

Target Trial Emulation with Real-World Data to Determine the Population-Level Cost-Effectiveness of Multi-Gene Panel Sequencing for Advanced Melanoma

Emanuel Krebs¹, D Weymann¹, C Ho^{2,3}, A Weppler^{2,3}, I Bosdet^{4,5}, A Karsan^{4,6}, T Hanna^{7,8}, S Pollard¹, D Regier^{1,9}

Background

- No randomized control trials of multi-gene panel sequencing have been completed in advanced melanoma.
- This study determined the cost-effectiveness of multi-gene panel sequencing compared to single-gene BRAF testing for advanced melanoma.

Methods

- In British Columbia (BC), Canada, the public healthcare system reimbursed a multi-gene panel in September 2016.
- Applying randomized trial design principles, our population-based retrospective study emulated a hypothetical pragmatic trial comparing multi-gene panel sequencing to single-gene BRAF testing. We drew on comprehensive patient-level clinical and health administrative data for all BC adults with a panel-eligible advanced melanoma diagnosis between September 2016 and December 2018.
- To emulate random treatment assignment, we 1:1 matched multi-gene panel patients to contemporaneous single-gene tested controls using genetic algorithm-based matching, a machine learning approach that maximized balance on 15 baseline clinical and sociodemographic covariates.
- Following matching, we estimated mean three-year survival time and costs (public healthcare payer perspective; 2021 CAD) and calculated the incremental net monetary benefit (INMB) for life-years gained (LYG) at conventional willingness-to-pay thresholds using inverse probability of censoring weighted linear regression and nonparametric bootstrapping.
- In addition to an intention-to-treat (ITT) effect, we estimated the per-protocol (PP) effect of initiating treatment within 90 days of receiving test results accounting for potential post-randomization confounding using inverse probability of treatment weights. We also estimated overall survival using Weibull regression and Kaplan-Meier survival analysis.



This research was supported by Genome British Columbia/Genome Canada (G05CHS) and the Terry Fox Research Institute.

Access to data provided by the Data Steward(s) is subject to approval, but can be requested for research projects through the Data Steward(s) or their designated service providers. All inferences, opinions, and conclusions drawn in this publication are those of the authors, and do not reflect the opinions or policies of the Data Steward(s).