Family history of cancer correlates with improved outcome from immunotherapy in NSCLC independent of somatic DNA damage response gene status

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Background

Among the few known underlying mechanisms of inherited cancer 728 and 652 patients were included in the pembrolizumab and Overall, 118 patients were included in the parallel DDR genes cohort, of susceptibility, germline DNA damage response and repair (DDR) genes chemotherapy cohort, respectively. We performed a perfect random case- which 20 FHC-high (16.9%) and 98 FHC-low/negative (83.1%). Relevant mutations are the most frequently involved. Acknowledging the immune control matching between the two cohorts and 607 patients from each baseline clinic-pathologic characteristics and the DDR genes profile data sensitive phenotype of cancer related to DDR genes defects, we cohort were randomly paired on the basis of the FHC, age (< 70 vs. \geq 70 are summarized in the OncoPrint provided (Figure 2). The prevalence of at previously showed that high burden of family history of cancer (FHC). years old), ECOG-PS (0-1 vs \geq 2), and burden of disease (\geq 2 vs < two least one DDR genes somatic mutations was 20% (4/20) and 24.5% namely FHC-high, was independently associated with prolonged overall metastatic sites). As compared to FHC-low/negative patients, FHC high (24/74) for FHC-low/negative and FHC-high patients, respectively (p = survival (OS) and progression free survival (PFS) to programmed deathwere confirmed to have a significantly longer OS (HR=0.67 [95%CI: 0.46- 0.6684). The median TMB for FHC-high was 6 Mut/Mb (range: 1 – 18), 1/programmed death ligand-1 (PD-1/PD-L1) checkpoint inhibitors. 0.95], p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281; Figure 1A), a significantly longer PFS (HR=0.65 whilst for the FHC-low/negative was 7.6 Mut/Mb (range: 0 - 42.8) (p = 0.0281). [95%CI: 0.48-0.89]; p = 0.0074; Figure 1B) and a higher disease control 0.6018) and no association between FHC and PD-L1 tumour expression **Patients and Methods** rate (DCR) (86.4 vs 67.5, p = 0.0096; Figure 1C), within the was reported. Figure 2 We present the outcomes analysis according to FHC from two large pembrolizumab cohort. On the contrary, no significant associations were multicenter cohorts of patients with metastatic non-small cell lung cancer found between FHC and OS (HR = 0.75 [95%CI: 0.54 - 1.04], p = 0.0866; (NSCLC) receiving either first-line pembrolizumab (PD-L1 expression \geq Figure 1D), PFS (HR = 1.06 [95%CI: 0.77 - 1.46], p = 0.7039; Figure 1E), 50%) or first-line chemotherapy. Patients were categorized FHC-high (in and DCR (69.7% vs 63.1%, p = 0.4475; Figure 1F), within the case of at least one cancer diagnosis in both straight and collateral family chemotherapy cohort. FHC was not associated with objective response rate lines) and FHC-low/negative. The role of FHC was validated through a (ORR) in either of the matched cohorts.

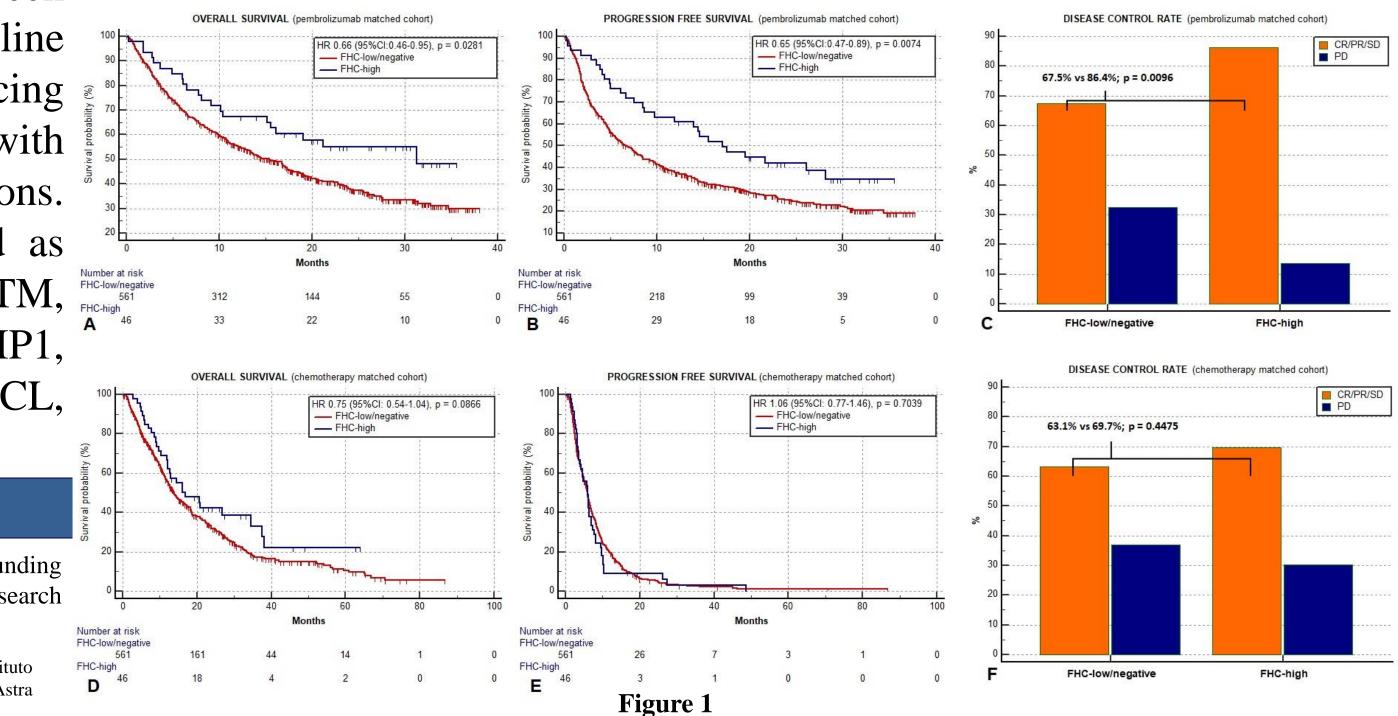
random case-control matching. To explore the association between somatic DDR genes alteration and FHC, we gathered relevant baseline clinic-pathologic information and targeted DNA tumour sequencing (FoundationOne CDx assay), from a parallel cohort of patients with NSCLC treated with various regimens at 4 of the participating institutions. The panel of 53 DDR genes defined by Ricciuti et al. was used as reference, identifying 24 genes of interest (MLH1, MSH6, PMS2, ATM, ^{FHC-low/negative} ATR, CHEK1, CHEK2, BAP1, BARD1, BRCA1, BRCA2, BRIP1, PALB2, RAD51, RAD51C, RAD52, FANCA, FANCC, FANCG, FANCL, POLD1, POLE, ERCC4, XRCC2).

Statements

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Results



Results

EGFR	
ALK	
ROS1	
PD-L1_expression	
TMB_class	
MLH1	1.7%
MSH6	0.8%
PMS2	0.8%
ATM	5%
ATR	3%
CHEK2	2.5%
BAP1	1.7%
BRCA2	4%
PALB2	3%
RAD51C	0.8%
FANCA	2.5%
POLD1	0.8%
ERCC4	0.8%
FHC status HIGH Genetic Alteration	LOW/NEGATIVE Missense Mutation Other Mutation Promoter Mutation Truncating Mutation No alterations
Genetic Alteration	Missense Mutation Other Mutation Promoter Mutation Truncating Mutation No alterations
	Negative Positive PD-L1 expression ≥50% 1-49% Neg NA TMB clas

Conclusions

FHC-high status identifies NSCLC patients with improved outcomes to pembrolizumab but not chemotherapy, suggesting its role as a surrogate marker for immunotherapy. Somatic DDR genes alterations are not associated with FHC and further prospective investigations with broader germline testing are warranted.

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High	Low	NA
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