Healthcare Innovations
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Implementation of precision oncology for breast cancer care in Brisbane: Q-IMPROvE

Amy McCart Reed[1], Therese McCurry[2], Peter Simpson[1], Po Inglis[2], Owen Ung[2,3], Kowsi Murrugappan[2,3], Nic Waddell[4], Cameron Snell[5], Natasha Woodward[6,7], Kathryn Middleton[6,8], Euan Walpole[8], Ken O'Byrne[8], Katharine Cuff[8], Vladimir Andelkovic[8], Kate Roberts[8], Karin Steinke[2], Gorane Santamaria[8], Nicole McCarthy[9], Helen Mar Fan[10], Lauren Kalinowski[1,11], Sunil Lakhani[1,12].

1 UQ Centre for Clinical Research, Faculty of Medicine, UQ; 2 RBWH; 3 UQ, Royal Brisbane Clinical Unit; 4 QIMR Berghofer MRI, genomiQa; 5 Mater Pathology; 6 Mater Misericordiae Ltd; 7 School of Medicine, Mater Clinical Unit, UQ; 8 Princess Alexandra Hospital; 9 Icon Cancer Care, Wesley Hospital; 10 Genetic Health Queensland; 11 Sullivan Nicolaides Pathology; 12 Pathology Queensland, RBWH.

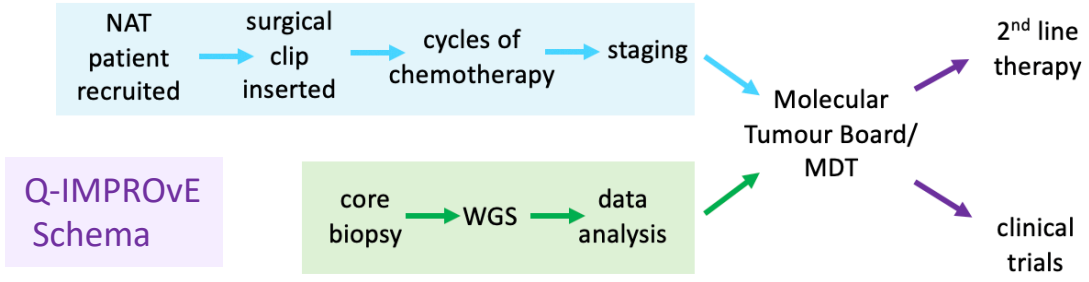
ABSTRACT

Purpose: The Q-IMPROvE (Qld IMplementation of PRecision Oncology in Breast Cancer) study has been undertaken to harness 'omics technology and national expertise to bring precision medicine to breast cancer care in Brisbane.

Method: We have joined together a team of researchers, pathologists, oncologists, surgeons and radiologists across Brisbane, underpinned by funding from Queensland Health through Queensland Genomics. Together, we have implemented a Whole Genome Sequencing (WGS) protocol in patients with high-grade breast cancer undergoing neoadjuvant therapy in an effort to ultimately improve second-line therapeutic decision-making and outcomes. Through our Molecular Tumour Board, we continue to evaluate the benefit of implementation of precision oncology in high-risk breast cancer patients by evaluating variant reports from genomiQa and assessing potential clinical intervention outcomes such as possible trials, pharmacogenomic implications and referrals to Genetics Health Queensland.

Results: We have established a pipeline from recruitment, through core biopsy collection (over three sites: RBWH, PAH, Mater), centralized sample processing at Pathology Queensland, sequencing and data analysis (genomiQa) and evaluation. We have established a regular Molecular Tumour Board meeting wherein clinicians present their patients, and the variant reports are discussed.

Conclusions: The ability of whole genome sequencing to identify changes predictive of specific therapeutic strategies, dose-modification of existing therapies (pharmacogenomics), as well as the potential to triage to clinical trials will be examined at the conclusion of this pilot study. We will determine whether there is benefit to the routine application of whole genome sequencing in the management of high-risk breast cancer patients.



RESULTS

- We have recruited 29 patients to the study
- 17 cases have been sequenced (tumour 180G and blood 90G)
- 7 cases have been discussed at the MTB, with the following outcomes discussed:
  - 5/7 cases have pathogenic somatic mutations (*TP53,PIK3CA, RB1, MAP2K4, TP53*)
  - 6/7 recorded a number of copy number variations (query pathogenic effects :*BRCA1/2, PTEN, MYC, CCND1*)
  - 2/7 recorded HRDetect score indicative of PARPi sensitivity
  - 3/7 recorded HRD score indicative of PARPi sensitivity
  - 0/7 recorded a tumour mutation burden >10 mut/MB which would indicate pembrolizumab sensitivity
- 2/7 have been identified as needing further intervention from Genetic Health Queensland – 1 to expedite an existing referral, and the second to confirm whether a *TP53* variant is somatic only, and that they are not Li Fraumeni.

CONCLUSIONS AND FUTURE DIRECTIONS

Our preliminary analysis shows the pipeline is feasible for implementation clinically and there are cases identified with the potential to be eligible for PARPi should they recur.
This study will be rolled out nationally with funding from MRFF Genomics Health Futures Mission.

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