Dear Editor,

Adrenocortical carcinomas (ACC) are rare but aggressive tumors. Currently, the single curative approach is complete surgery. Prognosis, response to treatment and recurrence remain unpredictable, which stresses the need for new biomarkers (Else et al. 2014). Recent exome sequencing approaches of tumors identified in 60% of ACC recurrent somatic mutations in 20 genes (Assié et al. 2014a, b, Juhlin et al. 2015, Zheng et al. 2016). Somatic mutations can be used as surrogate biomarkers for detecting circulating tumor DNA (ctDNA) in blood. This ctDNA corresponds to fragments of DNA released directly by tumor cells into the blood stream among the circulating cell-free DNA (ccfDNA). Discrimination of ctDNA from ccfDNA of non-tumoral origin is based on the detection of somatic mutations, specific of cancer cells. The amount of ccfDNA and the detection of ctDNA largely depend on tumor type and disease stage (Bettegowda et al. 2014). In ACC, ctDNA detection has been recently reported in one patient (Creemers et al. 2017). However, beyond this proof of concept, the proportion of ACC patients with detectable ctDNA is not established.

The aim of this study was to assess to which extent ctDNA can be detected in ACC patients, using two highly sensitive techniques: deep NGS and droplet digital PCR (ddPCR). We also assessed the evolution of ctDNA during the course of the disease.

We prospectively and randomly included 11 patients with ACC. For four patients, blood was sampled before primary surgery, for three patients at the time of a small relapse or metastasis occurring <2 years after primary surgery, and for four patients in the setting of a rapidly growing metastatic disease. Median age was 48 (range 31–81 years). Six patients had glucocorticoids hypersecretion. Two patients had androgen hypersecretion, while two patients presented no hypersecretion (Table 1). All patients were informed of the project, and signed a written consent for the genetic study of the tumor. A prior agreement from the local ethics committee was obtained, under the COMETE-TACTIC framework.

Tumor and leukocytes DNA were extracted for each patient. Next-generation sequencing (NGS) workflow based on a custom AmpliSeq (Thermofisher) panel was designed for sequencing the 20 genes known to be frequently mutated in ACCs, using a Ion Torrent PGM Sequencer (Life Technologies). Seventeen somatic mutations were detected in eight patients (Table 1). TP53 (5 hits) and CTNNB1 (3 hits) were the most affected genes, followed by NF1 (2 hits) and single-hit mutations in TERT, RPL22, ATRX, MED12 and MEN1. Four patients had more than one somatic mutation, ranging from 2 to 6. Tumor cellularity, clonality and heterozygosity status were assessed with our R algorithm TARGOMICS (Garinet et al. 2017, data not shown). Three patients presented no mutations in the genes studied.

For the eight patients with at least one somatic mutation identified in the tumor, ccfDNA was extracted from plasma collected either before surgery or at the time of relapse, metastases or follow-up obtained after double centrifugation of 20 mL of blood (BCT Cell-Free DNA Blood Collection Tube). Concentrations were variable, from 3 to 422 ng/mL of plasma (Table 1). For each patient, tumor mutations were searched in ccfDNA either by deep sequencing or by ddPCR. A library with a unique amplicon harboring the mutation was subsequently prepared for each patient relative to the mutation identified in the tumor DNA and sequenced with an expected depth of 100,000×.

Four mutations were detected by NGS, in two patients, 1 and 7 (Table 1). Notably, these patients displayed massively metastatic diseases, with a rapid evolution. Allelic ratios in tumors indicated that these mutations were present in all tumor cells. Concentrations of ccfDNA were high –17 and 422 ng/mL. For patient 1, the three somatic mutations – in RB1, TP53 and CTNNB1 genes – were
Table 1  Patients main clinical features.

<table>
<thead>
<tr>
<th>No.</th>
<th>Age</th>
<th>Gender</th>
<th>Time to surgery (months)</th>
<th>Primary in place</th>
<th>Metastases</th>
<th>Locoregional recurrence</th>
<th>Tumor burden</th>
<th>Disease progression*</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>44</td>
<td>M</td>
<td>21</td>
<td>No</td>
<td>Liver pancreas lung</td>
<td>Yes</td>
<td>Multiple large metastases</td>
<td>Progression</td>
</tr>
<tr>
<td>2</td>
<td>38</td>
<td>F</td>
<td>19</td>
<td>No</td>
<td>Lung</td>
<td>No</td>
<td>Micronodule</td>
<td>Stable</td>
</tr>
<tr>
<td>3</td>
<td>48</td>
<td>F</td>
<td>31</td>
<td>No</td>
<td>Lung</td>
<td>Yes</td>
<td>Micronodules</td>
<td>Stable</td>
</tr>
<tr>
<td>4</td>
<td>55</td>
<td>F</td>
<td>19</td>
<td>No</td>
<td>Liver lung</td>
<td>No</td>
<td>Multiple large metastases</td>
<td>Progression</td>
</tr>
<tr>
<td>5</td>
<td>31</td>
<td>F</td>
<td>Before</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
<td>Small primary</td>
<td>None</td>
</tr>
<tr>
<td>6</td>
<td>53</td>
<td>F</td>
<td>3</td>
<td>No</td>
<td>No</td>
<td>Yes</td>
<td>Multiple large nodules</td>
<td>Progression</td>
</tr>
<tr>
<td>7</td>
<td>42</td>
<td>F</td>
<td>Before</td>
<td>Yes</td>
<td>Lung</td>
<td>–</td>
<td>Massive primitive and metastases</td>
<td>Progression</td>
</tr>
<tr>
<td>8</td>
<td>81</td>
<td>F</td>
<td>21</td>
<td>No</td>
<td>Lung</td>
<td>Yes</td>
<td>35mm recurrence micrometastasis</td>
<td>Progression</td>
</tr>
<tr>
<td>9</td>
<td>21</td>
<td>F</td>
<td>Before</td>
<td>Yes</td>
<td>Lung</td>
<td>–</td>
<td>Large primary multiple micrometastases</td>
<td>Progression</td>
</tr>
<tr>
<td>10</td>
<td>53</td>
<td>F</td>
<td>30</td>
<td>No</td>
<td>Bone liver lung</td>
<td>No</td>
<td>Multiple large metastases (bone and liver) micrometastases (lung)</td>
<td>Progression</td>
</tr>
<tr>
<td>11</td>
<td>54</td>
<td>M</td>
<td>Before</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
<td>Massive primitive</td>
<td>–</td>
</tr>
</tbody>
</table>

found in ccfDNA. The allelic ratios were close – 11.7, 16.6 and 14.3% respectively. For patient 7, the somatic mutation in CTNNB1 was found, with an allelic ratio of 13.8%. For both patients, mutations were also detected with ddPCR. Allelic ratios – 15.2% and 15.3% for patient 1 and patient 7, respectively, were comparable to those obtained by NGS.

In contrast with these two patients, no ccfDNA mutation was detected for 6 out of 8 patients, neither by deep NGS nor by ddPCR (Table 1). Several parameters may impact detection of ccfDNA. First the tumor burden and progression may have a role. Indeed tumor volume was small and slowly/not progressing for three negative patients – patients 2, 3, 5 – and intermediate for one – patient 8. Yet, two of the six negative patients – patients 4 and 6 – also presented with a large and progressing tumor. Tumor burden is not fully associated with ccfDNA detection. The clonality of mutations may also have an
Table 1

Patients main clinical features.

<table>
<thead>
<tr>
<th>Steroid secretion</th>
<th>ENSAT stage</th>
<th>Tumor size (cm)</th>
<th>Weisk score</th>
<th>Ki67 (%)</th>
<th>Mutated genes (allelic ratio)</th>
<th>DNA Concentration (ng/mL of plasma)</th>
<th>CcfDNA</th>
<th>ddPCR allelic ratio (positive droplets/total)</th>
<th>Last follow-up</th>
<th>Specific death (time)</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>4</td>
<td>8</td>
<td>7</td>
<td>40</td>
<td>TPS53 c.611delT p. Leu204fs (93%)</td>
<td>17.3</td>
<td>301308</td>
<td>11.7%</td>
<td>15.2%</td>
<td>Yes (28)</td>
</tr>
<tr>
<td>A</td>
<td>4</td>
<td>6</td>
<td>7</td>
<td>9</td>
<td>TERT c.2657-46C&gt;T (17%)</td>
<td>3</td>
<td>–</td>
<td>&lt;0.1%</td>
<td>No (47)</td>
<td>–</td>
</tr>
<tr>
<td>GC</td>
<td>3</td>
<td>20</td>
<td>9/20</td>
<td></td>
<td>RPL22 c.305T&gt;C p. Val102Ala (5%)</td>
<td>6</td>
<td>121032</td>
<td>&lt;0.1%</td>
<td>No (36)</td>
<td>–</td>
</tr>
<tr>
<td>OC</td>
<td>4</td>
<td>10</td>
<td>8</td>
<td>20</td>
<td>TTF1 c.5017G&gt;T p.Glu1673* (75%)</td>
<td>31.5</td>
<td>0.0254</td>
<td>&lt;0.1%</td>
<td>Yes (27)</td>
<td>–</td>
</tr>
<tr>
<td>GC</td>
<td>1</td>
<td>2.5</td>
<td>1</td>
<td>5</td>
<td>TTF1 c.134C&gt;G p. Ser45Cys (13%)</td>
<td>9.4</td>
<td>21574</td>
<td>0.0254</td>
<td>No (17)</td>
<td>–</td>
</tr>
<tr>
<td>GC</td>
<td>2</td>
<td>10</td>
<td>9</td>
<td>40</td>
<td>TTF1 c.387A&gt;G p. Ser129ser (37%)</td>
<td>11</td>
<td>0</td>
<td>(0.1%</td>
<td>Yes (9)</td>
<td>–</td>
</tr>
<tr>
<td>GC</td>
<td>4</td>
<td>15</td>
<td>80</td>
<td>80</td>
<td>TPS53 c.76C&gt;T p.Arg26Cys (71%)</td>
<td>422</td>
<td>147166</td>
<td>13.8%</td>
<td>Yes (2)</td>
<td>–</td>
</tr>
<tr>
<td>A</td>
<td>3</td>
<td>6</td>
<td>9</td>
<td>35</td>
<td>MEN1 c.779A&gt;G p. Glu260Gly (84%)</td>
<td>19</td>
<td>109369</td>
<td>&lt;0.1%</td>
<td>No* (29)</td>
<td>–</td>
</tr>
<tr>
<td>GC MC</td>
<td>4</td>
<td>10</td>
<td>8</td>
<td>35</td>
<td>(TPS3 germine, 93%)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>Yes (6)</td>
<td>–</td>
</tr>
<tr>
<td>None</td>
<td>4</td>
<td>18</td>
<td>6</td>
<td>15</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>Yes (33)</td>
<td>–</td>
</tr>
<tr>
<td>GC</td>
<td>2</td>
<td>20</td>
<td>8</td>
<td>23</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>Yes* (0)</td>
<td>–</td>
</tr>
</tbody>
</table>

*RECIST criteria; **no Weiss score could be determined since only a biopsy was performed; *palliative care only at this time; +deceased from pulmonary infection after surgery; #determined on a lung metastases.

A, androgens; GC, glucocorticoids; MC, mineralocorticoids.

Impact. Indeed, no ctDNA could be detected for the two patients with subclonal mutations – patients 2 and 5. One tumor – patient 5 – was of borderline malignancy (Weiss score of 2), and it remains to be checked whether ctDNA can be detected in benign adrenal tumor.

It remains challenging to conclude whether ctDNA detection was negative because of a limited sensitivity. Indeed, one theoretical limitation of the sensitivity remains the initial quantity of DNA in the test sample.

In our study, quantities of ccfDNA were low (<10 ng/mL) for three patients – patients 2, 3 and 5 – and the number of DNA copies analyzed in ddPCR remained <300 for patients 2, 3 and 8. The minimum detectable ratio is thus lowered, and this is a detection limit de facto. However, it might be possible that some ACC do not release any ctDNA. This is the case for some tumor types, like glioma or renal cell carcinoma for which ctDNA is detected in less than 50% of patients, with currently no clear explanation.
Further studies will be needed to test this hypothesis. Compared to the study of Creemers and coworkers, who used a NGS panel (Creemers et al. 2017), our study used two of the currently most sensitive molecular biology technologies, including deep NGS and ddPCR. However, though being limited, our series suggest at least that patients with the most aggressive forms of the disease do secrete ctDNA. This subgroup of patients with aggressive disease is certainly the subgroup in which such a tool as ctDNA may have the most obvious applications, both in terms of prognosis and in terms of disease follow-up.

Amounts of ctDNA were monitored during follow-up, and our data suggest that quantity of ctDNA parallels disease evolution (Fig. 1). Patient 1 had a pancreatic recurrence, and no hepatic lesion at the time of first blood sampling. After 6 months, both ctDNA absolute quantity and allelic ratios increased from 2.7 to $9.9 \times 10^3$ copies of DNA in a 10 mL sample and from 13.5 to 27% respectively (Fig. 1A). This increase paralleled disease progression, with the appearance of liver metastases and growth of the pancreatic lesion (Fig. 1C and D). Patient 7 had small pulmonary and liver metastases at the time of first blood sampling. After one month, ctDNA absolute quantity remained similar, while allelic ratio decreased – from 56 to $48 \times 10^3$ copies of DNA in a 10 mL sample and from 13.8% to 8.9% of ctDNA respectively. Two months later, both ctDNA absolute quantity and allelic ratio increased importantly, reaching $264 \times 10^3$ copies and 31.6% of ctDNA. This rapid increase paralleled disease progression, with a rapid and massive growth of metastases (Fig. 1E, F and G), leading to patient’s death one month later. For both patients, quantities of non-tumoral ccfDNA were also at a higher level than observed in healthy controls and increased strongly when patient 7 was in terminal phase. This finding has been observed in other studies, and could be explained by an overall inflammation and excessive cell death releasing more ccfDNA (Zhang et al. 2017). Therefore, in clinical routine, ctDNA should be monitored with both the ratio relative to ccfDNA, and the absolute quantity. Monitoring ctDNA could help to monitor the response to treatment and disease progression in ACC patients. Further studies are needed, to compare ctDNA with imaging techniques for this purpose, both in terms of sensitivity.

In conclusion, ctDNA is detectable in a subset of ACC patients. When detected, ctDNA can be accurately quantified and seems to follow tumor dynamics. However, ctDNA could not be detected in several patients, including some with large tumor burden, and despite the use of highly sensitive technologies. Thus, despite some promising value, it is not currently possible to foresee the exact place of ctDNA in ACC management. Its applications...
as a potential biomarker remain to be determined on a larger cohort, with a longitudinal monitoring.

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Declaration of interest
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References


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