

Population-Based Precision Cancer Screening—Letter 

Karina Standahl Olsen and Eiliv Lund

We read with interest the commentary by Marcus and colleagues, reporting on a 2015 symposium entitled "Precision Cancer Screening in the General Population: Evidence, Epidemiology, and Next Steps" (1). We would like to draw attention toward the use of functional genomics-based biomarkers measured in blood, which we propose to be one of the most feasible ways to approach precision screening for cancer in the general population.

As described by Marcus and colleagues, cancer risk is influenced by our genes and by what factors we are exposed to through our surroundings and lifestyle, but more than a decade of genome-wide association studies has shown that there are very few genes (SNPs) with big effects (2). However, revealing and exploiting the functional, molecular mechanisms that make up the continuum of events between exposures and diseases may prove more useful.

A major issue in screening for breast cancer using mammography is that of overdiagnosis, which is costly to society and a burden to the patient. In addition, some cancers are clinically detected between screenings, often with a more aggressive phenotype. An evaluation of the Norwegian mammographic

screening program indicated an overdiagnosis of about 15% to 25% (3), and a different but simultaneous test could represent an improvement.

In the Norwegian Women and Cancer Post-genome Cohort (4), we have explored the use of transcriptomic profiling for early detection of breast cancer, using blood samples collected from healthy women. We have shown that blood samples collected up to 5 years before diagnosis display different transcriptomic profiles than blood samples from women who stay cancer free (5). Cancers that are clinically detected between screenings and are diagnosed with positive node status display the most prominent profiles, and the profiles do fluctuate with time. We are currently planning a pilot to test our transcriptomic biomarkers in conjunction with the national mammography screening program.

Our results, as well as current technological developments, point to the potential of using blood-based functional genomics biomarkers in cancer screening. Such biomarkers may provide identification of persons at risk of disease, discrimination between true- and false-positive results from other tests, and differentiation of aggressive tumors from indolent ones. Hence, blood-based functional genomics biomarkers may ultimately provide the precision in precision screening.

Department of Community Medicine, Faculty of Health Sciences, UiT The Arctic University of Norway, Tromsø, Norway.

Corresponding Author: Karina Standahl Olsen, Faculty of Health Sciences, UiT The Arctic University of Norway, Tromsø N-9037, Norway. Phone: +47 77 64 48 18; Fax: +47 77 64 48 31; E-mail: karina.s.olsen@uit.no

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References

- Marcus PM, Pashayan N, Church TR, Doria-Rose VP, Gould MK, Hubbard RA, et al. Population-based precision cancer screening: a symposium on evidence, epidemiology, and next steps. *Cancer Epidemiol Biomarkers Prev* 2016;25:1449–55
- Freedman ML, Monteiro ANA, Gayther SA, Coetzee GA, Risch A, Plass C, et al. Principles for the post-GWAS functional characterization of cancer risk loci. *Nat Genet* 2011;43:513–8.
- Division for Society and Health. Research-based evaluation of the Norwegian Breast Cancer Screening Program. Oslo, Norway: The Research Council of Norway; 2015.
- Dumeaux V, Borresen-Dale A-L, Frantzen J-O, Kumle M, Kristensen V, Lund E. Gene expression analyses in breast cancer epidemiology: the Norwegian Women and Cancer postgenome cohort study. *Breast Cancer Res* 2008;10:R13.
- Lund E, Holden L, Bøvelstad H, Plancade S, Mode N, Günther C-C, et al. A new statistical method for curve group analysis of longitudinal gene expression data illustrated for breast cancer in the NOWAC postgenome cohort as a proof of principle. *BMC Med Res Methodol* 2016;16:28.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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