Virchows Archiv (2019) 475 (Suppl 1):S1–S436
https://doi.org/10.1007/s00428-019-02631-8

Abstracts

31st European Congress of Pathology

Oral Free Paper Sessions

Sunday, 8 September 2019, 08:30 - 12:00, Galliéni 5
OFP-01 | Joint Session: Uropathology / Nephropathology

OFP-01-001
The influence of the presence of intraductal carcinoma of the prostate on the grade group system's prognostic performance
T. Tsuzuki[1], M. Kato[2]
[1] Department of Surgical Pathology, Aichi Medical University Hospital, Japan, [2] Department of Urology, Nagoya University Graduate School of Medicine, Japan

Background & Objectives: Although the presence of intraductal carcinoma of the prostate (IDC-P) influences biochemical failure in radical prostatectomy patients, no data are available regarding the impact of its integration into the classification Grade Group system. Thus, the aim of this study was to enhance the utility of the Grade Group (GG) system by integrating the presence of IDC-P.
Methods: This study was a retrospective evaluation of 1019 patients with prostate cancer who underwent radical prostatectomy between 2005 and 2013 without neoadjuvant or adjuvant therapy. Data on age, prostate-specific antigen (PSA) level at diagnosis, pathological T stage (pT), the presence of Gleason pattern 5 (GP5), the presence of IDC-P, and surgical margin status were analysed to predict PSA recurrence after prostatectomy.
Results: IDC-P was detected in 157 patients (15.4%). GGs were as follows: GG1 without IDC-P, n=163; GG2 without IDC-P, n=470; GG3 without IDC-P, n=160; GG4 without IDC-P, n=27; GG5 without IDC-P, n=42; any GG with IDC-P, [n=157; GG 2 (n=29); GG3 (n=60); GG4 (n=13); GG5 (n=55)]. Any GG with IDC-P showed a significantly worse prognosis than any other GG without IDC-P ($p< 0.0001$). In a multivariate analysis, integration of the IDC-P into the GGs was significant prognostic predictors ($P < 0.0001$).
Conclusion: Integrating the presence of IDC-P into the GG system will result in more accurate predictions of patient outcome.

OFP-01-002
Distinct genetic alterations and luminal molecular subtype in nested variant of urothelial carcinoma
V. Weyerer[1], R. Weisser[1], E.A. Moskalev[1], F. Haller[1], R. Stoehr[1], M. Eckstein[1], U. Zinnall[2], N.T. Gaisa[3], E. Compèrat[4], A. Perren[5], B. Keck[6], Y. Allory[7], G. Kristiansen[8], B. Wullich[6], A. Agaimy[1], A. Hartmann[1], S. Bertz[1]
[1] Institute of Pathology, University Hospital Erlangen, Friedrich-Alexander University Erlangen, Germany, [2] Institute of Medical Systems Biology, Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany, [3] Institute of Pathology, RWTH Aachen University, Germany, [4] Hôpital Tenon, HUEP, Sorbonne University, Paris, France, [5] Institute of Pathology, University of Bern, Switzerland, [6] Department of Urology and Paediatric Urology, University Hospital Erlangen, Friedrich-Alexander Universität Erlangen-Nuernberg, Germany, [7] Department of Pathology, Hôpital Foch, Universitè Versailles-Saint-Quentin-en-Yvelines, Universitè Paris-Saclay, Suresnes, Francle; Institut Curie, CNRS, UMR144, Paris, France, [8] Institute of Pathology, University Hospital Bonn, Germany

Background & Objectives: Nested variant of urothelial carcinoma (NVUC) is rare and only few small series exist. Molecular characteristics and the classifying marker profile as well as therapeutic targets of this specific variant are mostly unknown. Aim of this study was to characterise NVUC on the molecular level in one of the largest cohorts to date. In addition, we applied an immunohistochemical marker panel in order to define the molecular subtype of this variant.
Methods: 60 NVUC cases were collected from different departments. *TERT* promoter mutation analysis was carried out in all samples using SNaPshot analysis. Target sequencing of 48 cancer related genes by Next Generation Sequencing (NGS) analysis was performed in a subset of 26 cases. Immunohistochemical markers CD44, CK5, CK14, EGFR, p63, FOXA1, GATA3, CD24 und CK20 were used to elucidate the molecular subtype.
Results: A total of 62.5% of NVUC cases harbored a mutation of the *TERT* promoter. Additionally, *TP53* and *JAK3* were among the most frequently mutated genes identified by NGS analysis. Subtyping revealed that all NVUC express luminal markers such as CD24, FOXA1, GATA3 and CK20.
Conclusion: Summarized, NVUC belong to the luminal molecular subtype. Moreover, a subset of NVUC seems to be characterised by mutations of the Wnt- and inflammatory pathway, including *JAK3* mutations, indicating a different biological background compared to conventional urothelial bladder cancer.

OFP-01-003
A new auto-annotation method and machine learning strategy for detection and annotation of cancer areas in prostate biopsies
L. Björk[1,2], J. Gustafsson[3], F. Hikmet Noraddin[3], K. Eurèn[2], C. Lindskog[3]
[1] Karolinska Institutet, Sweden, [2] Contextvision, Sweden, [3] Uppsala Universitet, Sweden

Background & Objectives: Prostate cancer is one of the most diagnosed cancer forms and a leading cause of cancer-related death in males. The examination and Gleason scoring of prostate biopsies is however a major bottleneck in the pathology workflow, and studies have shown that the inter-observer variability in scoring is high. For increasing accuracy and speeding up the decision process, there is a high demand for implementation of an image analysis tool to support pathologists. The aim of the present investigation was to develop a strategy for un-biased, specific

[1] Department of Pathology, Postgraduate Program in Public Health, Faculty of Medicine, University of Fortaleza, Brazil, [2] Faculty of Medicine, University of Fortaleza, Brazil, [3] Pathology Division, Clinics Hospital, Faculty of Medicine, University of São Paulo, Brazil

Background & Objectives: Pathology teaching in Brazilian Medical Schools is a challenging scenario. The discrepancy between scarce time resources available and its cardinal role in Medicine demands innovative teaching tools. Students, as active learners also rely on non-orthodox online methods, from scientific material to YouTube videos. To evaluate the nature and quality of information freely available on YouTube about basic pathology, directed to students. To engage medical students into a critical review of pathology concepts by encouraging them to screen these videos for mistakes.
Methods: Second to Fourth year medical students evaluated YouTube videos from major Brazilian Portuguese speaking channels and gone through a basic pathology concepts check-list for errors. Videos and student annotations were reviewed by practicing pathologists.
Results: 65 videos were viewed by the students and reviewed, ranging from 2-82 minutes of duration (median 15 min); views ranged from 145 to 1026235; subscribers from 20 to 1611416. Authors were medical students (23), physicians (16, six pathologists), veterinary physicians (2), others with a biomedical background (19) and undisclosed (5). Four channels were linked to academic Institutions. Major errors were evidenced in 7 videos (44%), minor in (56%); academia-related channels evidenced less misconceptions than general channels (p=0.04). There was no statistical correlation between errors and the amount of views or subscribers (p=0.99), although one of the most influent channel (over 315k subs) had major and minor errors
Conclusion: YouTube is not a reliable source of information for technical knowledge, although this kind of activity was engaging as a "teaching from bad examples" by medical student's perception.

PS-09-011
Application of convolutional neural networks for glands instance segmentation in the images of colon epithelial neoplasms
I. Mikhailov[1], A. Khvostikov[1], A. Krylov[1], N. Oleynikova[1], P. Malkov[1], O. Kharlova[1], N. Danilova[1]
[1] Lomonosov Moscow State University, Russia

Background & Objectives: There are difficult tasks in the diagnosis of colon epithelial neoplasms: lack of quantitative criteria of basal dilation of the crypts and spread of the serration, determination of potential malignancy. Automatic mucous glands segmentation using a convolutional neural network (CNN) is the first step to real diagnostic algorithm development.
Methods: We propose a two step algorithm for glands segmentation. The first step produces semantic segmentation using a UNet-based CNN, while the second performs gland instance segmentation using a novel CNN architecture that predicts parameters for active contour model. This allows to segment each individual gland. We have designated closed-contour glands and "open glands" (glands with open contour).
Results: The network was first trained on Warwick-QU dataset (165 images), fine network tuning was performed on the collected PATH-DT-MSU dataset (19 images, colon biopsy material). 12 images were hyperplastic polyps; 6 images were SSA/P and one was normal colon tissue.
Our segmentation algorithm is characterised by Dice coefficient 0.87 on Warwick-QU and 0.78 on PATH-DT-MSU dataset. Dice coefficient decreased because of presence of «open glands» and the glands with adhered contours.
Conclusion: It is necessary to create alternative collections of annotated histological images of colon epithelial neoplasms and to use full-size images obtained in the pathology examination of the real colon biopsies because images are cut off and only contain closed-circuit glands (mag.x200, x400) in the Warwick-QU. In contrast there are full-size real images with the presence of "open glands" (mag.x100) in PATH-DT-MSU dataset.

PS-09-012
Using deep neural network to count Ki-67 positive cells in neuroendocrine tumours of the gastrointestinal tract
N. Mola[1], S. Leh[1]
[1] Haukeland University Hospital, Norway

Background & Objectives: Calculation of the Ki-67 index in neuroendocrine tumours (NET) of the gastrointestinal tract is time consuming. Automatic quantification of biomarker expression is a typical application of digital pathology. In the present study a cloud based machine-learning platform, Aiforia™, was used to train a deep convolutional neural network (CNN) in order to detect Ki-67 positive tumour cells in gastrointestinal NETs.
Methods: 29 digital slides of NETs (resolution 0.23 μm/pixel) were used as training data set. The images were uploaded to the Aiforia™ platform. The algorithm was trained by supervised learning. The algorithm consisted of two layers. The first layer detected tumour regions and the second layer segmented positive and negative tumour cell nuclei within the first layer. The performance of the algorithm was initially tested in non-annotated areas of the training data set.
Results: The interface for developing a CNN algorithm on the Aiforia™ platform was intuitive and user friendly. Erroneous detection of mucosa epithelium as tumour was overcome by additional annotations in order to represent all the possible variations of tumour cells as target and mucosa epithelium as background. In the second layer, cell nuclei segmentation was overall adequate, however especially overlapping nuclei continue to be an intricate task.
Conclusion: We present an easy to use machine-learning platform which has the potential to assist the pathologist in the calculation of the Ki-67 index in NETs. For a final evaluation an independent test set will be used and the model's results will be compared to the ground truth, manual counting by a pathologist.

PS-09-013
The new generation of AI tools: allowing pathologists to design their own algorithms
J. Gildenblat[1], C. Sagiv[1], N. Sagiv[1], I. Ben Shaul[1]
[1] DeePathology.ai, Israel

Background & Objectives: Digital pathology is the enabler for computer vision and deep learning algorithms. In the last few years many companies offer dedicate algorithms for various tasks in pathology that pathologists and researchers can use. In many cases, especially in pharma research, pathologists would like to design their own algorithms according to their data and needs. The aim of the DeePathology AI Platform is to provide pathologists with the ability to design customized algorithms on their own data. This approach can bridge the gap between the expert pathology knowledge and state of the art computer vision and machine learning capabilities.
Specifically, we plan to discuss the Cell Detection problem. The DeePathology.ai Cell Detection Studio is a do it yourself tool for pathologists to train deep learning cell detection algorithms on their own data. Using this tool, deep learning cell detection solutions can be easily created by the pathologist very quickly.
Methods: Common problems in the process of developing AI solutions for the medical field are highly unbalanced datasets on one hand and limited annotation resources on the other hand.
The use of Active Learning can dramatically help with both issues.
The task of Cell Detection is very important in digital pathology. For example, analyzing the quantity and density of immune cells can provide important indications on the progress of cancer.
This is a tedious task when manually done by pathologists and thus, automating this process is desirable.