NLRC5 germline variants as potential pharmacogenomic markers for immune checkpoint inhibitors

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I read with interest the recent report by Caulfield et al. In this elegant piece of work, the authors performed RNA-seq and whole exome sequencing (WES) on tumors from a small cohort of subjects that presented insulin-dependent diabetes after treatment by immune checkpoint inhibitors (ICIs), which is a rare but life-altering immune-related adverse effect (irAE) with undetermined underlying mechanisms. Their RNA-seq analyses suggested possible roles of tumorous ORM1, PLG, and G6PC gene expression, and their WES data highlighted a missense germline variant of the NLRC5 gene, the NLRC5 Pro191Leu (hg38, chr16:57025515C>T; rs74439742 in the dbSNP database), which was significantly enriched in patients that developed ICI-induced diabetes mellitus (ICI-DM). These findings, though based on data from a very limited number of patients (n=13), provided interesting clues about the possible mechanisms and biomarkers of ICI-DM.1

Despite the striking over-representation of the NLRC5 Pro191Leu variant in the ICI-DM patients compared with the general population (of European ancestry), this protein-coding mutation itself is more likely to be a non-causal marker given its predicted benign effect by multiple tools including Polyphen and SIFT, as shown in the gnomAD database (https://www.gnomad-sg.org). Nevertheless, this does not necessarily mean no causal role of the NLRC5 gene in ICI-DM, for the following reasons. First, as also discussed in Caulfield et al, the NLRC5 gene has been experimentally shown to play an important role in the development of IFNα-induced autoimmunity against pancreatic β cells, through not only transcriptional activation of HLA class I and antigen presentation-related genes, but also generation of β cell neoantigens by cross-talk with alternative splicing.1 Second, although the NLRC5 Pro191Leu amino acid change may confer non-significant impact on the function of NLRC5 protein, this variant is indeed significantly associated with the NLRC5 gene expression level in blood, as shown in the eQTLGen database (https://eqtlgen.org; rs74439742 T vs C, n=13100, Z-score=−5.1, p=2.8×10−7, FDR=8.6×10−4). This cis-eQTL relationship suggest a potential causal role of NLRC5 gene in the development of ICI-DM, though further studies are needed for validation. On the other hand, no NLRC5 genetic variants have been linked with type 1 diabetes (T1DM) at genomewide significance in GWAS studies so far, per queries in the GWAS Catalog (https://www.ebi.ac.uk/gwas) and IEU-GWAS (https://gwas.mrcieu.ac.uk) databases, which is consistent with the report by Caulfield et al that no significant difference in the allele-frequency of NLRC5 Pro191Leu was noted between the T1DM subjects and the controls in previously published T1DM datasets and the Type 1 Diabetes Genetics Consortium database.1 However, interestingly, summary statistics-based Mendelian randomization (SMR) analyses suggest a possible cause-and-effect relationship between NLRC5 and T1DM, as provided in the eQTLGen database (β_SMR=−0.40, P_SMR=3.3×10−5).

NLRC5, also known as MHC class I transactivator, has been widely recognized as a key transcriptional activator of MHC class I and antigen presentation genes. It has recently been shown to play crucial roles in cancer immune surveillance, and a recent study by the Kobayashi lab suggested the translational significance of NLRC5 gene expression in ICI-based immunotherapy in melanoma patients.2 Interestingly, strong coexpression is observed between NLRC5 and PDCD1/C2744/CTLA4 in tumors of a number of ICI-relevant cancer types, including melanoma, lung cancer, bladder cancer, breast cancer, colorectal cancer, and head-and-neck cancer, among others, per queries for TCGA

References:
data in the cBioPortal database (https://www.cbioportal.org; eg, TCGA BLCA, n=404: NLRC5 with PDCD1, Spearman’s r=0.78, p=2.9×10^{-34}; NLRC5 with CD274, Spearman’s r=0.65, p=2.2×10^{-48}; NLRC5 with CTLA4, Spearman’s r=0.76, p=6.1×10^{-31}). Considering the contributing effects exerted by genetic variants in anticancer immunity and ICI-response, NLRC5 variants could be potential biomarkers for ICI responsiveness and efficacy, similar as the previously identified marker SNPs associated with CTLA4, PDCD1, and CD274 genes.3 4 On the other hand, per query in the GTEx database (https://www.gtexportal.org/), although immune-related tissue types present the highest expression level of NLRC5 (ie, spleen and whole blood, median TPM, 63.98 and 35.93, respectively), it is also widely expressed in many other tissue types, and at a high level in lung, small intestine, and skin (median TPM, 24.63, 22.05, and 19.15, respectively). Therefore, if NLRC5 does play a role in irAE and with possible effects conferred by its germline variants, presumably ICI-DM is not the only form of manifestation. Indeed, as reviewed by Wang et al, NLRC5 is also implicated in a number of immune-related disorders, such as rheumatoid arthritis, inflammatory liver injury, and fibrosis in the liver, heart, and kidney.5

Taken together, current data by Caulfield et al and others suggest possible implications of NLRC5 in ICI-based cancer immunotherapy, with regard to both clinical efficacy and adverse effects. Further studies are warranted to test and validate the clinical utility of NLRC5 variants as potential pharmacogenomic markers for ICI-treatment efficacy and safety. Common germline polymorphisms located in NLRC5-related regulatory regions and/or demonstrate significant correlation with NLRC5 gene expression or methylation could be candidates of interest.

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