Adrenal

ADRENAL - TUMORS

Advantage and Trustworthy of Cortisol and Dexamethasone Evaluation in Different Biological Matrices in Patients with Adrenal Masses.

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SAT-166

Advantage and trustworthy of cortisol and dexamethasone evaluation in different biological matrices in patients with adrenal masses.

Biochemical function of adrenal masses is currently based on 1mg post-overnight dexamethasone suppression test (pDST). Several approaches are recently developed, in order to reduce false positive/negative samples, only in retrospective series. They are based on the correlation of some different parameters, i.e. late-night salivary cortisol (LNSC) *vs* serum and salivary cortisol pDST; LNSC *vs* serum and salivary cortisol and serum dexamethasone pDST; LNSC and cortisone *vs* serum cortisol and salivary cortisol and cortisone pDST. Although these findings offer a better diagnostic performance, several conditions are still disappointed. No information is traceable about the harvest time of diurnal salivary and serum samples and no study include neither the levels of salivary nor urinary dexamethasone pDST. Aim of our study is to combine all these strategies in order to avoid the underestimated biases and obtain more precise information about the true "cortisol condition" of the patients.

To reach this purpose we assess both cortisol and dexamethasone concentrations in several samples: saliva at 11PM before the drug administration, diurnal saliva and serum at 8AM and also the urine collection from 11PM to 8AM. Analytes levels are measured using a validated liquid chromatography-tandem mass spectrometry method. In this study we included 20 subjects without morphological adrenal alteration (MRI assessment), dyslipidemia, hypertension and impaired glucose tolerance (healthy controls) and 20 patients with adrenal incidentaloma showing different cortisol levels ranging from normal to ACTH-independent hypercortisolism. In both series, LNSC were similar to salivary cortisol pDST, even if they were greater in the patients with adrenal incidentalomas and subclinical cortisol secretion. Serum dexamethasone levels were in reference ranges, while salivary and urinary dexamethasone found in these matrices require additional sample numbers in order to establish appropriate cut-offs. Our preliminary results suggest that the combination of these findings could represent an improvement to assess the individual cortisol status.

Neuroendocrinology and Pituitary

PITUITARY TUMORS I

Integrated Analysis of Pituitary Adenoma Using Novel Approach of Non-Target Proteomics Along with RNA-Sequencing Analyses

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Objective: To clarify the relationship between proteomic expression and clinical feature of pituitary adenoma. Methods: We have previously developed non-target proteomics analysis, which enables to detect and quantify approximately 7,000 to 9,000 kinds of protein weave, in parallel with RNA-seq analysis, and then subjected to 14 cases of pituitary adenoma surgically removed at Chiba University Hospital. Bioinformatic evaluation including DEGs, heatmap and PCA analyses was performed to reveal underlying their molecular pathogenesis. Results: We successfully identified 789 differentially expressed proteins and 593 DEGs in non-target proteomics and RNA-seq, respectively. Intriguingly, PCA analysis demonstrated that tumors were clearly divided into 3 groups based on protein expression profile; functional pituitary adenomas consisting of two subtypes depending on Pit1 and T-pit linage, and non-functional tumors consisting of two distinct subtypes, with properties close to functional tumors and unique characteristics of hard tumor difficult to remove by endoscopic surgery. To address the underlying molecular biological functions in each group clustering analysis and heat-map were performed and we found that 3 groups were separated clearly with their own both gene and protein expression profile. Indeed, for instance, GO term of plasma membrane part was significantly enriched in hard tumor group, pathways of GH receptor signaling, GH hormone synthesis as in GH-positive group. Conclusions: We herein demonstrate that pituitary adenoma can be uniquely separated into certain categories through our novel non-target proteomics with coupling to RNA-seq, particularly providing novel group of hard tumor characteristics with enriched expression of both protein and mRNA in plasma membrane part. Thus our method would be beneficial and useful to elucidate underlying molecular pathogenesis for pituitary tumors, while further analysis is required.

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ADRENAL CASE REPORTS I

A Case of Hypoplastic Left Heart Syndrome and Paraganglioma

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SAT-191

INTRODUCTION:

Cyanotic heart disease and paragangliomas are two rare diagnosis. Co-occurrence of congenital cyanotic heart disease and pheochromocytomas/paragangliomas has been described, but the mechanism is unclear. In those patients where immediate cyanosis resulting from the congenital heart disease happens right after birth there is an association with an earlier detection of tumor compared to those with cyanotic heart disease later in life (26.6 years vs 46.3 years respectively) [1]. The objective of this case is to highlight this association, as a high degree of suspicion needs to be