



HHS Public Access

Author manuscript

JAMA Dermatol. Author manuscript; available in PMC 2021 September 01.

Published in final edited form as:

JAMA Dermatol. 2020 September 01; 156(9): 1004–1011. doi:10.1001/jamadermatol.2020.1729.

Prognostic Gene Expression Profiling in Cutaneous Melanoma: Identifying the Knowledge Gaps and Assessing the Clinical Benefit

Douglas Grossman, MD, PhD,

Huntsman Cancer Institute, Salt Lake City, Utah; Department of Dermatology, University of Utah, Salt Lake City; Department of Oncological Sciences, University of Utah, Salt Lake City; Department of Medicine, Division of Oncology, University of Utah, Salt Lake City

Nwanneka Okwundu, DO,

Huntsman Cancer Institute, Salt Lake City, Utah

Edmund K. Bartlett, MD,

Department of Surgery, Memorial Sloan Kettering Cancer Center, New York, New York

Michael A. Marchetti, MD,

Dermatology Service, Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, New York

Megan Othus, PhD,

Fred Hutchinson Cancer Research Center, Seattle, Washington

Daniel G. Coit, MD,

Department of Surgery, Memorial Sloan Kettering Cancer Center, New York, New York

Rebecca I. Hartman, MD, MPH,

Dana-Farber Cancer Institute, Harvard Medical School, Boston, Massachusetts; Department of Dermatology, Harvard Medical School, Boston, Massachusetts

Sancy A. Leachman, MD, PhD,

Corresponding Author: Douglas Grossman, MD, PhD, Huntsman Cancer Institute, 2000 Circle of Hope, Salt Lake City, UT 84112, (doug.grossman@hci.utah.edu).

Author Contributions: Drs Grossman and Swetter had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Study concept and design: Grossman, Hartman, Leachman, Berry, Korde, Lee, Curiel-Lewandrowski, Kim, Nelson, Swetter.

Acquisition, analysis, or interpretation of data: Grossman, Okwundu, Bartlett, Marchetti, Othus, Coit, Hartman, Leachman, Berry, Lee, Bar-Eli, Berwick, Bowles, Buchbinder, Burton, Chu, Curtis, Daud, Deacon, Ferris, Gershenwald, Grossmann, Hu-Lieskovan, Hyingstrom, Jeter, Judson-Torres, Kendra, Kirkwood, Lawson, Leming, Long, Marghoob, Mehnert, Ming, Polsky, Scolyer, Smith, Sondak, Stark, Stein, J. A. Thompson, J. F. Thompson, Venna, Wei.

Drafting of the manuscript: Grossman, Okwundu, Bartlett, Marchetti, Othus, Coit, Berry, Korde, Lee, Swetter.

Critical revision of the manuscript for important intellectual content: Grossman, Okwundu, Bartlett, Marchetti, Othus, Coit, Hartman, Leachman, Berry, Lee, Bar-Eli, Berwick, Bowles, Buchbinder, Burton, Chu, Curiel-Lewandrowski, Curtis, Daud, Deacon, Ferris, Gershenwald, Grossmann, Hu-Lieskovan, Hyingstrom, Jeter, Judson-Torres, Kendra, Kim, Kirkwood, Lawson, Leming, Long, Marghoob, Mehnert, Ming, Nelson, Polsky, Scolyer, Smith, Sondak, Stark, Stein, J. A. Thompson, J. F. Thompson, Venna, Wei, Swetter.

Statistical analysis: Marchetti, Othus, Lee.

Administrative, technical, or material support: Okwundu, Nelson.

Study supervision: Grossman.

Additional Contributions and Dedication: Glen Bowen, MD, contributed to discussions in the planning phase of this work and reviewed the first draft of the manuscript. He was keenly interested in developing new technologies like GEP testing to improve patient care. He was a tireless and creative champion for his patients, with an amazing sense of humor, who graced the Huntsman Cancer Institute for 20 years. His untimely death occurred just days before the manuscript was submitted, and this work is dedicated to his memory.

Department of Dermatology and Knight Cancer Institute, Oregon Health & Science University, Portland

Elizabeth G. Berry, MD,

Department of Dermatology and Knight Cancer Institute, Oregon Health & Science University, Portland

Larissa Korde, MD,

Division of Cancer Treatment and Diagnosis, National Cancer Institute, Bethesda, Maryland

Sandra J. Lee, ScD,

Dana-Farber Cancer Institute, Harvard Medical School, Boston, Massachusetts; Department of Data Sciences, Harvard Medical School, Boston, Massachusetts

Menashe Bar-Eli, PhD,

Department of Cancer Biology, The University of Texas MD Anderson Cancer Center, Houston

Marianne Berwick, PhD,

Departments of Dermatology and Internal Medicine, University of New Mexico Cancer Center, University of New Mexico, Albuquerque

Tawnya Bowles, MD,

Department of Surgery, Division of Surgical Oncology, University of Utah, Salt Lake City

Elizabeth I. Buchbinder, MD,

Dana-Farber Cancer Institute, Harvard Medical School, Boston, Massachusetts; Department of Internal Medicine, Harvard Medical School, Boston, Massachusetts

Elizabeth M. Burton, MBA,

Department of Surgical Oncology, The University of Texas MD Anderson Cancer Center, Houston

Emily Y. Chu, MD, PhD,

Department of Dermatology, Perelman School of Medicine University of Pennsylvania, Philadelphia

Clara Curiel-Lewandrowski, MD,

Department of Dermatology and University of Arizona Cancer Center, University of Arizona, Tucson

Julia A. Curtis, MD,

Department of Dermatology, University of Utah, Salt Lake City

Adil Daud, MD,

Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco; Department of Hematology/Oncology, University of California, San Francisco

Dekker C. Deacon, MD, PhD,

Department of Dermatology, University of Utah, Salt Lake City

Laura K. Ferris, MD, PhD,

Department of Dermatology and University of Pittsburgh Clinical and Translational Science Institute, Pittsburgh, Pennsylvania

Jeffrey E. Gershenwald, MD,

Department of Surgical Oncology, The University of Texas MD Anderson Cancer Center, Houston

Kenneth F. Grossmann, MD, PhD,

Huntsman Cancer Institute, Salt Lake City, Utah

Siwen Hu-Lieskovan, MD, PhD,

Huntsman Cancer Institute, Salt Lake City, Utah; Department of Medicine, Division of Oncology, University of Utah, Salt Lake City

John Hynstrom, MD,

Huntsman Cancer Institute, Salt Lake City, Utah; Department of Surgery, Division of Surgical Oncology, University of Utah, Salt Lake City

Joanne M. Jeter, MD,

Department of Internal Medicine and The Ohio State University Comprehensive Cancer Center, Columbus

Robert L. Judson-Torres, PhD,

Huntsman Cancer Institute, Salt Lake City, Utah; Department of Dermatology, University of Utah, Salt Lake City

Kari L. Kendra, MD, PhD,

Department of Internal Medicine and The Ohio State University Comprehensive Cancer Center, Columbus

Caroline C. Kim, MD,

Department of Dermatology, Tufts Medical Center, Boston, Massachusetts; Partners Healthcare, Newton Wellesley Dermatology Associates, Wellesley, Massachusetts

John M. Kirkwood, MD,

Department of Internal Medicine and UPMC Hillman Cancer Center, University of Pittsburgh, Pittsburgh, Pennsylvania

David H. Lawson, MD,

Department of Hematology and Medical Oncology, Emory University School of Medicine, Winship Cancer Institute of Emory University, Atlanta, Georgia

Philip D. Leming, MD,

Cincinnati Cancer Advisors, Cincinnati, Ohio

Georgina V. Long, MBBS, PhD,

Melanoma Institute Australia, The University of Sydney, Sydney, New South Wales, Australia; Faculty of Medicine and Health, The University of Sydney, Sydney, New South Wales, Australia; Department of Medical Oncology, Royal North Shore Hospital, Sydney, New South Wales, Australia; Charles Perkins Centre, The University of Sydney, Sydney, Australia

Ashfaq A. Marghoob, MD,

Dermatology Service, Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, New York

Janice M. Mehnert, MD,

Department of Medical Oncology, Robert Wood Johnson University Hospital, New Brunswick, New Jersey; Rutgers Cancer Institute of New Jersey, New Brunswick

Michael E. Ming, MD,

Department of Dermatology, Perelman School of Medicine University of Pennsylvania, Philadelphia

Kelly C. Nelson, MD,

Department of Dermatology, The University of Texas MD Anderson Cancer Center, Houston

David Polsky, MD, PhD,

Department of Dermatology, Ronald O. Perelman Department of Dermatology, Laura and Isaac Perlmutter Cancer Center, NYU Langone Health, New York University School of Medicine, New York, New York

Richard A. Scolyer, MD,

Melanoma Institute Australia, The University of Sydney, Sydney, New South Wales, Australia; Faculty of Medicine and Health, The University of Sydney, Sydney, New South Wales, Australia; Charles Perkins Centre, The University of Sydney, Sydney, Australia; Department of Tissue Pathology and Diagnostic Oncology, Royal Prince Alfred Hospital and NSW Health Pathology, Sydney, New South Wales, Australia

Eric A. Smith, MD, PhD,

Department of Pathology, University of Utah, Salt Lake City

Vernon K. Sondak, MD,

Department of Cutaneous Oncology, Moffitt Cancer Center & Research Institute, Tampa, Florida; Department of Oncologic Sciences, University of South Florida Morsani College of Medicine, Tampa

Mitchell S. Stark, PhD,

The University of Queensland Diamantina Institute, The University of Queensland, Dermatology Research Centre, Brisbane, Australia

Jennifer A. Stein, MD, PhD,

Department of Dermatology, Ronald O. Perelman Department of Dermatology, Laura and Isaac Perlmutter Cancer Center, NYU Langone Health, New York University School of Medicine, New York, New York

John A. Thompson, MD,

Fred Hutchinson Cancer Research Center, Seattle, Washington; Department of Oncology, University of Washington, Seattle; Seattle Cancer Care Alliance, Seattle, Washington

John F. Thompson, MD,

Melanoma Institute Australia, The University of Sydney, Sydney, New South Wales, Australia; Faculty of Medicine and Health, The University of Sydney, Sydney, New South Wales, Australia; Department of Melanoma and Surgical Oncology, Royal Prince Alfred Hospital, Sydney, New South Wales, Australia

Suraj S. Venna, MD,

Inova Schar Cancer Institute, Department of Medicine, Virginia Commonwealth University, Fairfax

Maria L. Wei, MD, PhD,

Helen Diller Family Comprehensive Cancer Center, University of California, San Francisco; Department of Dermatology, University of California, San Francisco; Dermatology Service, Veterans Affairs Medical Center, San Francisco, California

Susan M. Swetter, MD

Stanford University Medical Center and Cancer Institute, Stanford, California; Dermatology Service, Veterans Affairs Palo Alto Health Care System, Palo Alto, California

Abstract

IMPORTANCE—Use of prognostic gene expression profile (GEP) testing in cutaneous melanoma (CM) is rising despite a lack of endorsement as standard of care.

OBJECTIVE—To develop guidelines within the national Melanoma Prevention Working Group (MPWG) on integration of GEP testing into the management of patients with CM, including (1) review of published data using GEP tests, (2) definition of acceptable performance criteria, (3) current recommendations for use of GEP testing in clinical practice, and (4) considerations for future studies.

EVIDENCE REVIEW—The MPWG members and other international melanoma specialists participated in 2 online surveys and then convened a summit meeting. Published data and meeting abstracts from 2015 to 2019 were reviewed.

FINDINGS—The MPWG members are optimistic about the future use of prognostic GEP testing to improve risk stratification and enhance clinical decision-making but acknowledge that current utility is limited by test performance in patients with stage I disease. Published studies of GEP testing have not evaluated results in the context of all relevant clinicopathologic factors or as predictors of regional nodal metastasis to replace sentinel lymph node biopsy (SLNB). The performance of GEP tests has generally been reported for small groups of patients representing particular tumor stages or in aggregate form, such that stage-specific performance cannot be ascertained, and without survival outcomes compared with data from the American Joint Committee on Cancer 8th edition melanoma staging system international database. There are significant challenges to performing clinical trials incorporating GEP testing with SLNB and adjuvant therapy. The MPWG members favor conducting retrospective studies that evaluate multiple GEP testing platforms on fully annotated archived samples before embarking on costly prospective studies and recommend avoiding routine use of GEP testing to direct patient management until prospective studies support their clinical utility.

CONCLUSIONS AND RELEVANCE—More evidence is needed to support using GEP testing to inform recommendations regarding SLNB, intensity of follow-up or imaging surveillance, and postoperative adjuvant therapy. The MPWG recommends further research to assess the validity and clinical applicability of existing and emerging GEP tests. Decisions on performing GEP testing and patient management based on these results should only be made in the context of discussion of testing limitations with the patient or within a multidisciplinary group.

Prognostic gene expression profile (GEP) testing for cutaneous melanoma (CM) is designed to predict recurrence or metastatic risk based on expression patterns of a selected panel of genes from the primary tumor. Although routine GEP testing is not endorsed by the

American Academy of Dermatology (AAD)¹ or National Comprehensive Cancer Network (NCCN)² CM guidelines outside of a clinical trial or study, its use is becoming more prevalent. For example, the DecisionDx-Melanoma test (31-GEP, Castle Biosciences) is covered by Centers for Medicare & Medicaid Services (\$7193)³ for sentinel lymph node (SLN) biopsy (SLNB)–eligible patients. Approximately 1000 31-GEP tests are processed every month.⁴ Based on reported incidence in the US,⁵ up to 5% to 10% of cases are being tested. MelaGenix (NeraCare) is available in Europe, and a test from SkylineDx has been developed. A recent survey of pigmented lesion specialists revealed that 29% had ordered a prognostic GEP test, yet only half of these physicians reported that the test results influenced patient management.⁶ Although GEP testing has the potential to improve staging and guide interventions such as SLNB, surveillance imaging intensity, and adjuvant therapy, it is not clear which patients should be tested or how to act on the results.⁷ Additionally, there may be hazard for some patients forgoing SLNB based on results from GEP testing,⁸ including failure to qualify for adjuvant therapeutic options or a clinical trial. In November 2019, following 2 online surveys, the national Melanoma Prevention Working Group (MPWG) and other international melanoma specialists convened to review 3 different GEP test platforms in various stages of clinical development and outline recommendations for evaluating prognostic GEP tests based on current evidence and consensus. These results are discussed herein, along with challenges regarding future prospective clinical trials that aim to incorporate GEP testing into clinical decision-making.

Methods

Participants

The MPWG is an interdisciplinary group of dermatologists, medical oncologists, surgical oncologists, dermatopathologists, epidemiologists/statisticians, basic scientists, and patient advocates dedicated to evidence review for best practices in melanoma prevention and early detection. An MPWG Pigmented Lesion Subcommittee previously published consensus statements on melanoma screening⁹ and management of dysplastic nevi.¹⁰ The MPWG members and additional international melanoma specialists participated in 2 rounds of an online survey.

Review of the Literature

We reviewed journal articles published from 2015 to 2019 related to GEP testing in CM that were indexed in PubMed. Additionally, relevant abstracts presented at the American Society of Clinical Oncology from 2017 to 2019 were reviewed.

Online Survey Process

An MPWG GEP subcommittee (D.G., E.G.B., R.I.H., C.C.-L., C.C.K., S.A.L., K.C.N., and S.M.S.) held 2 conference calls to develop initial questions, review anonymous survey data, and refine subsequent questions. Participants were sent links by email to Qualtrics-based surveys, and 2 of us (D.G. and N.O.) collated the data. The University of Utah Institutional Review Board (No. 125960) approved this survey activity.

Summit Meeting

The GEP subcommittee convened a 2-hour meeting (November 20, 2019) during the Society for Melanoma Research Congress in Salt Lake City, Utah. Predesignated speakers conducted a literature review and discussions of CM guidelines regarding GEP testing, online survey results, use of GEP results as a biomarker, statistical considerations for clinical trials incorporating GEP testing, SLNB, and adjuvant therapy, and the merits of analyzing banked-tumor specimens from completed clinical trials.

Results

Why Routine Prognostic GEP Testing Is Not Endorsed by AAD/NCCN Guidelines

Current AAD¹ and NCCN² melanoma clinical practice guidelines do not specify particular interventions based on GEP test results, although they recognize that prognostic GEP testing may classify CMs according to low vs high risk for metastatic recurrence. Concerns persist regarding minimal overlap among gene panels across studies^{11–16} and whether GEP testing provides additional independent prognostic information compared with known clinicopathologic factors (ie, Breslow thickness, quantitative mitotic rate, ulceration, lymphovascular invasion, tumor-infiltrating lymphocytes, melanoma subtype, primary tumor site, regression, SLN status, American Joint Committee on Cancer [AJCC] stage, and patient age/sex). The eighth edition of the AJCC *Cancer Staging Manual* (AJCC8)¹⁷ international database has validated melanoma-specific survival (MSS) based on nearly 50 000 patients with stage I to III melanoma observed since 1998 from the US, Australia, and Europe, most of whom were pathologically staged with SLNB.^{18,19}

Without clinical trial assessment, the available evidence is insufficient to determine whether currently available GEP tests are simply a surrogate for a combination of known clinicopathologic factors associated with risk of recurrence/mortality. None of the published studies have evaluated all available clinicopathologic features of prognostic significance per international pathology reporting guidelines.²⁰ Contemporary assessment is further limited by lack of comparison in most studies to AJCC8,¹⁷ which incorporates additional microscopic positive nodes for staging; however, the utility of this prognostic factor may be less valuable because many patients no longer undergo complete nodal dissection following a positive SLNB result given the Multicenter Selective Lymphadenectomy Trial II (MSLT-II)²¹ and German Dermatologic Cooperative Oncology Group study (DeCOG-SLT)²² outcomes. There is also limited evidence that GEP testing informs the need for imaging surveillance, SLNB, or adjuvant treatment. Current data do not sufficiently address issues related to false-positive and false-negative GEP test results (ie, high-risk test patients who fare well, and low-risk test patients who do not). While the latest NCCN guidelines² note that prognostic GEP testing may have value as an adjunct to AJCC staging, further investigation of large, contemporary data sets of unselected patients (as has been performed in patients with breast cancer)^{23,24} was deemed necessary to define whether such testing can provide clinically actionable information.

Perceived Role of GEP Testing Among Melanoma Experts

In the current first-round online survey, the perceived clinical effect of GEP testing for early-stage (T1a/T1b) CM ranged from low to high, with more than 70% of respondents recognizing the potential value of accurately predicting patients with SLN positivity and those likely to relapse (eTable 1 in the Supplement). Because T1 tumors represent up to one-third of CM deaths,²⁵ GEP-based selection of those at highest risk for metastasis could potentially decrease melanoma mortality if adjuvant therapy were effectively used, although it has not yet been studied in this manner. There was also skepticism about the current ability of GEP testing to improve prognostication for T1 tumors, which are associated with greater than 95% 10-year MSS, according to AJCC8 staging from the worldwide collaborative data set.¹⁷ Most (61%-77%) respondents agreed that GEP testing could have high clinical effect for patients with stage II and III A disease by identifying those who might be spared from routine imaging surveillance and/or benefit from systemic adjuvant therapy. Although fewer than 50% of respondents agreed that clinical utility of GEP testing should be determined from highly annotated retrospective studies (eg, National Cancer Trials Network) rather than prospective clinical trials, most agreed that future studies should use multiple testing platforms.

In the second-round online survey and at the summit meeting, there was consensus regarding the value of representative cohorts and the need for prospective randomized clinical trials (similar to those performed for breast cancer^{23,24}) as all GEP platforms continue to evolve worldwide. While fewer than 50% of respondents agreed on the minimum acceptable prognostic accuracy for GEP testing, the majority (61%-80%) believed that worthwhile trials would address whether GEP testing could predict SLN positivity, compare favorably to SLNB in predicting risk of relapse, and identify patients who could be spared surveillance imaging and/or benefit from adjuvant therapy. Most (68%) respondents agreed that GEP testing had the greatest potential to influence the clinical management of patients with stage II disease.

Review of Currently Available GEP Testing Platforms

The 31-GEP Test—Two retrospective^{26,27} and 3 prospective²⁸⁻³¹ external validation studies have been published following the initial publication of 31-GEP test data in 2015.¹⁶ These studies demonstrated the prognostic ability of the 31-GEP test to identify low-risk (class 1) and high-risk (class 2) CM (Table 1). Despite differing study designs and variable follow-up, the performance of the 31-GEP test appeared consistent across studies and in a recent meta-analysis published following the summit meeting.³² When evaluated as an independent covariate in multivariate analyses of patients with mixed-stage disease, results have been independently associated with relapse; however, no studies reported multivariate analyses accounting for all known clinicopathologic variables associated with MSS (noted previously). Additionally, most patients were not staged according to AJCC8¹⁷ or compared with MSS from the AJCC8 data set, and follow-up times were insufficient to detect delayed recurrences for thin CM.³³⁻³⁵ Thus, the incremental value of the 31-GEP test beyond established clinicopathologic prognostic factors and AJCC8 staging remains uncertain. In evaluation of the limited data reported in a stage-specific manner, the 31-GEP test misclassified the majority of patients with stage I disease with melanoma

recurrence^{26,27,30,36}; in contrast, most patients with stage II and III disease with recurrence were correctly classified as class 2. The 31-GEP test was also evaluated as prognostic for SLN metastasis, although only unadjusted analyses were used.⁸

The Combined Clinicopathologic and GEP Platform—Statistical modeling merged clinicopathologic and GEP factors associated with nodal metastasis¹³ into a combined model (CP-GEP; Table 2). In a validation cohort, the CP-GEP model improved predictive capacity for SLN positivity.¹³ In partnership with SkylineDx, an external validation was performed.¹⁴ A revised CP-GEP model that included age, Breslow thickness, and expression of 8 target genes (including only 2 from the original GEP group¹³) yielded a negative predictive value of approximately 90%, and estimated that for T1/T2 tumors, an SLNB reduction rate of 40% could be achieved. Limitations of the published data include key differences between this external validation and the original CP-GEP model: age of the cohorts, inclusion of T4 tumors, use of only age and Breslow thickness as clinicopathologic factors, and use of a different gene set. Performance outcomes, such as area under the curve, sensitivity, specificity, false-positive and false-negative rates, and stage-specific breakdown, were not reported.¹⁴ This test recently became commercially available,³⁹ and further validation testing was published following the summit meeting.⁴⁰

The MelaGenix Platform—MelaGenix, which is commercially available in Europe, was developed from a panel¹² that was narrowed to 7 protective genes and 1 high-risk gene using a training cohort of 125 CMs.³⁷ This 8-GEP test was examined in a validation cohort (Table 2). Combining a dichotomized gene expression risk score (GRS) with SLN status improved prognostic performance, and when the GRS was examined as a continuous variable it complemented AJCC7 staging in predicting MSS. Recently, in patients with stage II disease, high GRS was associated with decreased recurrence-free survival, distant metastasis-free survival, and MSS.³⁸ Patients with low and high GRS had a 10-year MSS of 92% and 67%, respectively; 10-year MSS for AJCC substages was 88% (IIA), 82% (IIB), and 75% (IIC), suggesting that the GRS may add value to AJCC classification in defining both low-risk and high-risk patients.

Essential Elements for Incorporation of a GEP Test Into Melanoma Staging and Clinical Care Guidelines

New prognostic tests (including GEP) must improve the accuracy of the best, currently available risk prediction models by a clinically (and not solely statistically) significant amount and should thereby alter the treatment plan (eg, whether or not to increase surveillance, perform SLNB, or recommend adjuvant therapy). The test should add to the positive predictive value of current models (eg, by identifying more patients at high risk of relapse) while minimizing false-positive predictions (eg, by identifying patients who otherwise would have been predicted to relapse but who do not). Ideally, it should add to the negative predictive value of current models while minimizing false-negative predictions (eg, patients otherwise considered low risk but who will ultimately relapse).

A GEP test should preferably be developed from the primary tumors of patients with a relatively high incidence of events (a development/discovery set) and then evaluated with a

much larger test cohort that is more representative of the entire clinical spectrum of disease. If the GEP test performs well across the major parameters outlined previously and against the best risk prediction models currently available, it should then be evaluated in an unselected, large, independent validation set of patients (and preferably in more than 1 validation set) to ensure reproducibility and durability. The end points of these analyses must be well defined (eg, SLNB positivity, locoregional or distant recurrence, and disease-specific death) and analyzed separately.

There was consensus at the summit on the following concepts: (1) GEP test scores should be analyzed as continuous variables to avoid misleading interpretation of dichotomous low-risk and high-risk values that may not reflect true biologic significance; (2) GEP scores for a given end point should be evaluated against standard clinicopathologic variables and upcoming AJCC8 risk stratification models to ensure that they are additive; (3) GEP tests should be evaluated across the entire disease spectrum of intended use, to add value in high-risk patients and avoid harm in low-risk patients; (4) GEP test results should be reproducible, widely available, and cost-effective (not simply cost-additive) to be incorporated in national/international clinical practice guidelines; and (5) test validation must be performed while minimizing investigator or commercial bias.

Clinical Trial Considerations

Clinical research questions are best addressed by prospective randomized clinical trials, particularly if interventions based on GEP testing represent a change in standard care (such as surveillance, SLNB, and/or adjuvant therapy). Potential biomarkers such as GEPs, whether integral or integrated into trial design,⁴¹ should be analytically and clinically validated before they can be used in clinical trials to determine eligibility and assign or stratify patients for treatment. Analytic validation provides confirmation that the performance characteristics of the assay are reliable and suitable for the intended clinical trial.⁴² Clinical validation reflects the ability of the assay to predict the outcome of interest. Potential randomized clinical trial designs incorporating GEP testing in the context of SLNB or adjuvant therapy decision-making are shown in eTable 2 in the Supplement. Results from GEP testing also have the potential to inform decisions regarding use of imaging surveillance for higher-risk patients with stage IB to II disease and could be the subject of a clinical trial.

Although prospective clinical trials are desirable, given the anticipated cost and number of patients required (eTable 2 in the Supplement), summit participants believed it is important to first perform retrospective studies using representative clinically annotated banked specimens (with long-term outcomes data) to support evaluation of particular GEPs prospectively in future trials. For example, retrospective studies of large, contemporary data sets may be sufficient to determine if GEP testing could adequately predict SLN positivity. Unfortunately, GEP testing is not incorporated into ongoing adjuvant trials in patients with stage IIB/C disease (eg, KEYNOTE-716 [placebo vs pembrolizumab, [NCT03553836](#)] and Check Mate 76K [placebo vs nivolumab, [NCT04099251](#)]). However, several completed cooperative group trials (eg, S1404, E1609, E1697, EORTC1325) and industry-sponsored studies (CheckMate 238, CheckMate 915) containing well-annotated specimens might

provide opportunities to assess GEP test performance. We recognize that industry may be reluctant to sponsor a study that might identify patients who would not benefit from their GEP test or therapeutic product. Beyond the potential for tissue degradation with use of older biospecimens, there are also limitations to using completed trial data sets that include use of prior AJCC staging classifications that lack contemporary clinicopathologic factors, lack of uniform pathologic staging with SLNB, and outdated systemic/adjuvant therapies (eg, high-dose interferon or ipilimumab).

Discussion

A multidisciplinary group of melanoma specialists reviewed the current evidence and discussed recommendations for use of GEP testing in CM. The consensus of the MPWG is that there are insufficient data to support routine use of currently available prognostic GEP tests to inform management for patients with CM. The MPWG recommends further research to assess the validity and clinical applicability of existing and emerging GEP tests. Although current GEP platforms require significant amounts of tissue, it is likely that future technologies will enable testing from smaller specimens, potentially facilitating multiple parallel platform assessments. While spatial transcriptomics⁴³ is an exciting research technique, it requires extensive analytical validation and evidence of association with clinical outcomes before being evaluated as a clinical test. Cell-free circulating tumor DNA shows promise as a biomarker for the management of patients with stages III and IV melanoma, although the sensitivity of circulating tumor DNA assays is related to patient tumor burden.⁴⁴ Current data have not yet suggested a role for monitoring minimal residual disease in patients with resected stage I/II disease.⁴⁴

An international consortium for testing and comparing prognostic accuracy of multiple GEP platforms should be established in a standardized fashion. Such an initiative would also permit uniform reporting of prognostic testing data⁴⁵ in accordance with the REMARK (Reporting Recommendations for Tumor Marker Prognostic Studies) recommendations.⁴⁶ Additionally, net-benefit analysis may determine whether basing clinical decisions on a test would do more good than harm and would ideally include patient-reported outcomes and quality-of-life metrics, in contrast to traditional indices, such as sensitivity, specificity, or area under the curve, which are statistical abstractions and not necessarily informative about clinical value.⁴⁷ We acknowledge that funding for any trial initiative will be challenging.

Importantly, we must recognize that there may be non scientific elements involved in the adoption of new technologies into clinical practice that involve bias and other factors related to financial gain.^{48,49} Physicians who were collaborators in clinical studies may favorably influence their colleagues and perceive that the use of a new test could alter their reputation or revenue (either positively or negatively). Dermatologists may be biased in favor of a test that would allow them to perform more excisions and send fewer patients for SLNB, while surgical oncologists may be biased against a test that limits the use of SLNB. Medical oncologists and pharmaceutical companies may be biased against a test that limits the use of adjuvant therapy or in favor of one that expands its use. Finally, a prognostic test company will have financial motivation to maximize its utilization in as many clinical scenarios as possible. Rigorous peer review is essential to ensure that the validation data supporting use

of the technology are sufficient. The remedy to these different biases is transparency, regulatory oversight, and a shared intent to balance the necessity to protect patients from potentially inaccurate testing that may provide a false sense of security or perceived increased risk with the desire to develop and implement new, promising technologies.

Limitations

The limitations of our study include inability to review all relevant data, including proprietary industry data and other data published after the manuscript was submitted. Additionally, there was a relatively low combined response rate to both surveys.

Conclusions

The MPWG consensus is that there are insufficient data to support routine use of currently available prognostic GEP tests to inform management for patients with CM. The MPWG recommends further research to assess the validity and clinical applicability of existing and emerging GEP tests. Decisions on performing GEP testing and patient management based on these results should only be made in the context of discussion of testing limitations with the patient or within a multidisciplinary group.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Funding/Support:

This work was supported by the University of Utah Department of Dermatology (Drs Grossman and Okwundu), the Huntsman Cancer Foundation (Dr Grossman) at the University of Utah, the Melanoma Center at the Huntsman Cancer Institute (travel support for Dr Lee to attend summit meeting), the Hope Foundation (travel support for Dr Othus to attend summit meeting), the National Health and Medical Research Council of Australia (NHMRC) Program (Drs Long, Scolyer, and J. F. Thompson) and fellowship grants (Drs Long, Scolyer, and Stark), and grants from the American Skin Association (Dr Hartman) and the Sydney Medical School Foundation (Dr J. F. Thompson). This material is the result of work supported with resources and the use of facilities at the Veterans Affairs Palo Alto Health Care System in Palo Alto, California (Dr Swetter). The contents do not represent the views of the US Department of Veterans Affairs or the US Government.

Conflict of Interest Disclosures:

Dr Grossman reported receiving personal fees from Orlucent outside the submitted work. Dr Othus reported receiving grants from the National Cancer Institute during the conduct of the study, and serving as a consultant for Merck, Daiichi Sankyo, and GlycoMimetics and on the Data Safety and Monitoring Boards of Celgene and GlycoMimetics outside the submitted work. Dr Hartman reported receiving grants from the American Skin Association outside the submitted work. Dr Leachman reported receiving nonfinancial support (early access program) from Castle Biosciences outside the submitted work, as well as having manuscripts and abstracts published using the test with company support of the assay—all publications were peer reviewed and no personal or institutional payment or compensation was received. Dr Berry reported receiving personal fees from Bristol-Myers Squibb outside the submitted work. Dr Lee reported serving as a consultant for the Data Safety Monitoring Board of Genentech/Roche outside the submitted work. Dr Buchbinder reported receiving personal fees from Novartis and Partners Therapeutics outside the submitted work. Dr Daud reported receiving grants from Novartis, GlaxoSmithKline, Bristol-Myers Squibb, Merck, Pfizer, Incyte, Xencor, and OncoSec Medical outside the submitted work. Dr Ferris reported receiving grants from Castle Biosciences and grants and personal fees from DermTech outside the submitted work. Dr Gershenwald reported receiving personal fees from Merck, Novartis, Bristol-Myers Squibb, Syndax, and Castle Biosciences outside the submitted work. Dr Hu-Lieskovan reported receiving grants from Vaccinex and Bristol-Myers Squibb and personal fees from Bristol-Myers Squibb, Xencor, and Genmab outside the submitted work. Dr Jeter reported receiving grants from Bristol-Myers Squibb and Merck and serving as a consultant for Array Biopharma outside the submitted work. Dr Long reported receiving personal fees from Aduro, Amgen, Bristol-Myers Squibb, Mass Avery, Merck, Merck Sharp & Dohme, Novartis, OncoSec

Medical, Pierre-Fabre, Roche, and Sandoz outside the submitted work. Dr Mehnert reported receiving research grants from Amgen, AstraZeneca, Bristol-Myers Squibb, EMD Serono, Immunocore, Incyte, MacroGenics, Merck Sharp & Dohme, Novartis, Polynoma, and Sanofi; receiving personal fees for serving as a consultant for Amgen and Merck Sharp & Dohme; receiving honoraria from EMD Serono and Pfizer; and receiving personal fees for serving on advisory boards for Array BioPharma, Bristol-Myers Squibb, EMD Serono, and Sanofi/Regeneron. Dr Polsky reported a research contract with Novartis and receiving personal fees from Molecular MD and Physician's Education Resource outside the submitted work. Dr Scolyer reported receiving a NHMRC Program Grant and NHMRC Fellowship Grant during the conduct of the study and personal fees from Merck Sharp & Dohme, GlaxoSmithKline Australia, Bristol-Myers Squibb, Novartis Pharmaceuticals Australia Pty Ltd, Myriad, NeraCare, and Amgen outside the submitted work; support from Melanoma Institute Australia, The University of Sydney, The Royal Prince Alfred Hospital and New South Wales Health Pathology, and The Ainsworth Foundation is also acknowledged. Dr Sondak reported receiving personal fees from Bristol-Myers Squibb, Merck, Polynoma, and Regeneron outside the submitted work. Dr Stein reported receiving other (compensation to department for diagnostic services) from MoleSafe USA outside the submitted work. Dr J. F. Thompson reported grants from Australian NHMRC and grants from Sydney Medical School Foundation, The University of Sydney, during the conduct of the study and receiving honoraria and travel support from GlaxoSmithKline and Provectus Inc and personal fees for serving on advisory boards for BMS Australia and MSD Australia outside the submitted work. Dr Wei reported serving as an investigator for Castle Biosciences (no personal financial compensation). No other disclosures were reported.

Role of the Funder/Sponsor:

The funders had no role in the design and conduct of the study; collection, management, analysis, and interpretation of the data; preparation, review, or approval of the manuscript; and decision to submit the manuscript for publication.

REFERENCES

1. Swetter SM, Tsao H, Bichakjian CK, et al. Guidelines of care for the management of primary cutaneous melanoma. *J Am Acad Dermatol*. 2019;80(1):208–250.doi:10.1016/j.jaad.2018.08.055 [PubMed: 30392755]
2. National Comprehensive Cancer Network. NCCN Clinical Practice Guidelines in Oncology (NCCN Guidelines): cutaneous melanoma. Version 1.2020. Accessed December 19, 2019. https://www.nccn.org/professionals/physician_gls/pdf/cutaneous_melanoma.pdf
3. Centers for Medicare & Medicaid Services. Advanced diagnostic laboratory tests under the Medicare CLFS. Accessed June 26, 2020. <https://www.cms.gov/files/document/advanced-diagnostic-laboratory-tests-under-medicare-clfs.pdf>
4. Castle Biosciences announces Medicare coverage for the DecisionDx-Melanoma test in cutaneous melanoma. News release. Castle Biosciences. Accessed October 18, 2018. <https://ir.castlebiosciences.com/news-releases/news-release-details/castle-biosciences-announces-medicare-coverage-decisiondx>
5. National Cancer Institute. Cancer Stat Facts: melanoma of the skin. Accessed December 11, 2019. <https://seer.cancer.gov/statfacts/html/melan.html>
6. Varedi A, Gardner LJ, Kim CC, et al. Use of new molecular tests for melanoma by pigmented-lesion experts. *J Am Acad Dermatol*. 2020;82(1):245–247. doi:10.1016/j.jaad.2019.08.022 [PubMed: 31415835]
7. Grossman D, Kim CC, Hartman RI, et al. Prognostic gene expression profiling in melanoma: necessary steps to incorporate into clinical practice. *Melanoma Manag*. 2019;6(4):MMT32. doi:10.2217/mmt-2019-0016 [PubMed: 31871621]
8. Vetto JT, Hsueh EC, Gastman BR, et al. Guidance of sentinel lymph node biopsy decisions in patients with T1-T2 melanoma using gene expression profiling. *Future Oncol*. 2019;15(11):1207–1217. doi:10.2217/fon-2018-0912 [PubMed: 30691297]
9. Curiel-Lewandrowski C, Kim CC, Swetter SM, et al.; Melanoma Prevention Working Group–Pigmented Skin Lesion Sub-Committee. Survival is not the only valuable end point in melanoma screening. *J Invest Dermatol*. 2012;132(5):1332–1337.doi:10.1038/jid.2012.3 [PubMed: 22336950]
10. Kim CC, Swetter SM, Curiel-Lewandrowski C, et al. Addressing the knowledge gap in clinical recommendations for management and complete excision of clinically a typical nevi/dysplastic nevi: Pigmented Lesion Subcommittee consensus statement. *JAMA Dermatol*. 2015;151(2):212–218. doi:10.1001/jamadermatol.2014.2694 [PubMed: 25409291]

11. Winnepenninckx V, Lazar V, Michiels S, et al.; Melanoma Group of the European Organization for Research and Treatment of Cancer. Gene expression profiling of primary cutaneous melanoma and clinical outcome. *J Natl Cancer Inst.* 2006;98(7):472–482. doi:10.1093/jnci/djj103 [PubMed: 16595783]
12. Brunner G, Reitz M, Heinecke A, et al. A nine-gene signature predicting clinical outcome in cutaneous melanoma. *J Cancer Res Clin Oncol.* 2013;139(2):249–258. doi:10.1007/s00432-012-1322-z [PubMed: 23052696]
13. Meves A, Nikolova E, Heim JB, et al. Tumor cell adhesion as a risk factor for sentinel lymph node metastasis in primary cutaneous melanoma. *J Clin Oncol.* 2015;33(23):2509–2515. doi:10.1200/JCO.2014.60.7002 [PubMed: 26150443]
14. Mulder EEAP, Dwarkasing JT, Hollestein LM, et al. Validation of a clinicopathological and gene expression profile (CP-GEP) model for sentinel lymph node metastasis in primary cutaneous melanoma [abstract 1325P]. *Ann Oncol.* 2019;30 (suppl 5):v540. doi:10.1093/annonc/mdz255.014
15. Nsengimana J, Laye J, Filia A, et al. Independent replication of a melanoma subtype gene signature and evaluation of its prognostic value and biological correlates in a population cohort. *Oncotarget.* 2015;6 (13):11683–11693. doi:10.18632/oncotarget.3549 [PubMed: 25871393]
16. Gerami P, Cook RW, Wilkinson J, et al. Development of a prognostic genetic signature to predict the metastatic risk associated with cutaneous melanoma. *Clin Cancer Res.* 2015;21(1): 175–183. doi:10.1158/1078-0432.CCR-13-3316 [PubMed: 25564571]
17. Gershenwald JE, Scolyer RA, Hess KR, et al. Melanoma staging: evidence-based changes in the American Joint Committee on Cancer eighth edition cancer staging manual. *CA Cancer J Clin.* 2017;67 (6):472–492. doi:10.3322/caac.21409 [PubMed: 29028110]
18. Bajaj S, Donnelly D, Call M, et al. Melanoma prognosis—accuracy of the American Joint Committee on Cancer Staging Manual Eighth Edition. *J Natl Cancer Inst.* Published online 1 24, 2020. doi:10.1093/jnci/djaa008
19. Gershenwald JE, Scolyer RA. Melanoma staging: American Joint Committee on Cancer (AJCC) 8th edition and beyond. *Ann Surg Oncol.* 2018;25(8): 2105–2110. doi:10.1245/s10434-018-6513-7 [PubMed: 29850954]
20. Scolyer RA, Balamurgan T, Busam K, et al. *Invasive Melanoma, Histopathology Reporting Guide.* 2nd Edition. International Collaboration on Cancer Reporting; 2019.
21. Faries MB, Thompson JF, Cochran AJ, et al. Completion dissection or observation for sentinel-node metastasis in melanoma. *N Engl J Med.* 2017;376(23):2211–2222. doi:10.1056/NEJMoa1613210 [PubMed: 28591523]
22. Leiter U, Stadler R, Mauch C, et al.; German Dermatologic Cooperative Oncology Group (DeCOG). Complete lymph node dissection versus no dissection in patients with sentinel lymph node biopsy positive melanoma (DeCOG-SLT): a multicentre, randomised, phase 3 trial. *Lancet Oncol.* 2016;17 (6):757–767. doi:10.1016/S1470-2045(16)00141-8 [PubMed: 27161539]
23. Paik S, Shak S, Tang G, et al. A multigene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. *N Engl J Med.* 2004; 351(27):2817–2826. doi:10.1056/NEJMoa041588 [PubMed: 15591335]
24. Paik S, Tang G, Shak S, et al. Gene expression and benefit of chemotherapy in women with node-negative, estrogen receptor-positive breast cancer. *J Clin Oncol.* 2006;24(23):3726–3734. doi: 10.1200/JCO.2005.04.7985 [PubMed: 16720680]
25. Whiteman DC, Baade PD, Olsen CM. More people die from thin melanomas (≤ 1 mm) than from thick melanomas (> 4 mm) in Queensland, Australia. *J Invest Dermatol.* 2015;135(4):1190–1193. doi:10.1038/jid.2014.452 [PubMed: 25330295]
26. Zager JS, Gastman BR, Leachman S, et al. Performance of a prognostic 31-gene expression profile in an independent cohort of 523 cutaneous melanoma patients. *BMC Cancer.* 2018;18(1):130. doi:10.1186/s12885-018-4016-3 [PubMed: 29402264]
27. Greenhaw BN, Zitelli JA, Brodland DG. Estimation of prognosis in invasive cutaneous melanoma: an independent study of the accuracy of a gene expression profile test. *Dermatol Surg.* 2018;44(12):1494–1500. doi:10.1097/DSS.0000000000001588 [PubMed: 29994951]

28. Hsueh EC, DeBloom JR, Lee J, et al. Interim analysis of survival in a prospective, multi-center registry cohort of cutaneous melanoma tested with a prognostic 31-gene expression profile test. *J Hematol Oncol*. 2017;10(1):152. doi:10.1186/s13045-017-0520-1 [PubMed: 28851416]
29. Hsueh EC, DeBloom JR, Cook RW, McMasters K. Three-year survival outcomes in a prospective cohort evaluating a prognostic 31-gene expression profile (31-GEP) test for cutaneous melanoma (CM) [abstract 9519]. *J Clin Oncol*. 2019; 37(15)(suppl). doi:10.1200/JCO.2019.37.15_suppl.9519
30. Keller J, Schwartz TL, Lizalek JM, et al. Prospective validation of the prognostic 31-gene expression profiling test in primary cutaneous melanoma. *Cancer Med*. 2019;8(5):2205–2212. doi:10.1002/cam4.2128 [PubMed: 30950242]
31. Podlipnik S, Carrera C, Boada A, et al. Early outcome of a 31-gene expression profile test in 86 AJCC stage IB-II melanoma patients. a prospective multicentre cohort study. *J Eur Acad Dermatol Venereol*. 2019;33(5):857–862. doi:10.1111/jdv.15454 [PubMed: 30702163]
32. Greenhaw BN, Covington KR, Kurley SJ, et al. Molecular risk prediction in cutaneous melanoma: a meta-analysis of the 31-gene expression profile prognostic test in 1,479 patients. *J Am Acad Dermatol*. in press. doi:10.1016/j.jaad.2020.03.053
33. Crowley NJ, Seigler HF. Late recurrence of malignant melanoma. analysis of 168 patients. *Ann Surg*. 1990;212(2):173–177. doi:10.1097/00000658-199008000-00010 [PubMed: 2375648]
34. Kalady MF, White RR, Johnson JL, Tyler DS, Seigler HF. Thin melanomas: predictive lethal characteristics from a 30-year clinical experience. *Ann Surg*. 2003;238(4):528–535. doi:10.1097/01.sla.0000090446.63327.40 [PubMed: 14530724]
35. Lo SN, Scolyer RA, Thompson JF. Long-term survival of patients with thin (T1) cutaneous melanomas: a Breslow thickness cut point of 0.8 mm separates higher-risk and lower-risk tumors. *Ann Surg Oncol*. 2018;25(4):894–902. doi:10.1245/s10434-017-6325-1
36. Marchetti MA, Bartlett EK, Dusza SW, Bichakjian CK. Use of a prognostic gene expression profile test for T1 cutaneous melanoma: will it help or harm patients? *J Am Acad Dermatol*. 2019;80(6):e161–e162. doi:10.1016/j.jaad.2018.11.063 [PubMed: 30586612]
37. Gambichler T, Reinhold U, Tsagoudis K, et al. Gene-signature based prediction of relapse-free survival in melanoma patients with known sentinel lymph node status. *J Clin Oncol*. 2017;35:e21037. doi:10.1200/JCO.2017.35.15_suppl.e21037
38. Amaral TMS, Hoffmann M-C, Sinnberg T, et al. Clinical validation of a prognostic 11-gene expression profiling score in prospectively collected FFPE tissue of patients with AJCC v8 stage II cutaneous melanoma. *Eur J Cancer*. 2020;125:38–45. doi:10.1016/j.ejca.2019.10.027 [PubMed: 31838403]
39. SkylineDx launches melanoma test in United States to support cancer care. News release. SkylineDx. Accessed April 22, 2020. <https://www.skylinedx.com/news/skylinedx-launches-melanoma-test-in-united-states-to-support-cancer-care>
40. Bellomo D, Arias-Mejias SM, Ramana C, et al. Model combining tumor molecular and clinicopathologic risk factors predicts sentinel lymph node metastasis in primary cutaneous melanoma. *JCO Precis Oncol*. 2020;4:319–334. doi:10.1200/PO.19.00206 [PubMed: 32405608]
41. Schilsky RL, Doroshow JH, Leblanc M, Conley BA. Development and use of integral assays in clinical trials. *Clin Cancer Res*. 2012;18(6):1540–1546. doi:10.1158/1078-0432.CCR-11-2202 [PubMed: 22422406]
42. Williams PM, Lively TG, Jessup JM, Conley BA. Bridging the gap: moving predictive and prognostic assays from research to clinical use. *Clin Cancer Res*. 2012;18(6):1531–1539. doi:10.1158/1078-0432.CCR-11-2203 [PubMed: 22422405]
43. Thrane K, Eriksson H, Maaskola J, Hansson J, Lundeberg J. Spatially resolved transcriptomics enables dissection of genetic heterogeneity in stage III cutaneous malignant melanoma. *Cancer Res*. 2018;78(20):5970–5979. doi:10.1158/0008-5472.CAN-18-0747 [PubMed: 30154148]
44. Said R, Guibert N, Oxnard GR, Tsimberidou AM. Circulating tumor DNA analysis in the era of precision oncology. *Oncotarget*. 2020;11(2):188–211. doi:10.18632/oncotarget.27418 [PubMed: 32010431]
45. Rector TS, Taylor BC, Wilt TJ. Chapter 12: systematic review of prognostic tests. *J Gen Intern Med*. 2012;27(suppl 1):S94–S101. doi:10.1007/s11606-011-1899-y [PubMed: 22648680]

46. McShane LM, Altman DG, Sauerbrei W, Taube SE, Gion M, Clark GM; Statistics Subcommittee of the NCI-EORTC Working Group on Cancer Diagnostics. Reporting recommendations for tumour marker prognostic studies (REMARK). *Br J Cancer*. 2005;93 (4):387–391. doi:10.1038/sj.bjc.6602678 [PubMed: 16106245]
47. Vickers AJ, Van Calster B, Steyerberg EW. Net benefit approaches to the evaluation of prediction models, molecular markers, and diagnostic tests. *BMJ*. 2016;352:i6. doi:10.1136/bmj.i6 [PubMed: 26810254]
48. Robertson C, Rose S, Kesselheim AS. Effect of financial relationships on the behaviors of health care professionals: a review of the evidence. *J Law Med Ethics*. 2012;40(3):452–466. doi:10.1111/j.1748-720X.2012.00678.x [PubMed: 23061573]
49. Mitchell AP, Rotter JS, Patel E, et al. Association between reimbursement incentives and physician practice in oncology: a systematic review. *JAMA Oncol*. 2019;5(6):893–899. doi:10.1001/jamaoncol.2018.6196 [PubMed: 30605222]

Key Points

Question

What evidence is needed for incorporation of prognostic gene expression profile (GEP) testing into clinical practice for patients with melanoma?

Findings

Findings of GEP testing are needed from large, representative patient cohorts with adequate clinical follow-up to enable statistical modeling and validation, and these findings must be compared with known relevant melanoma clinicopathologic factors. The currently published evidence is insufficient to establish that routine use of GEP testing provides additional clinical value for melanoma staging and prognostication beyond available clinicopathologic variables.

Meaning

Before GEP testing is routinely used, the clinical benefit to the management of patients with melanoma must be established through further clinical investigation.

Author Manuscript

Author Manuscript

Author Manuscript

Author Manuscript

Table 1.

Summary of External Validation Studies of the 31-GEP Test

Source	Type	Patients	Findings	Recurrences correctly classified ^d
Zager et al ²⁶	Retrospective	<ul style="list-style-type: none"> • 523 Patients; 16 centers • 50% Stage I • 18% Stage II • 32% Stage III • Metastatic event or >5 y event-free f/u 	<ul style="list-style-type: none"> • Class 1: 5-y 88% RFS, 93% DMFS • Class 2: 5-y 52% RFS (HR, 2.1; 95% CI, 1.3-3.4, $P = .003$)^b • 60% DMFS (HR, 2.7; 95% CI, 1.5-4.8; $P = .002$)^b 	<ul style="list-style-type: none"> • Stage I^c: 35% (6/17) • Stage II: 77% (30/39) • Stage III: 76% (63/83)
Greenhaw et al ²⁷	Retrospective	<ul style="list-style-type: none"> • 256 Patients; single center • 86% Stage I • 14% Stage II • Mean f/u, 1.9 y 	<ul style="list-style-type: none"> • Class 1: 5-y 93% MFS • Class 2: 5-y 69% MFS • Breslow thickness and ulceration independently associated with class 2 	<ul style="list-style-type: none"> • Stage I^d: 0% (0/1) • Stage II: 83% (10/12)
Hsueh et al ^{28,29}	Prospective	<ul style="list-style-type: none"> • 342 Patients; 11 centers • 67% Stage I • 22% Stage II • 11% Stage III • Metastatic event or median event-free f/u, 3.2 y 	<ul style="list-style-type: none"> • Class 1A: 3-y 96% RFS; 97% DMFS • Class 1B: 3-y 91% RFS; 93% DMFS • Class 2A: 3-y 80% RFS; 84% DMFS • Class 2B: 3-y 62% RFS (class 2B HR, 4.24; 95% CI, 1.80-10.01; $P = .001$)^e; 80% DMFS (class 2B HR, 3.21; 95% CI, 1.06-9.69; $P = .04$)^e 	<ul style="list-style-type: none"> • Stages I-III^f: 60% (26/43) • Stage-specific performance not reported
Keller et al ³⁰	Prospective	<ul style="list-style-type: none"> • 159 Patients; single center (partial overlap with Hsueh et al²⁸) • 60% Stage I • 25% Stage II • 14% Stage III • Median f/u, 3.5 y 	<ul style="list-style-type: none"> • Class 1: 3-y 97% RFS; 99% DMFS • Class 2: 3-y 47% RFS (HR, 9.2; 95% CI, 3.0-28.5; $P = .0001$)^g • 64% DMFS (HR, 19.0; 95% CI, 2.1-170.5; $P = .009$)^h 	<ul style="list-style-type: none"> • Stage I^f: 0% (0/3) • Stage II: 86% (12/14) • Stage III: 92% (11/12)
Podlipnik et al ³¹	Prospective	<ul style="list-style-type: none"> • 86 Patients; 5 centers • 72% Stages IB-IIA • 28% Stages IIB-IIC • Median f/u, 26 mo 	<ul style="list-style-type: none"> • Class 1: 100% no recurrence • Class 2: 79% no recurrence (HR, 18.9; 95% CI, 1.8-2549.8; $P = .01$)ⁱ 	<ul style="list-style-type: none"> • Stages IB-IIC^f: 100% (7/7) • Stage-specific performance not reported
Vetro et al ⁸	Prospective	<ul style="list-style-type: none"> • 838 Patients^j; multicenter • T1/T2 patients with SLNB (or eligible) • Cohort 1: 326 T1/T2 patients with SLNB (or eligible) • Cohort 2: 512 T1/T2 patients with SLNB (or eligible) 	<ul style="list-style-type: none"> • Cohort 1 • Class 1A: 6.2% SLNB positive • Class 2B: 8.3% SLNB positive • Cohort 2 • Class 1A: 6.3% SLNB positive • Class 2B: 24.5% SLNB positive 	NA

Abbreviations: DMFS, distant metastasis-free survival; f/u, follow-up; GEP, gene expression profile; HR, hazard ratio; MFS, metastasis-free survival; NA, not applicable; RFS, recurrence-free survival; SLNB, sentinel lymph node biopsy.

^aFor class 2 result identifying patients who developed disease recurrence.

^bMultivariate Cox regression analysis based on 244 cases with complete data for Breslow thickness, mitotic rate, ulceration, SLNB, and GEP result.

^cPatients diagnosed from 2000 to 2014; American Joint Committee on Cancer (AJCC) edition used for staging not reported.

Author Manuscript

Author Manuscript

Author Manuscript

Author Manuscript

^dPatients diagnosed from 2013 to 2018; AJCC edition used for staging not reported.

^eMultivariate Cox regression analysis based on 49 cases with complete data for Breslow thickness, mitotic rate, ulceration, SLNB, and GEP result.

^fAJCC 7th edition used for staging.

^gMultivariate Cox regression analysis based on 159 cases with complete data for age, Breslow thickness, ulceration, SLNB, and GEP result.

^hMultivariate Cox regression analysis based on 159 cases with complete data for Breslow thickness, ulceration, SLNB, and GEP result.

ⁱMultivariate Cox regression analysis based on 86 cases with complete data for age, AJCC stage, and GEP result.

^jNot all patients in the cohort underwent SLNB, and percentage who underwent SLNB was not reported.

Table 2.

Summary of Published Studies Using Other GEP Platforms

Source	GEP test	Patients	Findings	Test performance
Meves et al ¹³	CP-GEP	<ul style="list-style-type: none"> Development cohort: 360 patients 	<ul style="list-style-type: none"> CP model: AUC, 0.78 (95% CI, 0.73-0.83) CP-GEP model: AUC, 0.89 (95% CI, 0.85-0.93; $P < .001$); HR, 17.32 (95% CI, 8.02-37.41)^d 	<ul style="list-style-type: none"> Sensitivity: 89%^b Specificity: 76% (cutoff point 0.1)
		<ul style="list-style-type: none"> Validation cohort: 146 patients 4 Centers 50% Stage I 18% Stage II 32% Stage III 	<ul style="list-style-type: none"> CP model: AUC, 0.68 (95% CI, not reported) CP-GEP model: AUC, 0.93 (95% CI, 0.87-0.97)^c 	<ul style="list-style-type: none"> Sensitivity: 100% Specificity: 80% Stage-specific breakdown not reported^d
Mulder et al ^{14, e}	CP-GEP	<ul style="list-style-type: none"> 211 Patients; single center 24% T1 43% T2 33% T3 27.5% SLNB positive 	<ul style="list-style-type: none"> SLNB reduction rate: 40% 	<ul style="list-style-type: none"> T1-T3: NPV, 89%^b T1-T2: NPV, 91% Complete stage-specific breakdown not reported^f
Gambichler et al ^{37, e}	8-GEP	<ul style="list-style-type: none"> 203 Patients; 2 centers Stages IA-IIIIC 	<ul style="list-style-type: none"> High GRS: 5-y 70% RFS (HR, 2.40; 95% CI, 1.18-4.89; $P = .015$)^g SLNB positive: 5-y 65% RFS (HR, 2.11; 95% CI, 1.02-4.37; $P = .046$) 	<ul style="list-style-type: none"> GRS plus SLNB: sensitivity of relapse detection increased from 38.7% (SLNB alone) to 67.7% Stage-specific breakdown not reported^h
Amaral et al ³⁸	8-GEP	<ul style="list-style-type: none"> 245 Patients 48% Stage IIA 32% Stage IIB 20% Stage IIC >2-y f/u 	<ul style="list-style-type: none"> High GRS: 5-y 82% MSS (HR, 1.55; 95% CI, 1.13-2.13; $P = .006$)^g 	<ul style="list-style-type: none"> GRS found to add value to AJCCⁱ classification in defining both low-risk and high-risk patients

Abbreviations: AJCC, American Joint Committee on Cancer; AUC, area under the curve; CP, clinicopathologic, f/u, follow-up; GEP, gene expression profile; GRS, gene expression risk score; HR, hazard ratio; MSS, melanoma-specific survival; NPV, negative predictive value; RFS, recurrence-free survival; SLNB, sentinel lymph node biopsy.

^aMultivariate Cox regression analysis based on 360 cases with complete data for age, tumor ulceration, Breslow thickness, SLNB result, and molecular factors (4 genes in original GEP group).

^bFor predicting SLNB positivity.

^cMultivariate Cox regression analysis based on 146 cases with complete data for age, Breslow thickness, SLNB result, and molecular factors (8 genes, including 2 from original GEP group).

^dPatients diagnosed from 2000 to 2014; AJCC edition used for staging not reported.

^eOnly the abstract was available for review.

^fPatients diagnosed from 2007 to 2017; AJCC edition used for staging not reported.

^gMultivariate analysis that included tumor thickness, age, and GRS.

^hYears of diagnosis and AJCC edition used for staging were not reported.

Patients diagnosed from 2000 to 2016; AJCC edition used for staging not reported.

Author Manuscript

Author Manuscript

Author Manuscript

Author Manuscript