

## In this issue

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This issue opens with a review on the (molecular) pathology of penile cancer by Emmanuel et al. (<https://doi.org/10.1007/s00428-019-02607-8>). Even though a less frequent form of cancer, also of penile cancer the pathobiology has been enlightened by high throughput genomic studies, which have shed new light on our understanding of its genesis and evolution with imminent impact on its management. This is reviewed in this paper.

Two papers in this issue address subjects concerning quality in pathology. Roos et al. (<https://doi.org/10.1007/s00428-019-02621-w>) asked the question how well in a single institution essential elements are covered in pathology reports produced in daily practice for complex surgical specimens, such as those of perihilar cholangiocarcinoma. The authors found that a substantial number of reports did not meet the requirements as compiled in the guidelines in the relevant dataset of the International Collaboration on Cancer Reporting (ICCR). Missing elements, such as resection margins which were often incompletely reported, were of potential clinical significance. Likewise, prognostic factors such as angio-invasive and perineural growth were not always mentioned. Reports edited by specialist hepatobiliary reports were significantly more complete. Typically, this type of problem can be radically solved when the choice is made for synoptic reporting, as is advocated by the ICCR. Equally important but in a completely different field is the paper by Bartosch et al. (<https://doi.org/10.1007/s00428-019-02639-0>), who established standards for fetal and neonatal biometric measurements, including organ weights and long bone lengths, based on autopsy data. This allowed the group to construct growth curves for gestational ages between 12 and 42 weeks, which are important for adequate assessment of organ development at post-mortem examination.

We also have the usual bouquet of papers on potential new prognostic factors. Yamada et al. (<https://doi.org/10.1007/s00428-019-02622-9>) studied the clinical course of solitary fibrous tumors, all confirmed by STAT6 immunohistochemistry and containing the NAB2-STAT6 fusion gene. The authors paid

specific attention to localization: pleuropulmonary, non-pleuropulmonary/non-central nervous system and central nervous system. Important additional parameters were association with hypoglycemia and histological evidence of dedifferentiation. They identified hypoglycemia, dedifferentiation and site as prognostically relevant, the latter as cerebromeningeal and intra-abdominal tumors were more aggressive. Strikingly, exon variations in the fusion gene were not associated with differences in outcome. Fischer (<https://doi.org/10.1007/s00428-019-02647-0>) looked at expression of stem cell factors ALDH1 and SOX2 in various serous ovarian tumors (high-grade and low-grade serous carcinomas, atypical proliferative serous tumors and serous tubal intraepithelial carcinomas). Not surprisingly, stem cell factors were expressed more often in high grade carcinomas. Of note, the two factors were found to be most often expressed in different cells, casting doubt on their biological association with stemness in this particular setting. No associations were found with prognosis in high grade lesions. The paper illustrates the complexity of the cancer stem cell concept in the context of human cancer. The cover image is from this paper and shows ALDH1/Ki67 double staining of a high grade serous ovarian carcinoma.

Of a totally different nature is the paper by Alabi et al. (<https://doi.org/10.1007/s00428-019-02642-5>), who used neural network based deep learning to extract prognostic information from multidimensional data collected on squamous cell carcinoma of the tongue, including clinical and pathological parameters. A feedforward neural network in the form of an online tool was trained to predict locoregional recurrence in early oral tongue squamous cell carcinoma. This approach allowed the authors to identify tumor budding and depth of invasion as the most relevant predictors of locoregional recurrence. They argue that neural network deep learning might replace the classical tool of logistic regression to support decision making in clinical oncology.

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