retrospectively analyzed abdominal CT scans performed at two university-affiliated hospitals (n = 483 and n = 514, respectively) from 2006 to 2019. This dataset was randomly divided into training set (181 CTs without adrenal nodule and 362 CTs with adrenal nodule) and test set (291 CTs without adrenal nodule and 163 CTs with adrenal nodule). All CT scans were contrast-enhanced and the phase with the highest contrast between adrenal gland and adjacent normal tissues was selected for multi-phase CT. The core algorithm of our deep learning algorithm for adrenal nodule (DLAAN) was MULAN (Multitask Universal Lesion Analysis Network) algorithm whose backbone was a convolutional neural network. DLAAN was composed of two stages. The first stage was to detect the CT slice where normal adrenal gland or adrenal nodule were located. The second stage was for fine localization of adrenal nodule on the corresponding CT slice. The performance of DLAAN was evaluated using the area under the receiver operating characteristic curve (AUROC) for patient-level classification and free-response ROC for nodule-level localization. The figure of merit for free-response ROC was calculated as an average sensitivity when 0.5, 1, 2, and 4 false positives per slice were allowed. **Results:** The AUROC of DLAAN was 0.927 (95% confidence interval: 0.900–0.955). With a threshold probability of 0.9, the sensitivity and specificity were 86.5% and 89.0%, respectively. When left and right adrenal nodules were analyzed separately, the AUROC was 0.910 for left adrenal nodule and 0.957 for right adrenal nodule, respectively. The accuracy of DLAAN according to the size of adrenal nodule was 0.890, 0.734, 0.981, 1.00 and 1.00 for no adrenal nodule, adrenal nodule sized 1–2 cm, 2–3 cm, 3–4 cm and > 4 cm, respectively. The performance of DLAAN for the localization of adrenal nodule which was estimated by average sensitivity was 0.812. The number of CTs with at least one false positive nodule was 93/454 (20.5%). **Conclusion:** Our proof of concept study of deep learning-based automatic detection of adrenal nodule on contrast-enhanced abdominal CT scans showed high accuracy for both the classification of patients with or without adrenal nodule and the localization of adrenal nodule, although the performance of the algorithm decreased for small sized adrenal nodules. External validation with different CT settings and patient population is needed to assess the generalizability of our algorithm.

Adrenal

ADRENAL – CLINICAL RESEARCH STUDIES

Gene Expression to Guide Glucocorticoid Replacement in Autoimmune Addison's Disease

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Objective: Deciding the optimal doses of glucocorticoid (GC) replacement treatment in autoimmune Addison's disease (AAD) is impeded by the lack of reliable biomarkers. This frequently results in over-treatment, with alarming and persistent side-effects, or under-replacement, which could be fatal. There is a need to think new in the quest for robust biomarkers to optimize GC replacement in AAD at an individual level.

Aim: We aimed to identify genes that are consistently up- or down-regulated in patients with AAD in response to different GC replacement doses. This information can be used to establish novel biomarkers to guide GC treatment in AAD.

Methods: Step 1: Global microarray expression analysis on RNA from whole blood before and after intravenous infusion of 100 mg hydrocortisone (HC) in 10 patients with AAD. To verify the results, we performed real-time PCR to compare gene expression levels of three of the highly differentially expressed genes (*FKBP5, MMP9,* and *DSIPI)* to compare gene expression levels before and two, four, and six hours after the HC infusion. Step 2: Rt-PCR to compare expression levels of 93 GC-regulated genes in normal versus very low morning cortisol levels in 27 patients with AAD.

Results: Step 1: Two hours after infusion of 100 mg HC, there was a marked increase in *FKBP5, MMP9,* and *DSIPI* expression levels. *MMP9* and *DSIPI* expression levels correlated with serum cortisol. Step 2: Expression levels of *CEBPB, DDIT4, FKBP5, DSIPI*, and *VDR* were increased and *ADARB1, ARIDB5,* and *POU2F1* decreased in normal versus very low morning cortisol. Normal serum cortisol levels positively correlated with *DSIPI*, *DDIT4,* and *FKBP5* expression.

Conclusions: We introduce gene expression as a novel approach to guide GC replacement in AAD. We suggest that gene expression of *DSIPI, DDIT4,* and *FKBP5* are particularly promising candidate biomarkers of GC replacement, followed by *MMP9, CEBPB, VDR, ADARB1, ARID5B*, and *POU2F1*.

Adrenal

ADRENAL – CLINICAL RESEARCH STUDIES

Genetic Alterations and Clinical Features in Brazilian Patients With Pheochromocytomas and Paragangliomas

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