editorial

memo (2022) 15:176–177
https://doi.org/10.1007/s12254-022-00831-8

memo
magazine of european medical oncology

Molecular profiling leading to personalized cancer treatment

Barbara Kiesewetter

Accepted: 25 July 2022
© The Author(s), under exclusive licence to Springer-Verlag GmbH Austria, part of Springer Nature 2022

Personalized medicine and molecular profiling represent inseparable terms. Only with the broad applicability and low-level access to genomics and next generation sequencing techniques has it been possible to implement precision medicine in the daily routine of medical oncology. In fact, the increasing feasibility of not solely tissue biopsies but also less invasive liquid biopsies is currently again offering new opportunities. As of 2022, molecular tumor profiling on (archived) formalin-fixed, paraffin-embedded (FFPE) tissues using DNA/RNA sequencing techniques allows identification of a wide number of cancer growth-related mutations and fusions that may proceed to treatment planning. However, we had to learn in the past that even if a druggable target exists, it is not given that it (1) is a defined driver of the distinct disease and (2) is clinically significant in the specific setting. Consequently, molecular profiling requests not only the technical abilities to perform such testing but also deep and concise understanding of the target, corresponding drugs, and tumor biology. Furthermore, we need to distinguish clinical settings where no standard is available and next generation sequencing is used to identify potential further therapies, such as in the relapsed/refractory setting after exhaustion of evidenced-based therapies (with multiple successful examples previously published, e.g., the Austrian example set in the EXACT trial by *Prager G et al.* [1]), versus settings where molecular targeted treatments are essential to the standard treatment algorithm. For the latter, EGFR-driven therapies in lung cancer constitute one of the earliest successful applications and recently a number of novel targeted drugs were approved in lung cancer, including KRAS, MET, and RET inhibitors. Hence, for both the salvage setting and increasingly for approved standard treatments, molecular profiling is crucial for optimal patient management.

In the current issue of *memo*, we provide an update on molecular profiling in salvage therapy selection and clinical routine. *Wolff et al.* [2] introduce different methods to classify molecular targets identified in precision medicine panels and how such tools can support multidisciplinary tumor boards and individual clinicians in clinical practice. For example, the ESCAT score, developed by an ESMO working group, provides a tier system to connect a target with a potential drug in a specific disease and estimates the level of evidence behind the distinct target/drug combination [3]. *Klocker et al.* [4] provide a concise overview on how molecular profiling has not only resulted in new therapeutic options in breast cancer, such as PIK3CA or BRCA mutations, but also explain the enormous opportunity of defining intrinsic subtypes with such methods. *Horvath et al.* [5] emphasize that in advanced (and more and more also early stage) lung cancer, no therapy at all can be planned any more without assessment of molecular targets due to a variety of target–drug combinations approved for routine therapy. They also discuss the opportunity of (re)sequencing following treatment failure, which possibly allows detection of mechanisms of acquired resistance. Finally, *Piringer et al.* [6] present molecular subtypes of colorectal cancer, including relevant treatments, and provide guidance of when to test which targets.

Conflict of interest B. Kiesewetter declares that she has no competing interests.

Ap. Prof. PDin Dr.in med.univ.et Dr.in scient. med.
B. Kiesewetter (✉)
Department of Medicine I, Division of Oncology, Medical University of Vienna, Währinger Gürtel 18–20, 1090 Vienna, Austria
barbara.kiesewetter@meduniwien.ac.at

References

1. Prager G, et al. Results of extended analysis for cancer treatment (EXACT) trial: a prospective translational study evaluating individualized treatment regimens in oncology. Oncotarget. 2019. https://doi.org/10.18632/oncotarget.26604.
2. Wolff L, Kiesewetter B. Applicability of ESMO-MCBS and ESCAT for molecular tumor boards. Memo. 2022; https://doi.org/10.1007/s12254-022-00800-1.
3. Mateo J, et al. A framework to rank genomic alterations as targets for cancer precision medicine: the ESMO Scale for Clinical Actionability of molecular Targets (ESCAT). Ann Oncol. 2018;29(9):1895–902.
4. Klocker EV, Balic M, Steger G. Molecular profiling leading to personalized treatment in breast cancer. Memo. 2022; https://doi.org/10.1007/s12254-021-00792-4.
5. Nagl L, Pall G, Wolf D, et al. Molecular profiling in lung cancer. Memo. 2022. https://doi.org/10.1007/s12254-022-00824-7.
6. Piringer G. Molecular profiling in colorectal cancer. Memo. 2022. https://doi.org/10.1007/s12254-022-00833-6.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

▸ For latest news from international oncology congresses see: http://www.springermedizin.at/memo-inoncology