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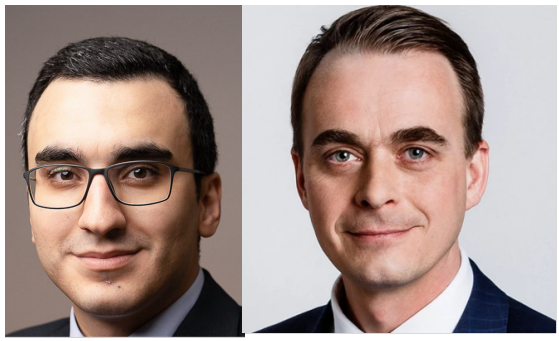

Molecular tumor board—editorial

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Precision oncology is transforming the landscape of cancer treatment by leveraging molecular profiling techniques to tailor therapeutic strategies to the unique genetic makeup of each patient's disease. Two recent articles delve into critical aspects of this evolving field: the role of molecular tumor boards (MTBs) and the integration of liquid biopsies into clinical practice.

Molecular tumor boards (MTBs) are pivotal in bridging the gap between complex molecular data and practical clinical applications. The article by Boos and Wicki emphasizes that MTBs facilitate a multidisciplinary approach, essential for interpreting molecular profiles and devising personalized treatment plans. MTBs typically involve oncologists, pathologists, molecular biologists, and bioinformaticians, who collaboratively analyze genomic data to identify actionable mutations and recommend targeted therapies or clinical trial enrollment.

Key questions addressed by Boos and Wicki include the aims and structure of MTBs, the types of cases discussed, and the selection of molecular panels. The authors highlight the importance of standardized next-generation sequencing (NGS) panels and bioinformatic tools to ensure consistency and accuracy across institutions. Moreover, the discussion outlines the necessity for continuous adaptation of diagnostic algorithms to incorporate technological advances like whole exome sequencing (WES) and comprehensive multi-omic profiling.

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Hasenleithner and Heitzer explore the promising role of liquid biopsies, specifically circulating tumor DNA (ctDNA) analysis, in managing advanced cancers. Liquid biopsies offer a noninvasive alternative to tissue biopsies, providing real-time insights into tumor dynamics and enabling the detection of clinically relevant biomarkers with high concordance to traditional methods. This approach is increasingly supported by international guidelines and is becoming integral to molecular diagnostics.

The article underscores the challenges associated with ctDNA analysis, such as tumor heterogeneity, sampling biases, and technical limitations. Despite these challenges, comprehensive genomic profiling (CGP) panels have proven effective in identifying actionable targets. The authors advocate for a balanced application of "tissue-first" and "plasma-first" strategies, tailored to individual patient scenarios, to maximize the clinical utility of molecular profiling.

The integration of liquid biopsies into the MTB framework enhances the ability to monitor disease progression and resistance mechanisms, offering a dynamic tool for precision oncology. MTBs play a crucial role in interpreting ctDNA data, ensuring that molecular findings are translated into actionable treatment recommendations. The interdisciplinary nature of MTBs facilitates the incorporation of liquid biopsy data into personalized cancer treatment regimens, potentially improving patient outcomes through more precise and timely interventions.

Both articles highlight the need for standardized data collection and the integration of new technologies to advance precision oncology. The structured collection of clinical and molecular data, combined with cross-institutional collaboration, will enable a deeper understanding of molecular phenotypes and their clinical implications. As new tumor-profiling technologies emerge, MTBs will remain at the

forefront of integrating these innovations into clinical practice, including the information obtained by liquid biopsy, driving scientific progress, and improving patient care.

Conflict of interest H. Taghizadeh and A. Gerger declare that they have no competing interests.

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