VIRTUAL ESMO congress 2020

1136P

Feasibility of linking the UK 100,000 genomes project and real-world evidence databases for a melanoma patient population

E. Scherrer[1], G.M. Hair[2], S. Mt-Isa[3], M. Pereira[4], G. Chan[4], I. Shui[2], P. Arumugam[4], M. Zarowiecki[4], K. Witkowska[4], T. Rahim[4], S. Turajlic[5], K.R. Litchfield[6], P. Lorigan[7], J. Larkin[5]

[1] Center for Observational and Real World Evidence, MSD, London, UK, [2] Center for Observational and Real-World Evidence, Merck Sharp & Dohme, Kenilworth, NJ, USA, [3] Biostatistics and Research Decision Sciences, MSD, London, UK, [4] Genomics England, Genomics England, London, UK, [5] Department of Medicine, The Royal Marsden Hospital NHS Foundation Trust, London, UK, [6] Swanton Lab, Francis Crick Institute, London, UK[7] Department of Medical Oncology, The Christie NHS Foundation Trust, Manchester, UK

Background

Linking genomic and real-world evidence (RWE) datasets has the potential to generate insights to inform clinical research or practice, including identifying biomarkers associated with treatment response. This study explored the feasibility of linking genomic and RWE data for melanoma patients within the UK 100,000 Genomes Project.

Methods

Anonymised whole-genome sequencing (WGS) data for patients with melanoma were linked, using unique identifiers, to corresponding records in RWE datasets maintained by the UK National Health Service and Public Health England (PHE). Examined characteristics included demographics, melanoma type and stage, and risk factors. The 20 most commonly mutated genes were determined for the categories of actionable genes, other cancer-related genes, and non-actionable and non-cancer-related genes. Treatment-related outcomes included time on treatment (to next line or death), and overall survival from the start of first line therapy.

Results

A total of 337 melanoma patients with WGS data were identified and linked to RWE records. While demographic data (e.g. age, gender, and race) were widely available, melanoma risk factors (e.g. UV exposure) and disease characteristics (e.g. tumour stage) were often missing. Treatment outcomes were difficult to estimate due to availability and discordant cut-off dates across WGS, treatment, and death datasets (April 2020, December 2017, and November 2019, respectively). Almost all patients (97%) had at least one mutated non-actionable but cancer-related gene. The most commonly mutated actionable genes were *BRAF* (42% of patients) — particularly to BRAF-V600E (30%) — and *NRAS* (28%). Among other cancer-related genes, *LRP1B* and *FAT4* were the most commonly mutated (40% and 37%).

Conclusions

Substantial and valuable WGS data are available for patients with melanoma within the 100,000 Genomes Project, and genomic characteristics appear consistent with other cohorts. However, RWE linkage is challenging, particularly as PHE clinical data are less current than the corresponding WGS data. Current efforts to secure further sources and increase data release frequency will improve feasibility.

Editorial acknowledgement

Adelphi Values PROVE.

Legal entity responsible for the study

Merck & Co., Inc., Kenilworth, NJ, USA.

Funding

Merck & Co., Inc., Kenilworth, NJ, USA.

Disclosure

E. Scherrer S. Mt-Isa: Full/Part-time employment: MSD, UK; Shareholder/Stockholder/Stock options: Merck & Co., Inc., Kenilworth, NJ, USA. G.M. Hair: Full/Part-time employment: Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA. M. Pereira, G. Chan, P. Arumugam, M. Zarowiecki, K. Witkowska, T. Rahim: Full/Part-time employment:

Genomics England. I. Shui: Full/Part-time employment: Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA. Shareholder/Stockholder/Stock options: Merck & Co., Inc., Kenilworth, NJ, USA; Shareholder/Stockholder/Stock options: Sanofi. S. Turajlic: Speaker Bureau/Expert testimony: Roche; Speaker Bureau/Expert testimony: AstraZeneca; Speaker Bureau/Expert testimony: Novartis; Speaker Bureau/Expert testimony: Ipsen. K.R. Litchfield: Speaker Bureau/Expert testimony: Roche Tissue Diagnostics. P. Lorigan: Advisory/Consultancy, Speaker Bureau/Expert testimony, Research grant/Funding (self), Research grant/Funding (institution), Travel/Accommodation/Expenses: Bristol-Myers Squibb; Advisory/Consultancy, Speaker Bureau/Expert testimony, Travel/Accommodation/Expenses: Merck Sharp & Dohme; Advisory/Consultancy, Speaker Bureau/Expert testimony: Pierre Fabre; Advisory/Consultancy, Speaker Bureau/Expert testimony: Novartis; Advisory/Consultancy, Speaker Bureau/Expert testimony: Amgen; Advisory/Consultancy, Speaker Bureau/Expert testimony: GlaxoSmithKline; Advisory/Consultancy, Speaker Bureau/Expert testimony: Roche; Advisory/Consultancy: Neracare/Melagenix. J. Larkin: Advisory/Consultancy, Research grant/Funding (institution): Bristol-Myers Squibb; Advisory/Consultancy, Research grant/Funding (institution): MSD; Research grant/Funding (institution): Roche; Advisory/Consultancy, Research grant/Funding (institution): Nektar Therapeutics; Research grant/Funding (institution): Covance; Research grant/Funding (institution): Immunocore; Research grant/Funding (institution): Pharmacyclics; Research grant/Funding (institution): Aveo; Advisory/Consultancy, Research grant/Funding (institution): Achilles Therapeutics; Advisory/Consultancy: AstraZeneca; Advisory/Consultancy: Boston Biomedical; Advisory/Consultancy: Eisai; Advisory/Consultancy: EUSA Pharma; Advisory/Consultancy: GlaxoSmithKline; Advisory/Consultancy: Ipsen; Advisory/Consultancy: Imugene; Advisory/Consultancy: Incyte; Advisory/Consultancy: iOnctura; Advisory/Consultancy: Kymab; Advisory/Consultancy: Merck Serono; Advisory/Consultancy: Novartis; Advisory/Consultancy: Pierre Fabre; Advisory/Consultancy, Research grant/Funding (institution): Pfizer; Advisory/Consultancy: Roche/Genentech; Advisory/Consultancy: Secarna; Advisory/Consultancy: Vitaccess.