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Presentation Title: Individualized breast cancer risk prediction using the OncoVue® model.

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Accurately predicting individualized probability of developing breast cancer over time is clinically useful for early detection and prevention. We explored the potential of improving upon the widely utilized Gail model for predicting individual risk of developing breast cancer by incorporating genetic information. Study participants were recruited into a case-control study conducted in six distinct geographic regions of the United States. All participants completed a questionnaire concerning clinical and lifestyle information and their DNA was genotyped for 117 common, functional polymorphisms (mostly SNPs) in candidate genes likely to influence breast carcinogenesis. Data from analysis of these SNP variants and personal history information was utilized to develop a predictive model. Multivariate logistic regression was applied to a discovery set of 5022 Caucasian women (1671 breast cancer cases and 3351 cancer-free controls age-matched within one year) in order to build a model consisting of three integrated components employing 22 SNPs in 19 genes and several epidemiological risk factors (OncoVue®). An independent sample set consisting of 1193 Caucasian women (400 cases and 793 controls) was used to validate the model. In both the discovery and validation sets, analyses of positive likelihood ratios demonstrated significant improvement of the integrated genetic model compared to the Gail model alone. OncoVue® exhibited improvement in individualized risk prediction by more effectively identifying women that are truly at higher risk for breast cancer (previously diagnosed breast cancer cases). Thus, incorporating genetic information with epidemiological factors resulted in better performance in estimating individual breast cancer risk among women.