Summary of the Hematopathology Working Group of the German Society of Pathology, Annual Meeting of the German Society of Pathology, Augsburg, May 2026

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The session opened with **T. M. Pentimalli** (Max Delbrück Center, Berlin), who showcased how high-resolution spatial transcriptomics combined with three-dimensional extracellular-matrix imaging can reconstruct the spatial ecosystem of human cancers. By mapping stromal and immune niches in unprecedented detail, his work reveals how the tumor micro-environment remodels during progression and highlights both the opportunities and the challenges of bringing spatial omics into routine clinical pathology.
S. Forster (Technical University Munich) then presented a mechanistic study on the CD70/CD27 axis in multiple myeloma. CD70 is aberrantly expressed on a subset of malignant plasma cells, especially at invasive tumor fronts and in hypoxic regions. Functional experiments using CD70-knock-out cell lines, blocking antibodies, and CD70-positive patient-derived xenografts demonstrated that CD70/CD27 signaling drives plasma-cell expansion and extramedullary disease. The data position CD70 as a marker of an aggressive, invasive myeloma cell state and a promising therapeutic target for high-risk disease.
The third talk, delivered by **J. Lippl and colleagues**, described an interpretable deep-learning model that detects MYC translocations directly from hematoxylin-eosin (H&E) stained slides of diffuse large B-cell lymphoma (DLBCL) and high-grade B-cell lymphoma (HGBCL). Trained on more than 2 000 cases, the model achieved an area under the ROC curve of ~0.80 for MYC rearrangements and ~0.76 for double-/triple-hit status. Importantly, the AI-derived score provided independent prognostic information for progression-free and overall survival, even in tumors lacking MYC alterations, and correlated with molecular features such as MYC/BCL2 expression and micro-environmental signatures. This approach offers a fast, inexpensive, and globally accessible alternative to molecular testing.
M. Bauer and collaborators explored the immunological consequences of long-term JAK inhibition in BCR-ABL1-negative myeloproliferative neoplasms. While both ruxolitinib and fedratinib initially suppressed JAK/STAT signaling, they diverged thereafter: ruxolitinib reduced HLA-II expression and could not be fully rescued by IFN-γ unless combined with epigenetic drugs, whereas fedratinib maintained or even increased HLA-I/II levels and STAT1 phosphorylation. Bone-marrow biopsies from treated patients mirrored these findings, linking distinct epigenetic (H3K27me3) alterations to the variable immune phenotypes observed with each inhibitor. The results underscore the need for biomarker-guided combination strategies when using JAK inhibitors.

In mantle-cell lymphoma, **M. Rudelius and colleagues** demonstrated that deletion of CDKN2A is associated with profound remodeling of the tumor micro-environment. Using spatial transcriptomics (Xenium 5K) and multiplex immunofluorescence on 82 cases, they showed that CDKN2A-deleted tumors harbor an immunologically "cold" milieu, enriched for immunosuppressive cell populations and multiple checkpoint molecules, and display disrupted immune-tumor connectivity. This genetic alteration therefore couples high proliferative signaling with immune exclusion, identifying a high-risk subgroup that may benefit from novel immunomodulatory therapies.

K. Kokkaliaris and colleagues introduced a quantitative three-dimensional imaging pipeline for large-tissue bone-marrow biopsies spanning the entire human lifespan. By processing 40 µm sections and performing whole-biopsy multiplex immunofluorescence, they captured extensive heterogeneity within endothelial and mesenchymal stromal compartments, identified distinct capillary and MSC subpopulations, and mapped the spatial relationships of purified hematopoietic stem and progenitor cells with key niche elements. This framework provides a comprehensive, age-resolved view of human hematopoiesis and establishes a foundation for future studies of aging and disease.

Finally, **J. Bosch-Schips and co-authors** presented a detailed clinicopathologic and molecular characterization of BCL6-rearranged follicular lymphoma (FL). Among 19 cases, two robust molecular subsets emerged: (1) STAT6-mutated FLs with CD23 expression and an IL-4-driven transcriptional program, and (2) STAT6-wildtype FLs with up-regulation of MYC-target genes such as BIRC5 and CXCL5. Both groups differed markedly from conventional BCL2-rearranged FL in gene-expression signatures, cytogenetic alterations (frequent 1p36 and 17p loss), and immunophenotype (loss of CD10). The study establishes BCL6-rearranged FL as a distinct entity and highlights STAT6 mutation status as a key driver of its heterogeneity.

Overall, the presentations illustrate a clear trend toward integrating spatially resolved omics, advanced imaging, and artificial intelligence approaches to dissect the tumor micro-environment and its genetic underpinnings. By linking specific molecular alterations (e.g., CD70, CDKN2A loss, BCL6 rearrangements) to distinct immune landscapes, the presented work paves the way for precision diagnostics and novel therapeutic strategies that target both the malignant cells and their surrounding niche.