Short report

Sensitivity and specificity of loss of heterozygosity analysis for the classification of rare germline variants in BRCA1/2: results of the observational AGO-TR1 study (NCT02222883)

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ABSTRACT

Variant-specific loss of heterozygosity (LOH) analyses may be useful to classify BRCA1/2 germline variants of unknown significance (VUS). The sensitivity and specificity of this approach, however, remain unknown. We performed comparative next-generation sequencing analyses of the BRCA1/2 genes using blood-derived and tumour-derived DNA of 488 patients with ovarian cancer enrolled in the observational AGO-TR1 trial (NCT02222883). Overall, 94 pathogenic, 90 benign and 24 VUS were identified in the germline. A significantly increased variant fraction (VF) of a germline variant in the tumour indicates loss of the wild-type allele; a decreased VF indicates loss of the variant allele. We demonstrate that significantly increased VFs predict pathogenicity with high sensitivity (0.84, 95% CI 0.77 to 0.91), poor specificity (0.63, 95% CI 0.53 to 0.73) and poor positive predictive value (PPV; 0.71, 95% CI 0.62 to 0.79). Significantly decreased VFs predict benignity with low sensitivity (0.26, 95% CI 0.17 to 0.35), high specificity (1.0, 95% CI 0.96 to 1.00) and PPV (1.0, 95% CI 0.85 to 1.00). Variant classification based on significantly increased VFs results in an unacceptable proportion of false-positive results. A significantly decreased VF in the tumour may be exploited as a reliable predictor for benignity, with no false-negative result observed. When applying the latter approach, VUS identified in four patients can now be considered benign.

INTRODUCTION

In cancer genetics, individual risk stratification and the choice of targeted therapies are increasingly dependent on the germline mutation status in disease-associated genes such as BRCA1 (MIM: 113705) and BRCA2 (MIM: 600185). Thus, the unambiguous classification of germline variants identified in a routine diagnostic setting is vitally important for the clinical management of the individuals seeking advice. Criteria for BRCA1/2 germline variant classification were continuously standardised, in particular through the work of the Evidence-based Network for the Interpretation of Germline Mutant Alleles (ENIGMA), the International Agency for Research on Cancer (IARC) and the American College of Medical Genetics and Genomics (ACMG).1–4 While common BRCA1/2 germline variants with a minor allele frequency (MAF) ≥1% in the general population are considered benign by default, the classification of rare BRCA1/2 germline variants with a MAF <1% remains challenging, especially for those that cannot be predicted protein-truncating based on their mutation type. For intronic and missense variants, the multifactorial likelihood analysis demonstrated utility for quantitative assessment of variant pathogenicity, a model based on variant location, in silico prediction of variant effect, cosegregation, family cancer history, co-occurrence with a pathogenic variant in the same gene, tumour pathology and case-control information.5 The multifactorial likelihood analysis, however, requires input data that may not be available for all rare BRCA1/2 germline variants.

In tumours with a hereditary disease cause, it is generally suggested that the heterozygous germline inactivation of a predisposition gene may be accompanied by a somatic inactivation of the wild-type allele by another deleterious variant, loss of the wild-type allele or promoter methylation.5 In 473 patients with ovarian cancer (OC (MIM: 167 000)) enrolled in the observational AGO-TR1 trial, we demonstrated that pathogenic germline variants in the BRCA1/2 genes very rarely associate with deleterious somatic variants or promoter methylation.5 In OC, more than 80% of the pathogenic BRCA1/2 germline variants showed significantly increased proportion of reads that support the variant allele (variant allele fractions (VFs)) in the tumour-derived versus blood-derived DNA, indicating loss of the wild-type alleles.5,6,7,8 Based on these findings, it was suggested that loss of heterozygosity (LOH) analyses might be useful to classify rare germline
variants in the BRCA1/2 genes.\textsuperscript{9,10} For rare germline variants in (candidate) cancer predisposition genes showing significantly increased VFs in the tumour, a potential role in cancer susceptibility was frequently suggested, as for example in the analyses of 429 patients with OC included in The Cancer Genome Atlas (TCGA) project.\textsuperscript{7} However, sensitivity along with specificity of 429 patients with OC included in The Cancer Genome Atlas increased VFs in the tumour, a potential role in cancer susceptibility genes showing significantly decreased VFs, were computed for each rare germline variant. Fisher’s exact test was applied to assess the significance level of deviating proportions of reads showing a variant allele between blood and tumour sample, with p values c0.05 after correction for multiple testing using the Benjamini-Hochberg approach\textsuperscript{13} considered significant. A significantly increased VF of a variant in the tumour suggests loss of the wild-type allele. A significantly decreased VF of a variant in the tumour suggests loss of the variant allele. Statistical analyses were performed using SPSS Statistics V25 and the epiR-Package under R V3.6.2.

Next-generation sequencing (NGS)
Targeted NGS of blood and tumour samples of 496 patients was performed using a customised gene panel covering the coding regions and exon-flanking sequences (±15 nt) of the BRCA1 (NM_007294.3) and BRCA2 (NM_000059.3) genes.\textsuperscript{8} The hybridisation-capture-based NGS method (Agilent SureSelect XT protocol optimised for 200 ng of genomic DNA) was suitable for the analysis of DNA derived from either blood or FFPE tumour samples. Sequencing was performed on a HiSeq4000 device (Illuminia, San Diego, California, USA). NGS analyses with a mean read coverage of at least 100× were considered successful. NGS data derived from both blood and corresponding FFPE tumour samples of 488 individuals achieved this threshold. The clinical characteristics of the 488 individuals were described in the online supplemental table 1. For the 488 individuals included, the mean read coverage was 455× (range 171×–882×) for NGS of blood-derived DNA and 570× (range 110×–1802×) for tumour-derived DNA. Bioinformatic analyses, including variant calling, were carried out using the VARBANK V2.10–2.24 pipeline of the Cologne Center for Genomics and the DDM1 platform (Sophia Genetics, Saint-Sulpice, Switzerland).

Germline variant classification
We employed criteria based on the ENIGMA and ACMG Guidelines for variant classification.\textsuperscript{4} Rare variants were defined as variants with a MAF <1% in large outbred control reference groups. Common variants with a MAF above this threshold were generally considered benign and excluded from this investigation. All rare variants in splice regions and non-synonymous single-nucleotide/indel variants were included in this investigation. CNVs were not considered. To determine MAFs, we used Exome Aggregation Consortium (ExAC)\textsuperscript{15} data of individuals of European, non-Finnish ancestry, excluding samples from TCGA. All rare BRCA1/2 germline variants were classified using a five-tier variant classification system as proposed by the IARC Unclassified Genetic Variants Working Group,\textsuperscript{12} namely, pathogenic=class 5, likely pathogenic=class 4, variant of uncertain significance (VUS)=class 3, likely benign=class 2 and benign=class 1. For reasons of clarity, class 4/5 are referred to as pathogenic variants and class 1/2 as benign variants in the following.

RESULTS
Germline analysis revealed 208 rare variants in 181 of the 488 patients (37.1%). One hundred and fifty-seven patients carried one (32.2%), 21 carried two (4.3%) and 3 patients carried three rare germline variants (0.6%) (online supplemental figure 1A). Of the 208 rare variants, 94 were pathogenic (class 4/5), 90 were benign (class 1/2) and 24 were of unknown significance (VUS, class 3). The combined BRCA1/2 genotypes of the 181 patients with rare variants are illustrated in online supplemental figure 1B). All rare variants were listed in the online supplemental table 2).

All rare germline variants were also detected in the corresponding tumour samples. Of the 94 pathogenic germline variants, 79 (84.0%) showed significantly increased VF in the tumour suggesting loss of the wild-type allele, with fold changes ranging from 1.15 to 2.05 (figure 1, online supplemental table 2). The VF differences of the remaining 15 class 4/5 variants (16%) were statistically not significant with fold changes ranging from 0.85 to 1.13. Of note, none of the class 4/5 variants showed a significantly decreased VF in the tumour. Of the 90 class 1/2 variants, 33 (36.7%) showed significantly increased VFs in the tumour with fold changes ranging from 1.22 to 2.02, 34 showed non-significant differences (37.8%, fold changes ranging from 0.87 to 1.16) and for the remaining 23 variants, VFs were significantly decreased in tumour samples (25.6%, fold changes ranging from 0.06 to 0.84) (figure 1, online supplemental table 2).

Variant classification based on significantly increased VFs shows a high sensitivity of 0.84 (95% CI 0.77 to 0.91), but a poor specificity of 0.63 (95% CI 0.53 to 0.73) and a poor positive predictive value (PPV) of 0.71 (95% CI 0.62 to 0.79). For this approach, the positive likelihood ratio (LR+) for pathogenicity is 2.29 (95% CI 1.72 to 3.05). Briefly, variant classification based on significantly increased VFs is hampered by the random distribution of VFs observed for benign variants. At least in a routine diagnostic setting, classification of rare BRCA1/2
germline variants may not be based on significantly increased VFs due to an unacceptable proportion of false-positive results.

As an alternative approach, a significantly decreased VF of a variant in the tumour, suggesting loss of the variant allele, may be useful to classify a rare BRCA1/2 germline variant as benign. Significantly decreased VFs were specific for benign variants and were not observed for pathogenic germline variants (figure 1).

Of the benign variants observed in 90 patients, 17 were recurrent and found at least twice in the sample set. For most of the recurrent benign variants, we found a high variability of fold changes, occasionally ranging from a significant decrease to a significant increase (figure 2). Classification of benign BRCA1/2 germline variants based on significantly decreased VFs results in a low sensitivity of 0.26 (95% CI 0.17 to 0.35) but a high specificity of 1.0 (95% CI 0.96 to 1.00) and a high PPV of 1.0 (95% CI 0.85 to 1.00). For this approach, the LR+ for benignity was 49.07 (95% CI 3.02 to 795.93) after Haldane-Anscombe correction (online supplemental table 3). A significantly decreased VF of a variant in the tumour may be exploited as a reliable predictor for benignity, with no false-negative result observed. This also holds true when analyses were performed for both genes separately (figure 1, online supplemental table 3). When applying this approach to the 24 VUS identified in our study sample, three distinct VUS found in four patients, that is, BRCA1 p.(Val525Ile), BRCA1 p.(Asp1152Asn) and BRCA2 p.(Lys2498del), may be considered benign (figure 2).

DISCUSSION

It was controversially discussed whether the results of LOH analyses may be useful for the classification of rare BRCA1/2 germline variants.7–10 14–18 Information from LOH analyses has not been implemented in the current ENIGMA variant classification system1 19 based on the previously published data16 suggesting that LOH analyses are not sufficiently reliable. Using paired analyses of blood-derived and tumour-derived DNA, we demonstrated that rare germline variants in the BRCA1/2 genes might be classified benign based on significantly decreased VFs in the tumour. This approach reached a specificity of 1.0 (95% CI 0.96 to 1.00), a PPV of 1.0 (95% CI 0.85 to 1.00) and a LR+ of 49.07 (95% CI 3.02 to 795.93). Given the fact that changes in VFs of benign variants occur randomly (figure 2), this approach shows a limited sensitivity of only 0.26 (95% CI 0.17 to 0.36). As of March 2020, more than 6,100 distinct BRCA1/2 germline VUS were listed in the ClinVar database, indicating the need for additional sources for the classification of BRCA1/2 germline variants. We suggest that large-scale comparative germline/tumour NGS analyses with sufficient read depths may significantly reduce the number of VUS, especially for VUS for which data regarding cosegregation, family cancer history, co-occurrence with a pathogenic variant in the same gene and case-control information are not available.1

Limitations of the study

In the overall study sample of patients with OC enrolled in the observational AGO-TR1 study, pathogenic germline mutations in non-BRCA1/2 OC predisposition genes such as RAD51C/D and BRIP1 were observed. However, the prevalence of pathogenic germline mutations in these genes was too low to perform meaningful calculations. Larger studies are required to quantify the sensitivity and the specificity of LOH analyses for the classification of rare germline mutations in additional OC predisposition genes. Moreover, this investigation was focused on patients with OC and FFPE samples with a high tumour content. It remains elusive to which extent our approach may be transferred to breast tumour analyses that are usually associated with lower BRCA1/2 LOH rates20 and probably lower tumour contents in FFPE samples.

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Contributors

JH and PH contributed equally to this work; and study concept and design: JH, PR, RS and EH; acquisition, analysis and interpretation of data: all authors; drafting the manuscript: JH, CE and EH; critical revision of the manuscript for important intellectual content: all authors; accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved: all authors; final approval of the submitted manuscript: all authors; obtained funding: PH; study supervision: PH, RS and EH; administrative, technical or material support: all authors.

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Competing interests

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Supplemental material

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Cancer genetics


