



7-9-2021

Clinical Outcomes of Molecular Tumor Boards: A Systematic Review

Kara L. Larson
University of Kentucky

Bin Huang
University of Kentucky, bhuan0@uky.edu


Heidi L. Weiss
University of Kentucky, heidi.weiss@uky.edu

Pamela C. Hull
University of Kentucky, Pam.Hull@uky.edu

Philip M. Westgate
University of Kentucky, philip.westgate@uky.edu

See next page for additional authors

Follow this and additional works at: https://uknowledge.uky.edu/markey_facpub

 Part of the [Biostatistics Commons](#), [Internal Medicine Commons](#), [Oncology Commons](#), and the [Pharmacy and Pharmaceutical Sciences Commons](#)

Right click to open a feedback form in a new tab to let us know how this document benefits you.

Repository Citation

Larson, Kara L.; Huang, Bin; Weiss, Heidi L.; Hull, Pamela C.; Westgate, Philip M.; Miller, Rachel W.; Arnold, Susanne M.; and Kolesar, Jill M., "Clinical Outcomes of Molecular Tumor Boards: A Systematic Review" (2021). *Markey Cancer Center Faculty Publications*. 169.
https://uknowledge.uky.edu/markey_facpub/169

This Review is brought to you for free and open access by the Markey Cancer Center at UKnowledge. It has been accepted for inclusion in Markey Cancer Center Faculty Publications by an authorized administrator of UKnowledge. For more information, please contact UKnowledge@lsv.uky.edu.

Clinical Outcomes of Molecular Tumor Boards: A Systematic Review

Digital Object Identifier (DOI)

<https://doi.org/10.1200/po.20.00495>

Notes/Citation Information

Published in *JCO Precision Oncology*, v. 5.

© 2021 by American Society of Clinical Oncology

Creative Commons Attribution Non-Commercial No Derivatives 4.0 License:

<https://creativecommons.org/licenses/by-nc-nd/4.0>

Authors

Kara L. Larson, Bin Huang, Heidi L. Weiss, Pamela C. Hull, Philip M. Westgate, Rachel W. Miller, Susanne M. Arnold, and Jill M. Kolesar

Clinical Outcomes of Molecular Tumor Boards: A Systematic Review

Kara L. Larson, PhD¹; Bin Huang, PhD^{1,2}; Heidi L. Weiss, PhD¹; Pam Hull, PhD¹; Philip M. Westgate, PhD³; Rachel W. Miller, MD^{1,4}; Susanne M. Arnold, MD^{1,5}; and Jill M. Kolesar, PharmD^{1,6}



PURPOSE We conducted this systematic review to evaluate the clinical outcomes associated with molecular tumor board (MTB) review in patients with cancer.

METHODS A systematic search of PubMed was performed to identify studies reporting clinical outcomes in patients with cancer who were reviewed by an MTB. To be included, studies had to report clinical outcomes, including clinical benefit, response, progression-free survival, or overall survival. Two reviewers independently selected studies and assessed quality with the Quality Assessment Tool for Before-After (Pre-Post) Studies with No Control Group or the Quality Assessment Tool for Observational Cohort and Cross-Sectional Studies depending on the type of study being reviewed.

RESULTS Fourteen studies were included with a total of 3,328 patients with cancer. All studies included patients without standard-of-care treatment options and usually with multiple prior lines of therapy. In studies reporting response rates, patients receiving MTB-recommended therapy had overall response rates ranging from 0% to 67%. In the only trial powered on clinical outcome and including a control group, the group receiving MTB-recommended therapy had significantly improved rate of progression-free survival compared with those receiving conventional therapy.

CONCLUSION Although data quality is limited by a lack of prospective randomized controlled trials, MTBs appear to improve clinical outcomes for patients with cancer. Future research should concentrate on prospective trials and standardization of approach and outcomes.

JCO Precis Oncol 5:1122-1132. © 2021 by American Society of Clinical Oncology

Creative Commons Attribution Non-Commercial No Derivatives 4.0 License

INTRODUCTION

Precision medicine, specifically testing tumor tissue for mutations with next-generation sequencing (NGS) and using these results to guide therapy, is a major advance in the treatment of cancer and is considered standard of care (SOC) for many cancer types, including lung cancer. Receiving a targeted therapy yields substantial benefit for patients, since randomized, controlled trials have demonstrated that they are more effective, less toxic, and improve quality of life compared with cytotoxic cancer treatments.¹

Despite the availability of clinical and affordable NGS, targeted therapies, and insurance coverage, the use of precision medicine remains low often because of insufficient support to guide clinicians in interpreting and acting on NGS results.²⁻⁴ As a response, many medical centers have instituted molecular tumor boards (MTBs) as a means to educate, interpret, and facilitate the use of precision medicine for oncology patients.⁵ Most MTBs consist of a multidisciplinary team of medical oncologists, surgeons, genetic counselors, pharmacists,

pathologists, radiologists, and basic scientists.⁶ This broad range of expertise allows for accurate and up-to-date confirmation of diagnoses and identification of actionable mutations and associated drugs, along with the ability to pair patients with open clinical trials. It can additionally identify potential germline mutations that would require further genetic testing and counseling for patients and their family members.

Many institutions have published descriptions of their MTBs outlining their aims, patient populations, and types of actionable mutations; however, data supporting the clinical utility of MTBs are lacking.⁷⁻⁹ Therefore, we focus on reports that also include clinical outcomes such as clinical benefit (CB), response, and/or progression-free survival (PFS). The purpose of this systematic review is to evaluate the effect of MTBs on clinical outcomes in patients with cancer.

METHODS

This review was performed following Preferred Reporting Items for Systematic Reviews and Meta-Analyses guidelines for systematic reviews.¹⁰

ASSOCIATED CONTENT

Appendix

Author affiliations and support information (if applicable) appear at the end of this article.

Accepted on June 9, 2021 and published at ascopubs.org/journal/po on July 9, 2021; DOI <https://doi.org/10.1200/P0.20.00495>

CONTEXT

Key Objective

What is the impact of a molecular tumor board on clinical outcomes?

Knowledge Generated

Molecular tumor boards reporting clinical outcomes had consistent structure and function. They are usually interdisciplinary, function as a consult service, and appear to improve clinical outcomes, including response and progression-free survival; however, studies are heterogeneous and data quality is limited.

Relevance

As the number of targetable mutations continues to increase and cancer care becomes even more complex, consultation with an interdisciplinary molecular tumor board can help guide therapy selection for patients with cancer.

Search Strategy and Inclusion and Exclusion Criteria

A PubMed search was conducted on April 1, 2020, using the following query: molecular tumor board [All Fields]. Further publications were found through additional means including a bibliography screen of all selected articles. Articles were excluded if they were not in English, were reviews, described MTBs for pediatric patients, or did not contain data about CB or survival. All remaining articles were screened for relevancy, and any duplicates were removed.

Data Analysis

Data extraction was performed by two researchers (K.L.L. and J.M.K.) for all publications examined. Any disagreement was discussed between the researchers, and a conclusion was reached. Because of data diversity and differences in study setup, a meta-analysis was not performed, and instead, data will be discussed using a description of the findings.

Calculations

The frequency of cases reviewed by each molecular tumor board (MTB) was calculated using the following formula:

$$\left(\frac{\text{number of patients reviewed}}{\text{number of patients referred}} \right) \times 100.$$

The frequency of actionable mutations was calculated using the following formula:

$$\left(\frac{\text{number of patients with an actionable mutation}}{\text{total number of patients reviewed by the MTB}} \right) \times 100.$$

The frequency of patients who received MTB-directed targeted therapy was calculated using the following formula:

$$\left(\frac{\text{number of patients that received MTB-directed therapy}}{\text{number of patients with actionable mutations}} \right) \times 100.$$

Outcomes were reported by the authors. For all cross-sectional cohort studies, CB, if not explicitly provided,

was calculated by adding the number of patients who achieved stable disease, partial response, or complete response (CR). Overall response rate (ORR), if not explicitly provided, was calculated by summing the number of patients who achieved partial response or CR. To calculate rates regarding outcomes, the following formula was used:

$$\left(\frac{\text{number of patients with CB or ORR}}{\text{number of patients receiving MTB-directed therapy}} \right) \times 100.$$

Finally, the outcomes if the trial employed and intention-to-treat design were calculated using the following formula:

$$\left(\frac{\text{number of patients with CB or ORR, respectively}}{\text{total number of patients referred to the MTB}} \right) \times 100.$$

Quality Assessment and Bias Determination

Quality assessment of the reviewed articles was performed using either the Quality Assessment Tool for Before-After (Pre-Post) Studies with No Control Group or the Quality Assessment Tool for Observational Cohort and Cross-Sectional Studies depending on the type of study being reviewed.¹¹ Each of the above tools were created and validated by the National Institutes of Health and were developed to determine the concepts that are necessary for critical review. Responses were yes, not reported (NR), or not applicable. Two researchers (K.L.L. and J.M.K.) performed the assessments independently, and any disagreements were discussed and resolved.

Additionally, the same researchers (K.L.L. and J.M.K.) reviewed the studies for risk using the tool To Assess the Risk of Bias in Cohort Studies validated by the Cochrane Institute.¹² Each study was rated as definitely yes, probably yes, probably no, and definitely no with the risk of bias increasing from yes to no.

RESULTS

A total of 71 articles were retrieved through a PubMed search. Titles and abstracts of 31 studies were reviewed for inclusion criteria. Ten articles were selected for a full

review, and four more were added after a screen of bibliographies and other additional resources. Fourteen total articles were reviewed for this systematic analysis (Fig 1).

Study Characteristics

For inclusion in this systematic review, the studies had to report CB, response rate, or survival among patients receiving MTB-recommended therapies. All studies were observational, and the majority were retrospective. About half of the studies screened fewer than 100 patients with a range of 34-2,579 for all studies. The majority of studies used large (more than 300 genes) commercial or in-house panels, with two using in-house whole-exome sequencing and one using a small (37 gene) panel. All studies took place in the United States,¹³⁻²² France,²³⁻²⁵ or the Netherlands²⁶ with the majority being single institution studies at academic medical centers. Eleven of the articles outlined MTBs that had reviewed patient cases for more than 1 year with only one reviewing for less than 1 year and two not reporting duration of review.

The authors for all publications analyzed similar aims for each of their tumor boards with one or all of the following stated:

1. To investigate the rate of mutations and examine their clinical utility,
2. To breakdown complex genomic reports and guide treatment,
3. To increase access to up-to-date precision medicine treatment options and clinical trials, and

4. To determine the efficacy of a precision medicine program.

The MTBs generally employed a consistent structure and operations, composed of an interdisciplinary team of clinicians and scientists, and operated essentially as a consult service, making recommendations to the treating physician rather than managing patients. Inclusion of a genetics counselor was common, but not universal. In most cases, treating physicians ordered NGS testing and then referred patients to the MTB for evaluation. In one study, the MTB was responsible for approving NGS, and in another study, all patients were enrolled in a prospective sequencing study with only a fraction of cases reviewed by the MTB (Tables 1 and 2). All MTBs, with one exception, made recommendations on the basis of pathogenic or likely pathogenic mutations, but one also included variants of unknown significance (Appendix Table A1).

Characteristics of the Patient Populations

Most of the MTBs described reviewed cases for multiple solid tumors with the exceptions of Kaderbhai et al²³ and Koopman et al²⁶ (non-small-cell lung cancer only), Parker et al¹⁷ (breast cancer only), and Rodriguez-Rodriguez et al²⁰ (gynecologic malignancies only). The mean and median patient age for all studies (with the exception of Tafe et al,²¹ which did not report age for their patients) was in the range of 50-68 years. The study population and/or eligibility requirements for MTB review were similar across all studies. The majority of patients had advanced-stage

FIG 1. Study schema.

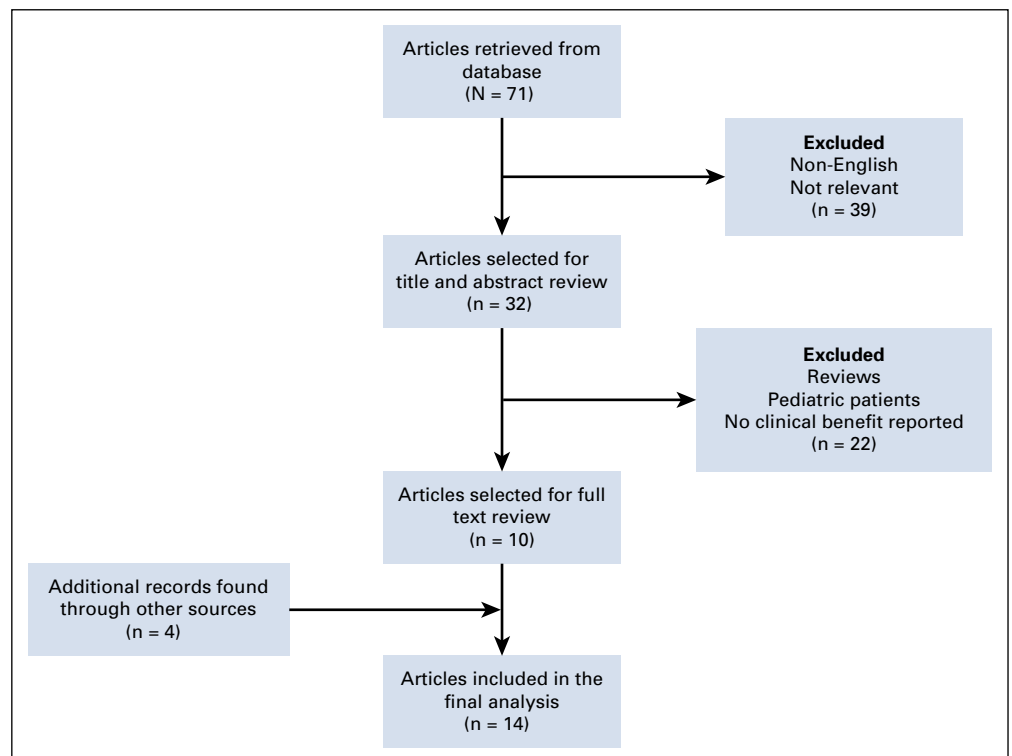


TABLE 1. Clinical Outcome of MTBs—Cross-Sectional Cohort Studies

Reference	Study Design	Scope of MTB	Sequencing Method	Tumor Types	Age (range), Years	Prior Lines of Therapy, Mean (range)	Patients Referred to MTB	Frequency Reviewed by MTB	Frequency of Actionable Mutations	Frequency of Receiving MTB Recommended Therapy	Outcomes If Received MTB Treatment	Outcomes If ITT
Bryce et al ¹³	Prospective	Consult Multidisciplinary Treatment recommendations	Commercial panels In-house whole exome	Solid and hematologic	53 (1.5-86)	NR	165	141 of 165 (85%)	92 of 141 (65%)	31 of 92 (34%)	CB: 13 of 31 (42%)	CB: 13 of 165 (8%)
Burkard et al ¹⁴	Prospective	Consult Multidisciplinary Treatment recommendations	Commercial panels In-house panels Single gene	Solid	57 (33-88)	2 (0-5)	38	38 of 38 (100%)	32 of 38 (84%)	9 of 32 (28%)	CB: 4 of 9 (44%) ORR: 2 of 9 (22%)	CB: 4 of 38 (11%) ORR: 2 of 38 (5%)
Harada et al ¹⁶	Retrospective	Consult Multidisciplinary Treatment recommendations Approved testing	Commercial panels Panels at another university	Solid	57 (range NR)	NR	191	132 of 192 (69%)	48 of 132 (36%)	15 of 48 (31%)	CB: 8 of 15 (53%) ORR: 3 of 15 (20%)	CB: 8 of 191 (4%) ORR: 3 of 191 (2%)
Kaderbhai et al ²³	Retrospective	Consult Oncologist and molecular biologists Treatment recommendations	In-house panel	NSCLC	61 (42-78)	2.3 ^a (1-7)	50	48 of 50 (96%)	29 of 48 (60%)	9 of 29 (31%)	CB: 7 of 9 (78%) ^b ORR: 4 of 9 (44%)	CB: 7 of 50 (14%) ORR: 4 of 50 (8%)
Koopman et al ²⁶	Retrospective	Consult Multidisciplinary Treatment recommendations	In-house panel	NSCLC	68 (36-89)	NR 68% with 0 32% with ≥ 1	129	110 of 129 (85%)	76 of 110 (69%)	25 of 76 (33%)	CB: 17 of 21 ^c (81%) ORR: 14 of 21 (67%)	CB: 17 of 129 (13%) ORR: 14 of 129 (11%)
Rodriguez-Rodriguez et al ²⁰	Prospective	Consult Multidisciplinary Treatment recommendations	Commercial panels	Gynecologic	61 (22-80)	NR but only rare or refractory included	69	68 of 69 (99%)	64 of 68 (94%)	25 of 64 (39%)	CB: 16 of 25 (64%) ORR: 10 of 25 (40%)	CB: 16 of 69 (23%) ORR: 10 of 69 (14%)
Schwaederle et al ¹⁸	Retrospective	Consult Multidisciplinary Treatment recommendations	Commercial panels	Solid	56 (29-75)	3 ^a (1-13)	34	34 of 34 (100%)	33 of 34 (97%)	12 of 33 (36%)	CB: 7 of 12 (58%) ORR: 3 of 12 (25%)	CB: 7 of 34 (21%) ORR: 3 of 34 (9%)
Tafe et al ²¹	Retrospective	Consult Multidisciplinary Treatment recommendations	In-house panel	Solid	NR	2 ^a (1-7)	35	35 of 35 (100%)	18 of 35 (51%)	2 of 18 (11%)	CB: 2 of 2 (100%) ORR: 1 of 2 (50%)	CB: 2 of 35 (6%) ORR: 1 of 35 (3%)
Trédan et al ²⁵	Prospective	Consult Multidisciplinary Treatment recommendations	Small in-house panel (ION torrent PGM)	Solid and hematologic	58 (44-63)	NR but only advanced disease	2,579	1,980 of 2,579 (77%)	1,032 of 1,980 (52%)	163 of 1,032 (15%)	CB: 80 of 182 ^d (43%) ORR: 23 of 182 (13%)	CB: 80 of 2,579 (3%) ORR: 23 of 2,579 (0.0%)
Trivedi et al ²²	Retrospective	Consult Multidisciplinary Treatment recommendations	Commercial panels	Solid	64 (37-82)	2.4 (1-6)	54	54 of 54 (100%)	54 (100%)	12 of 54 (22%)	CB: 9 of 12 (75%) ORR: 0 of 12 (0%)	CB: 9 of 54 (17%) ORR: 0 of 54

Abbreviations: CB, clinical benefit; ITT, intention to treat; MTB, molecular tumor board; NR, not reported; NSCLC, non-small-cell lung cancer; ORR, overall response rate.

^aMedian.

^bProgression-free survival of 3 months considered stable disease.

^cOutcomes of four individuals on clinical trials NR.

^dSome patients got more than one MTB-recommended therapy.

TABLE 2. Clinical Outcome of MTBs—Before-After Studies

Reference	Study Design	Scope of MTB	Sequencing Method	Tumor Types	Ages (range), Years	Prior Lines of Therapy, Mean (range)	Patients Referred to MTB	Frequency Reviewed by MTB	Frequency of Actionable Mutations	Frequency of Receiving MTB-Recommended Therapy	Outcomes If Received MTB Treatment	Outcomes If ITT
Dalton et al ¹⁵	Retrospective	Consult Multidisciplinary Treatment recommendations	Commercial panels	Solid	59 (17-73)	2 (0-10)	155	155 of 155 (100%)	132 of 155 (85%)	28 of 132 (22%)	Median PFS (n) MTB (22): 5 months, 95% CI, 2.9 to NR Conv. (54): 3 months, 95% CI, 2.4 to 5 6-month PFS probability (n) MTB: 43%, 95% CI, 26 to 71 Conv.: 20%, 95% CI, 11 to 35	NA
Parker et al ¹⁷	Retrospective	Consult Multidisciplinary Treatment recommendations	Commercial panels	Breast	59 (range NR)	3 ^a (1-13)	43	43 of 43 (100%)	40 of 43 (93%)	17 of 40 (43%)	CB: 7 of 17 (41%) ORR: 5 of 17 (29%) PFS ratio \geq 1.3 in 7 of 17 (41%)	CB: 7 of 43 (16%) ORR: 5 of 43 (12%)
Radovich et al ¹⁹	Prospective	Consult Multidisciplinary Treatment recommendations	Commercial panels	Solid	55 (range NR)	4 ^a (2-6)	168	168 of 168 (100%)	NR	44 of NR	PFS ratio \geq 1.3 MTB: 19 of 44 (43%) Conv.: 3 of 57 (5%) $P < .0001$ Median PFS MTB: 86 days Conv.: 49 days HR = 0.55 (95% CI, 0.38 to 0.84)	NA
Réda et al ²⁴	Prospective	Consult Multidisciplinary Treatment recommendations	In-house WES but recommendations limited to panel	Solid	65 (24-94)	2 ^a (1-8)	506	386 of 506 (76%)	342 of 506 (68%) (included VUS)	79 of 342 (23%)	PFS ratio \geq 1.3 MTB: 12 of 48 (25%) Conv.: 23 of 89 (26%) NS $P = .8$ (χ^2 test)	NA

Abbreviations: CB, clinical benefit; conv., conventional; HR, hazard ratio; ITT, intention to treat; MTB, molecular tumor board; NA, not applicable; NR, not reported; NS, not significant; ORR, overall response rate; PFS, progression-free survival; VUS, variants of unknown significance; WES, whole-exome sequencing.

^aMedian.

TABLE 3. Quality Assessment of Before-After Studies

Quality Criteria	Dalton et al ¹⁵	Parker et al ¹⁷	Radovich et al ¹⁹	Réda et al ²⁴
Clearly stated question or objective	No	No	Yes	No
Study eligibility clearly described	Yes	No	Yes	Yes
Participants' representative	Yes	Yes	Yes	Yes
All eligible patients enrolled	Yes	NR	NR	NR
Sample size sufficient	No	No	Yes	No
Intervention clearly described	Yes	Yes	Yes	Yes
Outcomes clearly defined, valid, reliable, and assessed consistently	No	No	Yes	No
Outcome assessors blinded	No	No	No	No
Loss to follow-up \leq 20%	Yes	Yes	NR	Yes
Statistical methods provide <i>P</i> for pre- to postchanges	No	Yes	Yes	No
Outcome measures taken multiple times before and after intervention	NA	NA	NA	NA
Statistical analysis for group to individual effect	NA	NA	NA	NA

Abbreviations: NA, not applicable; NR, not reported.

disease and had received several prior therapies with most having exhausted all SOC options.

Quality Assessment

Study quality was analyzed using the quality assessment tools provided by the National Institutes of Health.¹¹ If the main outcomes of a study included comparing survival on an MTB-directed treatment with patients' prior treatment, the study was classified as before-after, and quality was assessed with Quality Assessment Tool for Before-After (Pre-Post) Studies with No Control Group (Table 3). All other studies were classified as cross-sectional cohort studies, and quality was assessed with Quality Assessment Tool for Observational Cohort and Cross-Sectional Studies (Table 4). Most groups reported similar eligibility requirements or described their patient populations, and almost all patients were followed until progression on MTB therapy, and therefore used an appropriate timeframe to measure patient outcomes. Physician or patient choice, insurance, geographic location of clinical trials, and waiting to exhaust SOC options were the main reasons for not accepting MTB recommendations.

Bias analysis was performed using the tool from the Cochrane Institute.¹² Nine of the 14 studies did not include a matched control, neither a cohort of untreated patients nor by comparing MTB-recommended therapies with the patients' prior therapy. This resulted in those studies receiving the lowest score in that category, but the overall level of bias was low (Table 5).

Genetic Testing and Actionable Mutations

The types of sequencing varied among studies and within studies. The majority of samples were sent to commercial Clinical Laboratory Improvement Amendments laboratories with the most common being FoundationOne. Some researchers used on-site clinical laboratories to perform all DNA extraction and sequencing. The types of testing used

included whole-exome sequencing, gene panels, and comparative genomic hybridization. Each study defined an actionable mutation differently with four^{18-20,22} of the 14 studies not defining actionability at all. Those studies that used on-site clinical laboratories also varied in their decision making in regard to somatic calls, using different databases, and publications, to determine each patient's mutation profile. We calculated actionability rates for each study that provided sufficient data as described in methods. The frequency of actionable mutations ranged from 36% to 100%. Of note, the only MTB that considered tumor mutation burden an actionable mutation was the most recently published.²⁴ We diagrammed these actionability rates along each study timeline in Appendix Figure A1 (for those studies that included the timeframe of data collection). In general, rates of actionability increased over time, likely because of new targets and drug approvals. Exceptions were Koopman et al,²⁶ who only evaluated lung cancer, where the most common targetable driver mutations have been known for decades, and Parker et al¹⁷ and Rodriguez-Rodriguez et al,²⁰ who focused on breast and gynecological malignancies, respectively, where new targetable have been slow to be identified.

Clinical Outcomes

To assess clinical outcomes, studies were divided into before-after or cross-sectional cohort studies. For the cross-sectional cohort studies, the percentage of patients receiving MTB-recommended targeted therapies ranged from 11% to 39%. Although reasons for not receiving an MTB-directed therapy were not frequently reported, when reported, the most common reasons were lack of actionable mutations, rapidly progressive disease, and when clinical trials were recommended by the MTB, patients were unwilling to travel or ineligible.¹⁴ The frequency of patients achieving a CB from MTB-directed therapies ranged from 42%¹⁴ to 100%,²¹ although one study²¹

TABLE 4. Quality Assessment of Cross-Sectional Cohort Studies

Quality Criteria	Bryce et al ¹³	Burkard et al ¹⁴	Harada et al ¹⁶	Kaderbhai et al ²³	Koopman et al ²⁶	Rodriguez-Rodriguez et al ²⁰	Schwaederle et al ¹⁸	Tafe et al ²¹	Trédan et al ²⁵	Trivedi et al ²²
Clearly stated question or objective	No	No	No	No	No	No	No	No	No	No
Defined population	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Participation rate of $\geq 50\%$	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Participant recruited from the same population	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Sample size justification	No	No	No	No	No	No	No	No	No	No
Exposures measured before the outcome	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sufficient timeframe	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Different levels or exposures examined	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Exposure measures clearly defined	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Outcome measures clearly defined	No	No	No	No	No	No	No	No	No	No
Outcome assessors blinded	No	No	No	No	No	No	No	No	No	No
Loss to follow-up $\leq 20\%$	Yes	Yes	Yes	NR	NR	Yes	NR	NR	NR	Yes
Compounding variables measured	No	No	No	No	No	No	No	No	No	No

Abbreviations: NA, not applicable; NR, not reported.

reported clinical outcomes for only two patients. Kaderbhai et al²³ and Koopman et al²⁶ reported excellent CB rates of 78% and 81%, respectively, in patients with non–small-cell lung cancer. ORRs ranged from 0% to 67% reported by Trivedi et al²² and Koopman et al,²⁶ respectively, with none of the patients in Trivedi's study achieving a partial or CR.

For the before-after studies, the percentage of patients receiving MTB-recommended targeted therapies ranged from 22% to 43%. There were two prospective trials reported, the first by Radovich et al¹⁹ who prospectively compared the PFS ratio and PFS for 168 patients referred to their MTB. Of these, 67 were lost to follow-up or had insufficient follow-up duration and were excluded. Of the remainder, 44 received a genomically targeted therapy and 57 received nontargeted therapy. Patients with an actionable mutation and receiving a targeted therapy had improved PFS (mean 86 days) compared with those not receiving genomic therapy (mean 49 days, hazard ratio: 0.55, 95% CI, 0.37 to 0.84). In addition, 43.2% of those with a targeted therapy achieved a PFS ratio of ≥ 1.3 , compared with only 5.3% of those with nontargeted therapy, $P < .0001$. Réda et al²⁴ evaluated 506 patients who were referred for NGS and were able to perform sequencing on 386. The primary end point was feasibility of the

approach, defined as proportion of individuals who received a recommendation on the basis of their genomic report. Overall, 79 received a recommended therapy; however, there was no difference proportion of patients achieving a PFS of ≥ 1.3 between genomically targeted and standard therapy.

DISCUSSION

Somatic genomic sequencing has added additional layers of complexity to diagnosing and treating cancer. Molecular tumor boards have been developed to assist with assessing and acting on genomic reports.^{6,27} All the studies analyzed for this review stated similar aims for their molecular tumor boards, using them as an opportunity to break down the complexity of genomic testing and reporting, increase access to up-to-date treatments and clinical trials, and better understand the clinical utility of precision medicine in oncology.

Nine of the 14 studies analyzed for this review had CB and/or response rate as the primary outcome. None of these studies were randomized nor were they controlled for non-MTB-directed outcomes, thus making it difficult to determine the effectiveness of molecular targeted therapies and the recommendations of their MTBs. ORRs in these

TABLE 5. Risk of Bias of All Studies

Bias Criteria	Rodriguez-													
	Bryce et al ¹³	Burkard et al ¹⁴	Dalton et al ¹⁵	Harada et al ¹⁶	Kaderbhai et al ²³	Koopman et al ²⁶	Parker et al ¹⁷	Radovich et al ¹⁹	Réda et al ²⁴	Rodriguez et al ²⁰	Schwaederle et al ¹⁸	Tafe et al ²¹	Trédan et al ²⁵	Trivedi et al ²²
Selection of exposed and nonexposed cohorts drawn from the same population	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Confident in the assessment of exposure	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Confident that the outcome was not present at start of study	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Exposed and unexposed matched for all variables	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Confident in the assessment of the presence or absence of prognostic factors	4	4	4	4	4	4	4	4	4	4	4	4	4	4
Confidence in the assessment of outcome	3	3	3	3	3	3	3	2	3	3	3	3	3	3
Follow-up of cohorts adequate	2	2	2	2	2	2	2	2	2	2	2	2	2	2
Cointerventions similar between groups	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

NOTE. 1, definitely yes; 2, probably yes; 3, probably no; 4, definitely no.
Abbreviation: NA, not applicable.

studies ranged from 0% to 67%, which favorably compared with previously published ORRs of 5% in unmatched phase I trials²⁸ and 6% for all phase I trials in a single institution.²⁹ Trédan et al²² not only had the largest patient cohort but also used the smallest gene panel for their NGS testing, resulting in a relatively low rate of patients with an actionable mutation. Koopman et al²⁶ reported a high CB in patients receiving an off-label drug, but the authors indicated stricter criteria for off-target therapies than other studies, denoting that mutations in downstream pathways were not considered for off-target therapies of an upstream protein.

The three studies that either used patients' PFS ratio or compared PFS between patient groups allowed for a more direct analysis of the efficacy of the MTB-directed therapies. Of these, one was positive,¹⁹ one trended toward superiority,¹⁵ and one found no difference.²⁴ Since PFS typically decreases with every subsequent therapy, a minor increase in PFS2 may be noteworthy in this population.³⁰

Comparing outcomes across a wide variety of reports with different primary outcomes, patient populations, and criteria for recommendations makes definitive conclusions

difficult; however, generally, positive benefits were seen. Outcomes reported in trials without a control arm did appear to be much better than in other salvage situations such as phase I trial responses from the era before targeted therapy.^{29,30} Among those trials with a control arm, while not conclusive, MTBs provide CB and at least do no harm. In addition, overall impressions from the authors of each study were positive in regard to the utility of the MTBs at their respective institutions and suggested that each MTB helped to inform treatment decisions and increase access to genetic counseling for patients.

Although clinical trials comparing targeted therapies with standard therapies in those with a biomarker are almost universally positive, the reported benefit of NGS for the selection of therapy has been mixed. Several NCI-MATCH study arms demonstrate promising results. In arm H, patients with BRAFV600 mutations were treated with dabrafenib and trametinib. This arm met its primary end point, with an ORR of 33%.³¹ The MOSCATO trial concluded that NGS improved outcomes, but only among a small subset of patients with targetable mutations.³² The SHIVA trial was a

randomized phase II trial that included patients with a mutation in one of the three pathways, hormone receptors, PI3K, or RAF, and matched them to one of the 11 different targeted therapies. In this trial, there was no improvement in survival after treatment with targeted therapies.³³ The SHIVA trial has been criticized for its design, for both assigning therapies with unproven activity for the targets and using an algorithm that only considered mutations in the targeted arm, whereas physician discretion was allowed in the control arm. The number of patients eligible for targeted therapies increased between 2006 and 2018, likely because of more targeted therapy approvals every year, but that fewer than 7% actually benefitted, whereas only 16% were eligible.³⁴

Advances in NGS technologies are also identifying additional patients with actionable mutations. High tumor mutation burden, an indication for pembrolizumab in any tumor type,³¹ loss of heterozygosity, an indication for poly (ADP-ribose) polymerase inhibition for prostate cancer,³²

and certain RNA fusions, which confer sensitivity to specific targeted therapies, are now routinely reported on many NGS panels.³³ In addition, there is an increasing awareness of the ability of somatic mutation testing to identify potential germline mutations.³⁵ In addition to being targetable with small molecules, these germline mutations are clinically important to the patient's family members and support the need for inclusion of genetic counselors in the MTB team.

As the number of eligible patients continues to rise, it will become increasingly important for clinicians to accurately interpret complex genomic test results and to have increased access to therapies and clinical trials. Resources such as interprofessional MTBs can help clinicians navigate the complex world of precision medicine and provide these advanced treatments to their patients. Furthermore, as larger cohorts of data become available and shared, standardizing the components of an MTB, such as the definition of actionability, use of off-target drugs, and the types of sequencing will be imperative.

AFFILIATIONS

¹Markey Cancer Center, University of Kentucky, Lexington, Kentucky

²Kentucky Cancer Registry, University of Kentucky, Lexington, Kentucky

³Department of Biostatistics, University of Kentucky, Lexington, Kentucky

⁴Department of Obstetrics and Gynecology, University of Kentucky, Lexington, Kentucky

⁵Department of Internal Medicine, University of Kentucky, Lexington, Kentucky

⁶Department of Pharmacy Practice and Science, University of Kentucky, Lexington, Kentucky

CORRESPONDING AUTHOR

Jill M. Kolesar, PharmD, Department of Pharmacy Practice and Science, College of Pharmacy, 789 S Limestone St, Lexington, KY 40536; e-mail: Jill.Kolesar@uky.edu.

SUPPORT

Supported by Grant No. P30 CA177558 from the National Cancer Institute.

AUTHOR CONTRIBUTIONS

Conception and design: Bin Huang, Heidi L. Weiss, Philip M. Westgate, Rachel W. Miller, Jill M. Kolesar

Provision of study materials or patients: Susanne M. Arnold

Collection and assembly of data: Kara L. Larson, Rachel W. Miller, Jill M. Kolesar

Data analysis and interpretation: Bin Huang, Heidi L. Weiss, Pam Hull, Philip M. Westgate, Rachel W. Miller, Susanne M. Arnold, Jill M. Kolesar

Manuscript writing: All authors

Final approval of manuscript: All authors

Accountable for all aspects of the work: All authors

AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

The following represents disclosure information provided by the authors of this manuscript. All relationships are considered compensated unless otherwise noted. Relationships are self-held unless noted. I = Immediate Family Member, Inst = My Institution. Relationships may not relate to the subject matter of this manuscript. For more information about ASCO's conflict of interest policy, please refer to www.asco.org/rwc or ascopubs.org/po/author-center.

Open Payments is a public database containing information reported by companies about payments made to US-licensed physicians ([Open Payments](http://OpenPayments)).

Kara L. Larson

Employment: Boehringer Ingelheim

Susanne M. Arnold

Research Funding: AstraZeneca, Genentech, Merck Sharp & Dohme, Nektar, Exelixis, Ohio State University, National Cancer Institute, Kura Oncology, Regeneron

Jill M. Kolesar

Stock and Other Ownership Interests: Helix Diagnostics

No other potential conflicts of interest were reported.

REFERENCES

- Lee C, Davies L, Wu Y, et al: Gefitinib or erlotinib vs chemotherapy for EGFR mutation-positive lung cancer: Individual patient data meta-analysis of overall survival. *J Natl Cancer Inst* 109, 2017
- F1CDx technical specifications, in *Foundation Medicine* (ed), 2020. https://info.foundationmedicine.com/hubfs/FMI%20Dossiers/FMI_Commercial_Dossier_F1CDx.pdf
- Lynch J, Berse B, Chun D, et al: Epidermal growth factor receptor mutation testing and erlotinib treatment among veterans diagnosed with lung cancer in the United States Department of Veterans Affairs. *Clin Lung Cancer* 18:401-409, 2017

4. Lynch J, Berse B, Dotson W, et al: Utilization of genetic tests: Analysis of gene-specific billing in Medicare claims data. *Genet Med* 19:890-899, 2017
5. Berger MF, Mardis ER: The emerging clinical relevance of genomics in cancer medicine. *Nat Rev Clin Oncol* 15:353-365, 2018
6. Bourret P, Cambrosio A: Genomic expertise in action: Molecular tumour boards and decision-making in precision oncology. *Social Health Illn* 41:1568-1584, 2019
7. Basse C, Morel C, Alt M, et al: Relevance of a molecular tumor board (MTB) for patients' enrolment in clinical trials: Experience of the Institut Curie. *ESMO Open* 3:e000339, 2018
8. Hirshfield KM, Talkunov D, Zhong H, et al: Clinical actionability of comprehensive genomic profiling for management of rare or refractory cancers. *Oncologist* 21:1315-1325, 2016
9. Knepper TC, Bell GC, Hicks JK, et al: Key lessons learned from Moffitt's molecular tumor board: The clinical genomics action committee experience. *Oncologist* 22:144-151, 2017
10. PRISMA: Transparent reporting of systematic review and meta-analyses. 2015. <http://www.prisma-statement.org>
11. NIH: Study quality assessment tools. 2014. <https://www.nhlbi.nih.gov/health-topics/study-quality-assessment-tools>
12. Sterne J, Savovic J, Page M, et al: RoB 2: A revised tool for assessing risk of bias in randomized trials. *BMJ* 366:l4898, 2019
13. Bryce AH, Egan JB, Borad MJ, et al: Experience with precision genomics and tumor board, indicates frequent target identification, but barriers to delivery. *Oncotarget* 8:27145-27154, 2017
14. Burkard MF, Demin DA, Kenny PA, et al: Implementation and clinical utility of an integrated academic-community regional molecular tumor board. *JCO Precis Oncol* 10.1200/PO.16.00022
15. Dalton BW, Forde PM, Kang H, et al: Personalized medicine in the oncology clinic: Implementation and outcomes of the Johns Hopkins molecular tumor board. *JCO Precis Oncol* 10.1200/PO.16.00046
16. Harada S, Arend R, Dai Q, et al: Implementation and utilization of the molecular tumor board to guide precision medicine. *Oncotarget* 8:57845-57854, 2017
17. Parker BA, Schwaederle M, Scur MD, et al: Breast cancer experience of the molecular tumor board at the University of California, San Diego Moores Cancer Center. *J Oncol Pract* 11:442-450, 2015
18. Schwaederle M, Parker BA, Schwab RB, et al: Molecular tumor board: The University of California San Diego Moores Cancer Center experience. *Oncologist* 19:631-636, 2014
19. Radovich M, Kiel PJ, Nance SM, et al: Clinical benefit of a precision medicine based approach for guiding treatment of refractory cancers. *Oncotarget* 7:56491-56500, 2016
20. Rodriguez-Rodriguez L, Hirshfield KM, Rojas V, et al: Use of comprehensive genomic profiling to direct point-of-care management of patients with gynecologic cancers. *Gynecol Oncol* 141:2-9, 2016
21. Tafe LJ, Gorlov IP, De Abreu FB, et al: Implementation of a molecular tumor board: The impact on treatment decisions for 35 patients evaluated at Dartmouth-Hitchcock Medical Center. *Oncologist* 20:1011-1018, 2015
22. Trivedi H, Acharya D, Chamrathy U, et al: Implementation and outcomes of a molecular tumor board at Herbert-Herman Cancer Center, Sparrow Hospital. *Acta Med Acad* 48:242-247, 2019
23. Kaderbhai CG, Boidot R, Beltjens F, et al: Use of dedicated gene panel sequencing using next generation sequencing to improve the personalized care of lung cancer. *Oncotarget* 7:24860-24870, 2016
24. Réda M, Richard C, Bertaut A, et al: Implementation and use of whole exome sequencing for metastatic solid cancer. *EBioMedicine* 51:102624, 2020
25. Trédan O, Wang Q, Pissaloux D, et al: Molecular screening program to select molecular-based recommended therapies for metastatic cancer patients: Analysis from the ProfilER trial. *Ann Oncol* 30:757-765, 2019
26. Koopman B, van der Wekken AJ, ter Elst A, et al: Relevance and effectiveness of molecular tumor board recommendations for patients with non-small cell lung cancer with rare or complex mutational profiles. *JCO Precis Oncol* 4:393-410, 2020
27. van de Haar J, Hoes L, Voest E: Advancing molecular tumour boards: Highly needed to maximise the impact of precision medicine. *ESMO Open* 4:e000516, 2019
28. Tsimberidou A-M, Iskander NG, Hong DS, et al: Personalized medicine in a phase I clinical trials program: The MD Anderson Cancer Center Initiative. *Clin Cancer Res* 18:6373-6383, 2012
29. Mahipal A, Nguyen D: Risks and benefits of phase 1 clinical trial participation. *Cancer Control* 21:193-199, 2014
30. Bailey CH, Jameson G, Sima C, et al: Progression-free survival decreases with each subsequent therapy in patients presenting for phase I clinical trials. *J Cancer* 3:7-13, 2012
31. Marabelle A, Fakih M, Lopez J, et al: Association of tumour mutational burden with outcomes in patients with advanced solid tumours treated with pembrolizumab: Prospective biomarker analysis of the multicohort, open-label, phase 2 KEYNOTE-158 study. *Lancet Oncol* 21:1353-1365, 2020
32. Mateo J, Porta N, Bianchini D, et al: Olaparib in patients with metastatic castration-resistant prostate cancer with DNA repair gene aberrations (TOPARP-B): A multicentre, open-label, randomised, phase 2 trial. *Lancet Oncol* 21:162-174, 2020
33. Gambardella V, Tarazona N, Cejalvo JM, et al: Personalized medicine: Recent progress in cancer therapy. *Cancers (Basel)* 12:1009, 2020
34. Marquart J, Chen EY, Prasad V: Estimation of the percentage of US patients with cancer who benefit from genome-driven oncology. *JAMA Oncol* 4:1093-1098, 2018
35. Raymond VM, Gray SW, Roychowdhury S, et al: Germline findings in tumor-only sequencing: Points to consider for clinicians and laboratories. *J Natl Cancer Inst* 108:djv351, 2016



APPENDIX

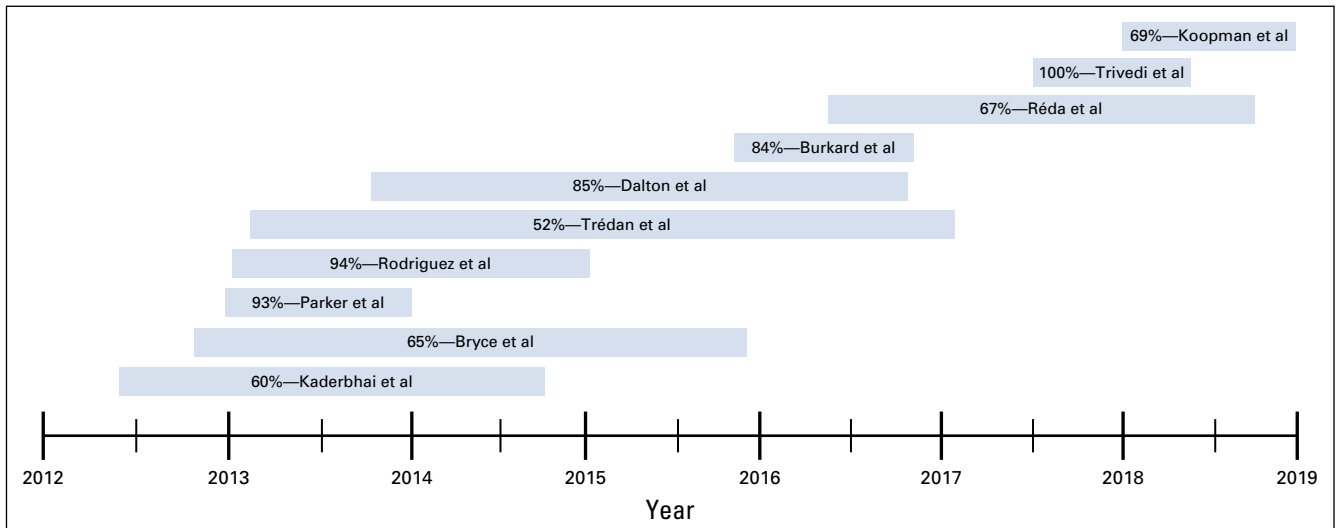


FIG A1. Actionability rates by year.

TABLE A1. Definitions of Actionability as Provided by the Authors

Reference	Definition of Actionability
Bryce et al ¹³	An aberration with known functional significance that could be therapeutically targeted with an FDA-approved drug or clinical trial
Burkard et al ¹⁴	Allowed for identification of a molecular-targeted clinical trial or off-trial treatment
Dalton et al ¹⁵	Offered a target for a drug approved by the FDA, an FDA-approved drug off-label, a clinical trial, or was a potential germline mutation for a hereditary syndrome
Harada et al ¹⁶	Variants classified as predictive or prognostic of any tumor types or have been reported in cancer and had available clinical trials
Kaderbhai et al ²³	Associated with FDA-approved drugs, potentially targetable when associated with a clinical trial or potential sensitivity to a drug
Koopman et al ²⁶	Tier 1 or 2 according to 2017 American College of Medical Genetics guidelines or existence of effective targeted therapy options
Parker et al ¹⁷	An FDA-approved drug or in clinical trials that targeted at low nanomolar concentrations or was the primary target of an antibody
Radovich et al ¹⁹	NR
Réda et al ²⁴	Class I-III variants with some class IV according to European Society of Medical Oncology Scale for Clinical Actionability of Molecular Tests guidelines, included some VUS
Rodriguez-Rodriguez et al ²⁰	NR
Schwaederle et al ¹⁸	NR
Tafe et al ²¹	Associated with available (approved, off-label, or experimental) targeting of the affected pathway
Trédan et al ²⁵	NR
Trivedi et al ²²	Linked as either a positive or negative biomarker for an approved therapy or enrollment criteria for an open clinical trial

Abbreviations: FDA, US Food and Drug Administration; NR, not reported; VUS, variants of unknown significance.