Molecular signature induced by RNASET2, a tumor antagonizing gene, in ovarian cancer cells

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ABSTRACT:

Using the Hey3Met2 human ovarian cancer cell line, we previously found the RNASET2 gene to possess a remarkable in vivo tumor suppressor activity, although no in vitro features such as inhibition of cell proliferation, clonogenic potential, impaired growth in soft agar and increase in apoptotic rate could be detected. This is reminiscent of the behavior of genes belonging to the class of tumor antagonizing genes (TAG) which act mainly within the context of the microenvironment. Here we present transcriptional profiles analysis which indicates that investigations of the mechanisms of TAG biological functions require a comparison between the in vitro and in vivo expression patterns. Indeed several genes displaying a biological function potentially related to tumor suppression could not be validated by subsequent in vivo expression analysis. On the other hand the fact that we could find congruency for three genes both in vivo and in vitro adds a warning to a too much stringent categorization of this class of genes which relies on the sensitivity of the methodological approaches.

RNASET2, A NEW MEMBER OF THE GROWING CLASS OF TUMOR ANTAGONIZING GENES

Among the gynecological malignancies, ovarian cancer is considered to be the most lethal tumor, with an incidence of 42,000 new cases per year in Europe [1] and 22,000 cases in the USA [2]. In more than 60% of the patients, the diagnosis is made in advanced stage, owing both to the lack of symptoms and the to fact that a panel of highly predictive biomarkers for screening and early stage detection is still missing. It is estimated that 80% of the patients with advanced disease will develop recurrence and succumb to the illness, despite their good initial responsiveness to primary therapy.

We reckon that one of the main reasons for such regrettable scenario is a poor understanding of the biological bases of ovarian cancer pathogenesis. Indeed, one of the salient feature of these tumors is their high heterogeneity, both at the morphological and biological levels, which make the contribution of genetic lesions difficult to interpret in a causative way. Among human cancers located in the ovary, those derived from the ovarian surface epithelium are the most frequent [3] and all epithelial ovarian cancer subtypes have been postulated to originate from the single layer of cells representing the ovary’s surface epithelium (OSE cells) [4]. These cells are known to undergo repeated cycles of proliferation due to the recurrent growth and rupture of ovarian follicles during the ovulatory cycle and one feature of this phenomenon is a well-characterized interaction between the ovarian mesenchymal and surface epithelial cells [5]. Any imbalance in the microenvironmental homeostasis has therefore the potential to contribute to ovarian cancerogenesis, and a growing interest has indeed been placed toward the active role for stromal misregulation in the progression of neoplasias [6]. Within this frame, a special class of genes has been recently described that
seems to play a crucial role in tumor suppression by means of regulating the cross-talk between stromal and epithelial cells. These genes belong to the growing but still poorly characterized class of tumor autonously/malignancy suppressor genes (TAMSG) [7], whose principal feature is their ability to suppress malignant growth in vivo but not in vitro.

We have recently reported a preliminary biological characterization of one of these genes, called RNASET2, which codes for an extracellular RNase highly conserved among the phyla from viruses to humans, suggesting an evolutionary important function [8].

In a xenograft model for ovarian cancer, we found RNASET2 to carry out a strong immunosuppressive activity by recruiting cells of the monocyte/macrophage lineage into the tumor mass. This subset of cells represents the main component of the host immunological response [9]. Although the main function of RNASET2 was found to take place in the context of the microenvironment, namely in the extracellular compartment, we could not completely rule out that this conserved RNase might also carry out a cell-autonomous role, as suggested by a recent work on S. cerevisiae [10].

This was basically the rationale that prompted us to further investigate the cell-autonomous expression profile induced by RNASET2 in ovarian cancer cells.

**IN VITRO WHOLE GENOME TRANSCRIPTIONAL PROFILING OF CONTROL AND RNASET2-OVEREXPRESSION HUMAN OVARIAN CANCER CELLS**

As previously reported, using the Hey3Met2 human ovarian cancer cell line, we found the RNASET2 gene to possess a remarkable in vivo tumor suppressor activity, irrespective of the protein’s catalytic activity [9]. Noteworthy, when tested in vitro, the same cell clones did not show inhibition of cell proliferation, changes in the clonogenic potential, impaired growth in soft agar, and increase in apoptotic rate.

As stated in the previous section, although these data strongly suggest that RNASET2 might represent a new member of the family of TAMSG (acting mostly in a non-cell autonomous fashion), we could not formally rule out a cell-autonomous effect elicited by this gene on the cancer cells, which might have escaped detection by our panel of in vitro standard assays. We therefore decided to carry out a more thorough analysis to shed light on this issue.

Accordingly, we defined the expression profile of the RNASET2-overexpressing Hey3Met2 cells and compared it with that of control cells. An Agilent Whole Human Genome Oligo Microarray was employed with total RNA extracted from Hey3Met2 clones transfected with wild-type or a catalytically mutant form of RNASET2 (whose cDNA was mutagenized as the two CAS catalytic sites). Total RNA from Hey3Met2 cells, transfected with the empty vector, was used as a control.

Sixty-five genes were found to be modulated by at least one of the two RNASET2 protein forms tested (i.e. either wild-type or catalytically dead RNASET2), with a fold-inductions or repression greater than 2 and a p-value smaller than 0.01. These genes were further organized by hierarchical clustering using squared Pearson correlation into 2 clusters, as shown in Figure 1. Overall, for several of these genes we noticed a trend for a higher degree of change in their expression levels in Hey3Met2 cells transfected with wild-type rather than catalytically-mutant RNASET2 expression vectors. This might, hypothetically, suggest some influence of RNASET2 ribonucleolytic
<table>
<thead>
<tr>
<th>GENE SYMBOL</th>
<th>GENE DESCRIPTION</th>
<th>FOLD. CHANGE WT</th>
<th>FOLD. CHANGE MUT</th>
<th>GENE ONTOLOGY</th>
</tr>
</thead>
<tbody>
<tr>
<td>MDK</td>
<td>midkine (neurite growth promoting factor 2)</td>
<td>-2.5</td>
<td>-2.0</td>
<td>heparin binding; glycosaminoglycan binding</td>
</tr>
<tr>
<td>MCAM</td>
<td>melanoma cell adhesion molecule</td>
<td>-3</td>
<td>-2.8</td>
<td>cell adhesion; motility</td>
</tr>
<tr>
<td>AREG</td>
<td>amphiregulin</td>
<td>-2.1</td>
<td>-3.8</td>
<td>growth factor activity; cell invasion</td>
</tr>
<tr>
<td>NNMT</td>
<td>nicotinamide N-methyltransferase</td>
<td>-4.1</td>
<td>-5.1</td>
<td>cell migration</td>
</tr>
<tr>
<td>PLAU</td>
<td>plasminogen activator,urokinase</td>
<td>-2.0</td>
<td>-1.2</td>
<td>wound healing; fibrinolysis and degradation of extracellular matrix</td>
</tr>
<tr>
<td>DDIT4</td>
<td>DNA-damage-inducible transcript 4</td>
<td>-4.3</td>
<td>-2.2</td>
<td></td>
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<tr>
<td>CPA4</td>
<td>Carboxypeptidase A4</td>
<td>-3.8</td>
<td>-1.3</td>
<td>peptidase activity; zinc ion binding</td>
</tr>
<tr>
<td>RELB</td>
<td>v-erb reticulum endotheliosis viral oncogene homolog B</td>
<td>-2.1</td>
<td>-1.8</td>
<td>DNA binding; transcription factor activity; transcription regulator activity</td>
</tr>
<tr>
<td>JDP2</td>
<td>Jun dimerization protein 2</td>
<td>-3.4</td>
<td>-2.4</td>
<td>DNA binding; transcription factor activity; transcription regulator activity</td>
</tr>
<tr>
<td>DMKN</td>
<td>demokine</td>
<td>-6.7</td>
<td>-6.2</td>
<td>Rab GTPase binding</td>
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<tr>
<td>PTPRH</td>
<td>protein tyrosine phosphatase receptor type H</td>
<td>-2</td>
<td>-1.5</td>
<td>phosphoprotein phosphatase activity; transmembrane receptor protein phosphatase activity</td>
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<tr>
<td>DSE</td>
<td>dematan sulfate epimerase</td>
<td>+2.1</td>
<td>+1.2</td>
<td>racemase and epimerase activity; chondroitin-glucuronate 5-epimerase activity</td>
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<tr>
<td>LIMCD1</td>
<td>LIM and cysteine-rich domains 1</td>
<td>+2.6</td>
<td>+2.3</td>
<td>zinc ion binding; transcription factor binding; transcription regulator activity</td>
</tr>
</tbody>
</table>
Figures 2: In vitro and in vivo validation of the microarray expression profile for 13 putative RNASET2-responsive genes by real-time RT-PCR. A) qPCR assays were performed for each gene using the same RNA samples from the RNASET2-overexpressing Hey3M1 cells clones used for microarray hybridization. The panel below the graph compares the in vitro expression data from microarray hybridization and qPCR assay. B) qPCR expression data for the same genes in tumors grown in vivo in immunocompromised mice following s.c. inoculation of RNASET2-transfected and control Hey3M1 clones.

In order to define the cellular processes/pathways affected by RNASET2, all differentially expressed genes were cross-referenced to the Gene Ontology (GO) database to identify functional categories over-represented in the panel of genes associated with the two clusters.

The GO analysis was done at GO FAT level of biological process and molecular function, whereas Expression Analysis Systematic Explorer (EASE) biological theme analysis was carried out online (at http://david.meb.unsw.edu.au) using DAVID [11]. The GO survey did not show any significant enrichment, probably due to the small number of genes analyzed (54 genes in cluster 1 and 11 genes in cluster 2). Nevertheless, within the above mentioned gene set a few associated categories were shown to represent biologically relevant process that were worth investigating.

Since TAG-MEM genes are postulated to encode for products involved in the cross-talk between the cancer cell and the tumor microenvironment [12, 13], we selected five RNASET2-responsive genes, mainly because of their involvement in cell adhesion and migration. The five selected genes are MDCK, encoding a non-apoptotic growth factor over-expressed in various human malignant tumors and recently suggested as a new biomarker for ovarian cancer [14-16], AREG (cell invasion breast cancer), a regulator of cancer cells invasiveness which was reported to be frequently overexpressed in colon, breast, prostate, pancreas, lung and ovarian cancer [17-19], MUC1, a well-known marker of poor prognosis in epithelial ovarian cancer, whose gene product promotes the growth, invasion and metastatic potential of malignant cells [20-22], PLAU (Plasminogen Activator Urokinase-type), which promotes fibrinolysis and degradation of extracellular matrix [23], and NMMT (nonsmooth muscle N-methyltransferase), a serum tumor marker for colorectal cancer recently identified as novel regulator of cell migration [24, 25].

Moreover, on the basis of both biological function we decided to validate a few genes that were also shown to be down-regulated after RNASET2 overexpression. The first is DAB2, a gene differentially regulated in inflammatory conditions, and whose role in activating Rab5 function was recently defined [50]. The genes encoding for the transcription factors RELB and JDP2 were also selected, due to their involvement in the NF-kB pathway and cell proliferation/differentiation, respectively [27-30].
The DDT4 gene was chosen due to its role in RAS-mediated transformation of ovarian epithelial cells [31]. Significantly, transfection of DDT4 expression vectors in immortalized human ovarian surface epithelial cells has been shown to render the cells tumorogenic in substitution for oncogenic Ras mutations.

Recent studies have suggested a relation between CP44 gene expression and prostate cancer aggressiveness, possibly due to its role in extracellular peptide processing [32]. We thus included CP44 in the panel of genes to be further investigated.

The PTP4A1 gene, encoding a member of the protein tyrosine phosphatase (PTP) family [33], was also selected, since PTP proteins are known to regulate a variety of cellular processes including cell growth, differentiation, mitotic cycle, and oncogenic transformation.

Finally, two genes that were up-regulated by RNASE2 were also selected for validation: LMCDC1, belonging to the category of the LMID1 tumor suppressor gene, and D5E (dermatitis sulfite epidermese), where protein product elicits specific cytotoxic T lymphocytes responses in cancer patients [34,35]. Table 1 provides a list of the fifteen genes selected for validation.

**VALIDATION AND COMPARISON OF THE TRANSCRIPTIONAL PROFILES IN VITRO AND IN VIVO**

To validate these genes, real-time RT-PCR (qPCR) assays were performed on the same RNA samples used for microarray hybridization. In order to allow for cross-references of the expression data, the sequence of all primer pairs was designed to span the region of the cDNA corresponding to the hybridization probe placed on the microarray chip. As shown in figure 2A, the pattern of gene expression changes observed following microarray hybridization was confirmed by qPCR for the most tested genes. The only exception was represented by the D5E and PLAU genes, whose expression pattern in Hey3Met2 cells expressing the catalytically-mutant RNASE2 protein turned out to be down-regulated by microarray hybridization but upregulated by qPCR. However, for both genes the observed change in expression was highly significant (1.0 fold for microarray hybridization vs. -1.4 fold by qPCR for D5E and -1.2 fold by microarray hybridization vs. -1.01 fold by qPCR for PLAU, respectively). Moreover, for both genes the expression pattern observed by qPCR in Hey3Met2 cells expressing wild-type RNASE2 was in agreement with that observed by microarray hybridization.

As expected, for using a more sensitive test, the observed fold-changes in the expression levels were slightly higher for several genes when tested by qPCR. For example, the RNASE2-mediated downregulation of the CP44, D5EKN and MCLAM genes that was observed by microarray hybridization turned out to be much more evident when assayed by qPCR. Of note, the fold-change expression for the RNASE2 gene turned out to be much higher by qPCR, in keeping with previous expression data obtained by western blot analysis carried out on the same clones (data not shown). We next asked whether some of these genes could have any relevance in RNASE2-mediated tumor suppression in vivo. To this end, total RNA extracted from xenograft tumors [9] was used to assess whether the expression pattern was congruent with the qPCR data. Clearly at variance with the in vitro setting, the in vivo tumor population is rather heterogeneous, comprising both human Hey3Met2 cancer cells and host-derived mouse stromal cells. The results of this survey are shown in figure 2B. As shown, the RNASE2-mediated changes in the expression levels that we previously observed in vitro were not confirmed for most tested genes in the in vivo setting. Indeed, significant changes in the expression pattern that were found to be in agreement with those previously observed in vitro could be reported for just three genes, namely LMCDC1, D5E and RELB.

As for the remaining genes, whereas some of them (i.e. CP44, MCLAM and AXXC) are almost unresponsive to RNASE2 expression in vivo, others showed obvious changes in expression pattern mediated by RNASE2, but these changes were in the opposite direction with respect to those observed in vitro.

**FUTURE DIRECTIONS**

Undoubtedly, the observed RNASE2-mediated modulation of LMCDC1, D5E and RELB gene expression deserves further investigation, since it has been detected in vitro and subsequently confirmed in vivo. These three genes thus represent bona fide candidate effector genes for RNASE2-mediated tumor suppression. A panel of ovarian cancer cell lines, characterized for RNASE2 expression levels, is available in our laboratory and will be used to investigate the relationship between RNASE2 levels expression of these three genes and putative phenotypic outcomes. Furthermore a RNASE2 knock-down model recently established in our laboratory in the OVCAR3 ovarian cancer cell line will further contribute to investigate this issue.

As for the putative mechanism by which these three genes might contribute to RNASE2-mediated tumor suppression, it is worth noting that two of them show a plausible link with cellular functions related to tumor rejection by the immune system. Indeed, it is well established that one of the several biological functions of this pleiomorphic enzyme is the modulation of host immune system [8]. Accordingly, the RELB gene has long been associated with adaptive immune responses mediated by dendritic cells [38,39]. Moreover, since RELB is directly
involved in the NF-κB pathway, it is tempting to postulate a role for RNASET2 in RELB-mediated control of tumor-associated macrophages (TAMs) polarization. In fact, tumor progression is thought to involve a gradual switch of macrophage polarization from M1 to M2 class, which is paralleled by a gradual inhibition of NF-κB activity [36]. This role for the NK-κB pathway in macrophage polarization might therefore be relevant, considering that RNASET1 is apparently able to recruit specific subclass of stromal macrophages in the Hey3Mey2 ovarian cancer model studied by our group [9]. It will be of interest in future studies to define whether RNASET2 derived from cancer cells could influence the NF-κB pathway by changing the RELB expression levels in cells of the monocyte-macrophage lineage. Moreover, due to the observed downregulation of RELB in Hey3Mey2 cells expressing RNASET1, a cell-autonomous role for RNASET2 cannot be completely ruled out, since the RELB protein is known to promote cancer cell survival by inducing the expression of proteins with anti-apoptotic roles, such as Survivin and Bcl-2 [37]. A close inspection of the RELB yeast orthologue’s behaviour in yeast cells could be very instructive in this regard.

The second RNASET2-responsive gene that might be related to immune cell function is DSE. It encodes for dematin sulfate epimerase, an enzyme involved in D-glucuronic acid to L-iduronic acid conversion in the dermatan sulfate biosynthetic pathway [38]. The DSE gene was originally identified on the basis of the ability of its gene product to be recognized with high efficiency by a subset of cytotoxic T lymphocytes in certain tumors [39]. Moreover, expression of DSE was found to be altered in laryngeal cancer versus normal when compared to normal tissue samples [39]. Significantly, abnormal dermatan sulfate composition has also been reported in both ovarian carcinomas and ovarian cancer cell lines [40], providing further support for a potential role of DSE in our ovarian model.

As for the third gene whose change in expression level was confirmed in vivo (LAMC2), its direct involvement in RNASET2-mediated tumor suppression is rather speculative. LAMC2 encodes for a poorly characterized cysteine-rich and LAM domain-containing protein, which has been so far implicated in cardiac hypertrophy [41]. However, LAM-domain proteins belonging to the related CRP family have been described as potent tumor suppressor genes [42] and, most importantly, the related LIMD1 gene has been recently reported to display functional properties reminiscent of tumor antagonizing genes [7].

Taken together, the results of our studies provides a clear indication that investigations of the molecular mechanisms through which TAG-MSG carry out their biological functions necessitate a thorough comparison between the in vitro and in vivo expression patterns. Indeed, several genes displaying a biological function potentially related to tumor suppression, and thus defined as candidate based on their in vitro expression pattern, were not validated by subsequent in vivo expression profiling.

On the other hand, the fact that the same changes in the expression levels of a few genes (i.e. RELB, LIMD1 and DSE) were observed both in vitro and in vivo deserves some comment. We recall that the results gathered in the present report highlight some of the limitations inherent in the conceptual process of categorizing relevant biological processes. In our case, the strict categorization of tumor antagonizing genes as genes endowed with an asymmetric behavior (i.e. suppressing tumorigenesis without affecting in vitro growth) was clearly dependent on the sensitivity of the methodological approach employed. In fact, using the highly sensitive microarray analysis some genes’ features were detected in a congruent fashion in both the in vitro and in vivo.

The three above-mentioned genes are therefore worth to be investigated in-depth, as they could represent not only relevant candidates for the carcinogenic process taking place in our ovarian cancer model, but they could also be instrumental and paradigmatic of a more molecularly-oriented classification of the growing family of tumor antagonizing genes.

We reckon that the latter issue is not irrelevant in contributing some conceptual and experimental support for a more systemic search and characterization of tumor antagonizing genes. To this end, it is worth reminding that the genome of a cancer cell is usually characterized by DNA losses and given the limited number of tumor suppressor genes identified and characterized so far, we are probably seeing just the "tip of the iceberg": with a large fraction of genes (including TAGs) protecting against malignant growth yet undiscovered.

REFERENCES
Publications


