mechanisms of action in ACC development.

We also demonstrated that miR-483-3p and miR-483-5p expression levels were significantly higher in carcinomas compared with the benign or normal counterparts. Concordantly, overexpression of miR-483-3p and miR-483-5p were recently reported in childhood adrenocortical tumors (Doghman et al. 2010) and adult ACC (Patterson et al. 2011) respectively. However, Soon et al. (2009b) observed a non-significant trend for miR-483 overexpression in adult ACC versus adenomas, where the lack of statistical significance could result from the relatively limited sample size. miR-483-3p and miR-483-5p are derived from different arms (3' and 5' arms respectively), of the same miRNA precursor. Although both miR-483-3p and miR-483-5p were significantly upregulated in carcinomas, we noted that the 3'-strand was much more abundant than the 5'-strand.

Overexpression of miR-483-3p may be a common alteration of tumor cells in several different tumor
miRNAs associated with survival in ACC

Recently, Soon et al. (2009b) identified two miRNAs (i.e. miR-483-5p and miR-195) associated with survival in ACC using Exiqon miRCURY LNA microarray, however these miRNAs were not significantly associated with survival in our cohort using both Agilent microarray and qRT-PCR methods (data not shown). The discrepancy could be due to differences in sample characteristics, platforms, and data analysis methods.

In this study, we demonstrate that ACC can be divided into different subgroups with different clinical outcomes based on their miRNA expression profiles. Cluster 3 is associated with poorer outcome, in which most patients were died of the disease. The overall survival is apparently better in the other two clusters in which most patients are still alive. However, no distinct histologic features were found between the two subgroups (data not shown). Survival analysis revealed that high expression of miR-503, miR-1202, and miR-1275 are significantly associated with poor survival of ACC patients. Notably, increased expression of miR-503 has been observed in various human tumors, including parathyroid carcinoma (Corbetta et al. 2010), retinoblastoma (Zhao et al. 2009), and ACC (Soon et al. 2009b, Tombol et al. 2009). However, to our knowledge, the association between miR-503 expression and survival has not been reported in any cancer type. Functionally, miR-503 has been shown to directly target cell cycle regulators, which leads to induction of G1 cell cycle arrest in various cancer cell lines and promotion of cell differentiation in monocytes and myeloblasts (Forrest et al. 2010, Sarkar et al. 2010). Although miR-503 is important for promoting cell cycle arrest and differentiation, its role in tumor progression has yet to be
elucidated. The other two miRNAs demonstrating significant association with survival, miR-1202 and miR-1275, have not been described in any cancer types. Nothing is known about their expression levels and function.

In conclusion, our findings show deregulation of a subset of miRNAs in ACC together with a potential role of miR-483, miR-195, and miR-497 in the pathogenesis of this neoplasm. Our study also reveals that high expression of miR-503, miR-1202, and miR-1275 are associated with poor survival of ACC patients, suggesting their potential prognostic value in ACC.

**Supplementary data**

This is linked to the online version of the paper at http://dx.doi.org/10.1530/ERC-11-0082.

**Declaration of interest**

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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**Author contribution statement**

D M Ö, S C, C L, and W-O L conceived and designed the experiments; D M Ö, S C, D V-F, P A, and H X performed the experiments; D M Ö, S C, D V-F, P A, and H X, and W-O L analyzed the data; M B, C L, A H, and J Z contributed to clinical and histopathological information of the cases; D M Ö, S C, C L, and W-O L wrote the manuscript; All authors have read and approved the final version of the manuscript.

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