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Original Research

Comprehensive analysis of cancers of unknown primary for the biomarkers of response to immune checkpoint blockade therapy

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KEYWORDS

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Abstract Background: Cancer of unknown primary (CUP) accounts for approximately 3% of all malignancies. Avoiding immune destruction is a major cancer characteristic and therapies aimed at immune checkpoint blockade are in use for several specific cancer types. A comprehensive survey of predictive biomarkers to immune checkpoint blockade in CUP were explored in this study.

Methods: About 389 cases of CUP were analysed for mutations in 592 genes and 52 gene fusions using a massively parallel DNA sequencing platform (next-generation sequencing [NGS]). Total mutational load (TML) and microsatellite instability (MSI) were calculated from NGS data. PD-L1 expression was explored using immunohistochemistry (with 5% cutoff value).

Results: High TML was seen in 11.8% (46/389) of tumours. MSI-high (MSI-H) was detected in 7/384 (1.8%) of tumours. Tumour PD-L1 expression was detected in 80/362 CUP (22%). A small proportion of CUP cases harboured genetic alterations of negative predictive biomarkers to immune checkpoint inhibitors (predictors to hyperprogression) including *MDM2* gene amplification (2%) and loss of function *JAK2* gene mutations (1%). Amplifications of *CD274* (*PD-L1*) and *PDCD1LG2* (*PD-L2*) genes were also rare (1.4% and 0.8%, respectively). The most frequently mutated genes were *TP53* (54%), *KRAS* (22%), *ARID1A* (13%), *PIK3CA* (9%), *CDKN2A* (8%), *SMARCA4* (7%) and *PBRM1*, *STK11*, *APC*, *RBI* (5%, respectively).

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Conclusions: Using a multiplex testing approach, 28% of CUP carried one or more predictive biomarkers (MSI-H, PD-L1 and/or TML-H) to the immune checkpoint blockade, providing a novel option for treatment in patients with CUP.

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1. Introduction

Cancer of unknown primary (CUP) are a heterogeneous group comprising approximately 3–5% of all malignancies and are associated with poor prognosis [1–3]. Usually, extensive tumour sample investigations are performed to identify the presumed tissue of origin [3–5], but in true CUP, by definition, the diagnosis of the primary cancer cannot be verified. Recently, we [6] and others [7–10] have identified numerous genetic alterations in common cancer pathways [11] in CUP, providing an opportunity to administer pathway-specific (targeted) therapies in CUP. All these studies identified at least one clinically targetable genetic alteration in CUP. In contrast to the previous studies, we utilised an extended next-generation sequencing (NGS) panel composed of 592 genes and used Archer Panel to explore the gene fusions.

In the last couple of years, a dramatic improvement in advanced cancers therapy has been achieved with immune checkpoint blockade. To date, five immune checkpoint inhibitors (pembrolizumab, nivolumab, atezolizumab, avelumab and durvalumab) targeting either programmed death 1 (PD-1) or its ligand (PD-L1) have received the US Food and Drug Administration (FDA) approval (<https://www.fda.gov/>) and caused a paradigm shift in treatment of various cancer types including melanoma, non-small cell lung carcinoma, renal cell carcinoma, advanced bladder carcinoma, Merkel cell carcinoma, gastroesophageal junction adenocarcinoma and classical Hodgkin lymphoma [12–23]. Several predictive biomarkers for immune checkpoint inhibitors have been proposed (PD-L1 status in tumour and inflammatory cells, tumour mutational load and microsatellite instability [MSI] status) and some have achieved companion diagnostics status (e.g. PD-L1 immunohistochemistry in certain cancer lineages and MSI status in all tumours regardless of a lineage). In addition, recent breakthrough studies revealed several predictors of hyperprogression after the therapy with the immune checkpoint inhibitors (e.g. *JAK1/2*, *MDM2* and *EGFR*) [24–26]. A comprehensive molecular profiling (biomarkers) of CUP with regard to immune checkpoint inhibitors has not been conducted so far. Therefore, we decided to explore a comprehensive survey of predictive biomarkers to immune checkpoint inhibitors in a large cohort of CUP profiled at a single institution.

2. Results

2.1. Patients and histopathologic characteristics

Three hundred eighty-nine patients (53% female and 47% male) were included in the study cohort. The average patient's age was 62.7 years. No clinically recognised primary tumour site was identified in any of the patients tested (Table 1) [3].

Histologically, CUP were classified as adenocarcinomas ($n = 175$, 45%), carcinomas not otherwise specified ($n = 120$, 31%), squamous cell carcinomas ($n = 30$, 8%) or other subtypes ($n = 64$, 16%) (Table 1). Referring laboratories' immunohistochemical analyses for markers of tissue of origin (e.g. wide-spectrum cytokeratins [AE1/AE3, Cam5.2], CK7, CK20, PSA, oestrogen receptor, progesterone receptor, CDX2, TTF1, napsin-A, thyroglobulin, calcitonin, neuroendocrine markers: NSE, chromogranin, synaptophysin) were non-conclusive in all analysed cases (i.e. more than one possible site of origin was considered) [3]. Board-certified pathologists reviewed all cases and selected appropriate slides for molecular profiling.

2.2. Predictive biomarkers to immune checkpoint inhibitors

Fig. 1 (Venn diagram) summarises total mutational load (TML), PD-L1 status and MSI status for the subgroup of CUP tumours that had PD-L1, MSI and TML information available ($n = 362$).

In the complete cohort of 389 tumour analysed, TML-high was seen in 11.8% (46/389) of CUPs, similar to the rate observed in common cancers profiled at Caris (Non-small cell lung cancer (NSCLC), bladder carcinoma, Fig. 3). In contrast to other common cancers, MSI-high (MSI-H) rate was detected in 7/389 (1.8%) of CUP cases (Fig. 3). Subsequent immunohistochemistry (IHC) analysis of MSI-H cases showed combined loss of expression of MSH2 and MSH6 or MLH1 and PMS2 mismatch repair proteins in five cases and isolated PMS2 loss in one case, while one case was not evaluable (Table 2). In addition, 12 microsatellite stable cases by NGS were also confirmed by IHC as mismatch repair proficient (no loss of expression of mismatch repair proteins).

Expression of PD-L1 (on $\geq 5\%$ cancer cells) was seen in 22.5% (82/365) of tumours, while the presence of PD-1

Table 1
Demographic and pathologic characteristics of the CUP cohort.

Gender	N (%)
Male	186 (47%)
Female	203 (53%)
Age	Years
Average (range)	62.7 (18–90)
Histology	N
Adenocarcinoma	175 (45%)
Carcinoma NOS	120 (31%)
Squamous cell carcinoma	30 (8%)
NSCC	15 (3.8%)
Mucinous carcinoma	14 (3.6%)
Neuroendocrine carcinoma	9 (2.3%)
Sarcomatoid and spindle cell carcinoma	8 (2%)
Carcinosarcoma	2 (0.5%)
Pleomorphic carcinoma	2 (0.5%)
Serous carcinoma	2 (0.5%)
Signet ring carcinoma	2 (0.5%)
Other rare cancer subtypes	10 (2.5%)
Total	389

ACC = adenoid cystic carcinoma; NOS = not otherwise specified carcinoma; NSCC = non-small cell carcinoma; SCC = small cell carcinoma; TCC = transitional cell carcinoma.

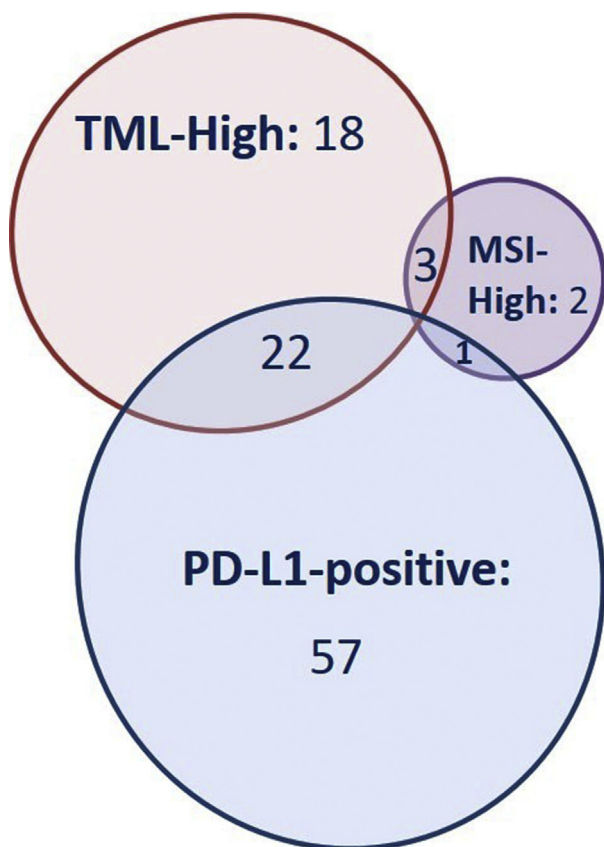


Fig. 1. Venn diagram showing the relationship between TML-H, MSI-H and PD-L1+ CUP cases. Three hundred sixty-two cases were analysed for all three predictive biomarkers: 103 cases had at least one of the three predictive biomarkers to immune checkpoint blockade and 259 CUP cases were with all three biomarkers negative result (TML-low/MSS/PD-L1-negative cases).

expressing tumour infiltrating lymphocytes was seen in 58.7% (37/63) of cases.

2.3. Individual gene alterations detected by NGS

Fig. 2 and Supplemental Table 1 illustrate detected gene alteration frequencies in the entire cohort.

A total of 70 different genes were found with pathogenic and presumed pathogenic mutations ranging in incidence from 0.3% to 54%; the most frequently mutated gene was *TP53* (54%), followed by *KRAS* (22%), *ARID1A* (13%), *PIK3CA* (9%), *CDKN2A* (8%), *SMARCA4* (7%), *PBRM1*, *STK11*, *APC*, *RBI* (5%, respectively) and *PTEN*, *BRAF*, *NF2*, *BAP1* (4%, respectively). *ERBB2* (*HER2*) was mutated in 1.5% of cases while *BRCA1* and *BRCA2* were each mutated in 1%.

Gene amplifications of *CCND1* (5%), *FGF3*, *FGF4*, *FGF19* (3%, respectively; all located on chromosome 11q13.3 near *CCND1*), *ERBB2*, *MYC* (3%, respectively) were most frequent, while *AKT2*, *MCL1*, *KRAS*, *CCNE1* and *MDM2* were each amplified in ~2% of the cases. Of note, amplifications of *CD274* (*PD-L1*), *PDCD1LG2* (*PD-L2*) and *JAK2* (all located at chromosome 9p24.1) were rare (1.4, 0.8 and 1.1%, respectively).

Targetable gene fusions were identified in five cases including two *FGFR2* fusions, two *RET* fusions and one *RAF1* fusion. Tumours in which fusions were identified as cancer driver events carried a significantly lower TML (average 6/Mb) than the complete cohort (11.0/Mb, $p < 0.001$).

3. Discussion

Numerous studies have identified potential predictive biomarkers to drug therapies in cancers of various, well-defined lineages [27–29]. Recent work from The Cancer Genome Atlas demonstrated that the tissue of origin of a particular cancer may be much less relevant to prognosis and response to therapy than identification of causative mutations and optimal predictive biomarkers [30,31]. Along those observations, several CUP cases that harboured activating *EGFR* mutations were successfully treated with *EGFR* inhibitors (e.g. gefitinib) [6,32,33]. Also, CUP cases harbouring potentially actionable *ERBB2* and *EGFR* gene copy alterations benefited from targeted treatments [34,35]. In our present study, we failed to detect new cases with actionable *EGFR* gene alterations, so CUP remains a rare candidate for *EGFR* inhibitors.

Recent advances in cancer treatment with immune checkpoint inhibitors significantly improved outcomes in several different cancer lineages (e.g. NSCLC, melanoma, urothelial carcinoma). Very limited data are available regarding the treatment of CUP patients with

Table 2
Molecular profile of the 7 CUP cases with MSI-H status.

Case	MSI-NGS	MMR-SEQ (mutation)	IHC MMRP	Other NGS	TML	PD-L1
#1	MSI-H	Wild type	No loss (MSH6 fail?)	<i>BRAF V600E</i>	10	Negative
#2	MSI-H	Wild type	MLH1/PMS2 loss	<i>CTNNB1</i>	11	Negative
#3	MSI-H	<i>MSH2</i> (R621X), <i>MSH6</i> (F1088fs)	MSH2/MSH6 loss	<i>KRAS G12D</i>	16	Not performed
#4	MSI-H	Wild type	MLH1/PMS2 loss	<i>BRAF V600E</i>	66	Negative
#5	MSI-H	<i>MSH6</i> (F1088fs/S616F), <i>PMS2</i> mutation result unknown	Isolated PMS2 loss	<i>KRAS A59T</i>	48	Negative
#6	MSI-H	Wild type	MLH1/PMS2 loss	<i>KRAS G12V</i>	9	Positive (5%, 3+)
#7	MSI-H	<i>MSH2</i> (D680X 49)	Loss of MSH2/MSH6	<i>MSH2 D603V</i>	31	Negative

IHC = immunohistochemistry; MMRP = mismatch repair protein; MSI-H = microsatellite instability-high; NGS = next-generation sequencing; PD-L1 = programmed death-ligand 1; TML = tumour mutational load.

immune checkpoint inhibitors, presumably due to the lack of routine testing for predictive immuno-oncology biomarkers. Recently, Groschel *et al.* [8] reported success with pembrolizumab, a checkpoint inhibitor (anti-PD1 drug), in a patient with CUP exhibiting focal high-level amplification of chromosome 9p including the *PD-L1* gene [*CD274*]; Similarly, Kato *et al.* [9] reported a successful response to combined treatment with nivolumab and trametinib in a CUP patient whose cancer was MSI-H due to an *MLH1* mutation. In our cohort, we identified 7 CUP cases harbouring MSI-H status, but the clinical response data were not available. We believe that the wider implementation of the FDA approval of immune therapy for all MSI-H cancers will lead to increased utilisation of the therapy and subsequently evaluation if its efficacy in this cancer type.

Several predictive biomarkers have recently emerged for checkpoint inhibitors and include immunohistochemical PD-L1 status and DNA MSI status. Tumour mutational (neoantigen) load has been recently associated with response to immune checkpoint inhibitors in malignant melanomas [36,37]. High TML is also a characteristic of mismatch repair deficient tumours and measurement of MSI had been associated with response to pembrolizumab in a variety of tumours exhibiting MSI-H and TML-H [38]. The FDA has recently approved mismatch repair deficiency (defined as either identification of loss of mismatch repair protein expression or identification of microsatellite DNA alterations) as a biomarker for Pembrolizumab for adult and paediatric patients with unresectable or metastatic solid cancers, irrespective of lineage (<https://www.fda.gov/Drugs/InformationOnDrugs/ApprovedDrugs/ucm560040.htm>). In this large cohort of CUP, we demonstrated the presence of a high TML in 12% of cases. Also, most recently, high tumour mutational load (burden) (defined as ≥ 10 mutations per megabase) was found to be predictive of response to Opdivo (nivolumab) plus Yervoy (ipilimumab) combination therapy (Phase 3 CheckMate-227 trial) [39].

We also identified a small subset of MSI-H CUP, which in some cases may have been associated with Lynch syndrome; however, we have not pursued

germline testing in any of the cases. In Fig. 3, we compare the status of predictive biomarkers for immune checkpoint inhibitors in CUP with four other major cancer types (melanoma, NSCLC, bladder and kidney carcinomas) that have the FDA-approved immune checkpoint treatment modalities. Although no optimal predictive biomarker to assign patients for therapy with immune checkpoint inhibitors has been identified, expression of PD-L1 by immunohistochemistry is most commonly used for that purpose. Several different antibodies and thresholds are in use for associating protein expression with specific drugs in specific tumours [15,16,40]. No uniform threshold is applied in the literature [41], but for the SP142 antibody, a frequently cited threshold is 5% positivity in cancer cells, which we used in our study. With this approach, we identified 22.5% positivity for PD-L1 in CUP. This represents one of the most frequent detection rates of PD-L1 in a cancer cohort [42]. When presence of any one of the three biomarkers was taken into account, 28% of CUP cases were potentially eligible for treatment with immune checkpoint inhibitors. These findings, along with the two recently described successful CUP cases treated with immune checkpoint blockade [8,9], clearly indicate a potential for this novel treatment approach with CUP patients.

In addition to the aforementioned biomarkers, our study also revealed a small proportion of CUP cases harbouring the presence of negative predictive biomarkers (*MDM2* amplification and loss of function *JAK2* mutations) to immune checkpoint inhibitors (predictors to hyperprogression). These biomarkers along with *JAK1* are associated with cancer progression following anti-PD-1/PD-L1 therapy [24,25].

Our study had limitations; the lack of clinical (follow-up) data did not allow us to explore the clinical relevance of the observed findings. However, we believe that our study as well as recently recognised predictive value in determination of MSI and TML status using NGS will lead to immune checkpoint inhibitors therapy in the selected patients with CUP.

In conclusion, our study showed that a substantial proportion of CUP patients are potential candidates for

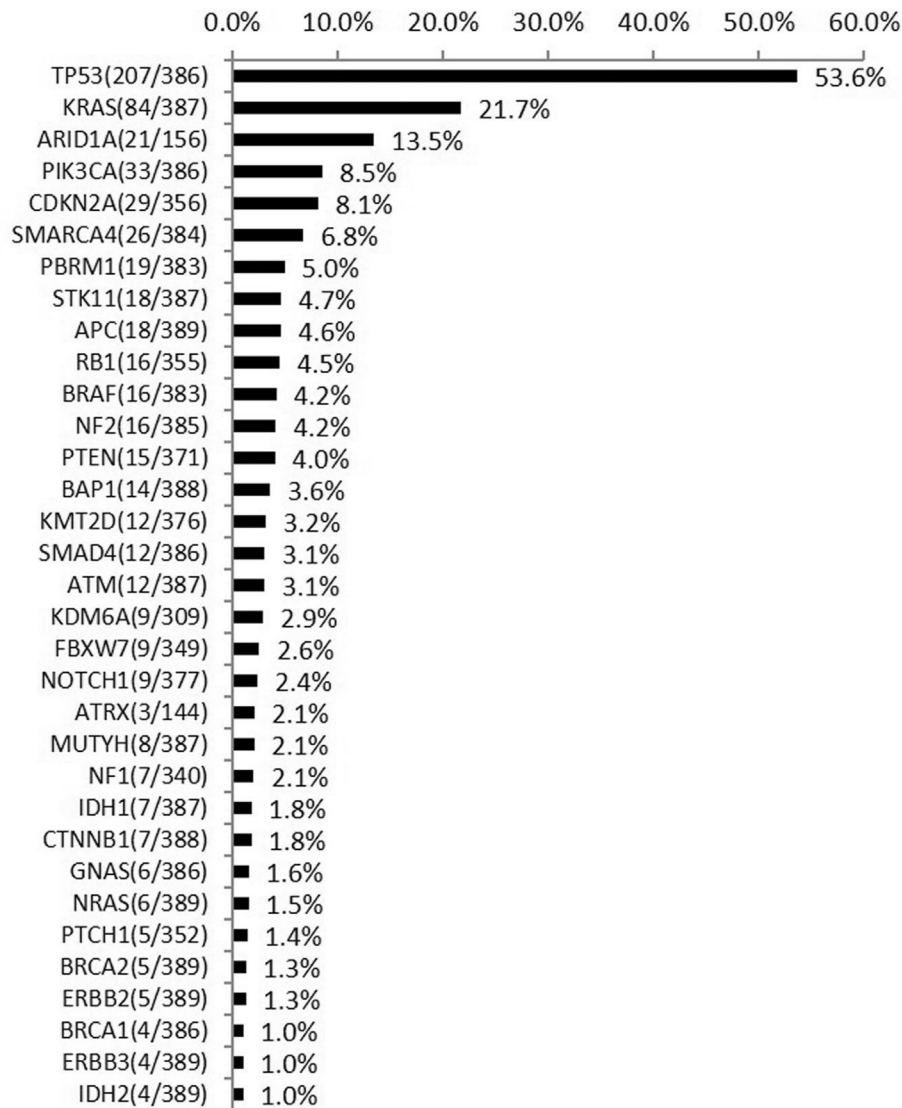


Fig. 2. **Most commonly mutated genes in CUP.** Genes with pathogenic mutations occurring with $\geq 1\%$ frequency in the CUP cohort are presented.

immune checkpoint therapy, but to achieve maximum detection success multiplatform testing may be necessary.

4. Materials and methods

Formalin-fixed paraffin-embedded tissue samples from 389 consecutive patients with verified CUP [3] were used in the study. All the tested cases were previously characterised as CUP by the referring pathologists and oncologists (mainly from the United States) who submitted the specimens for molecular profiling over 34-month period. The haematoxylin and eosin stained slides were re-reviewed by a board-certified pathologist (Z.G.) to confirm the diagnosis of CUP. All assays were performed in CLIA/CAP/ISO15189 certified clinical laboratory (Caris Life Sciences, Phoenix, AZ).

The samples were analysed with massively parallel, NGS platform that included 592 genes (NGS, NextSeq,

Illumina, San Diego, CA) [43]. TML was calculated using nonsynonymous missense mutations; common germline variants excluded. A high TML was considered ≥ 17 mutations/Mb. This threshold was previously validated and was based on the MSI and NGS data comparisons (more info is available here: https://www.carismolecularintelligence.com/wp-content/uploads/2016/12/TN0291-v1_Total-Mutational-Load-Immuno-therapy-REVERSED-PAGES.pdf). Copy number variation was tested by NGS and was determined by comparing the depth of sequencing of genomic loci to a diploid control as well as the known performance of these genomic loci. Calculated gains ≥ 6 copies were considered amplified.

MSI was calculated from the NGS data by direct analysis of short tandem repeat tracts in the target regions of sequenced genes. The count only included alterations that resulted in increases or decreases in the number of repeats; MSI-H was defined as ≥ 46 altered

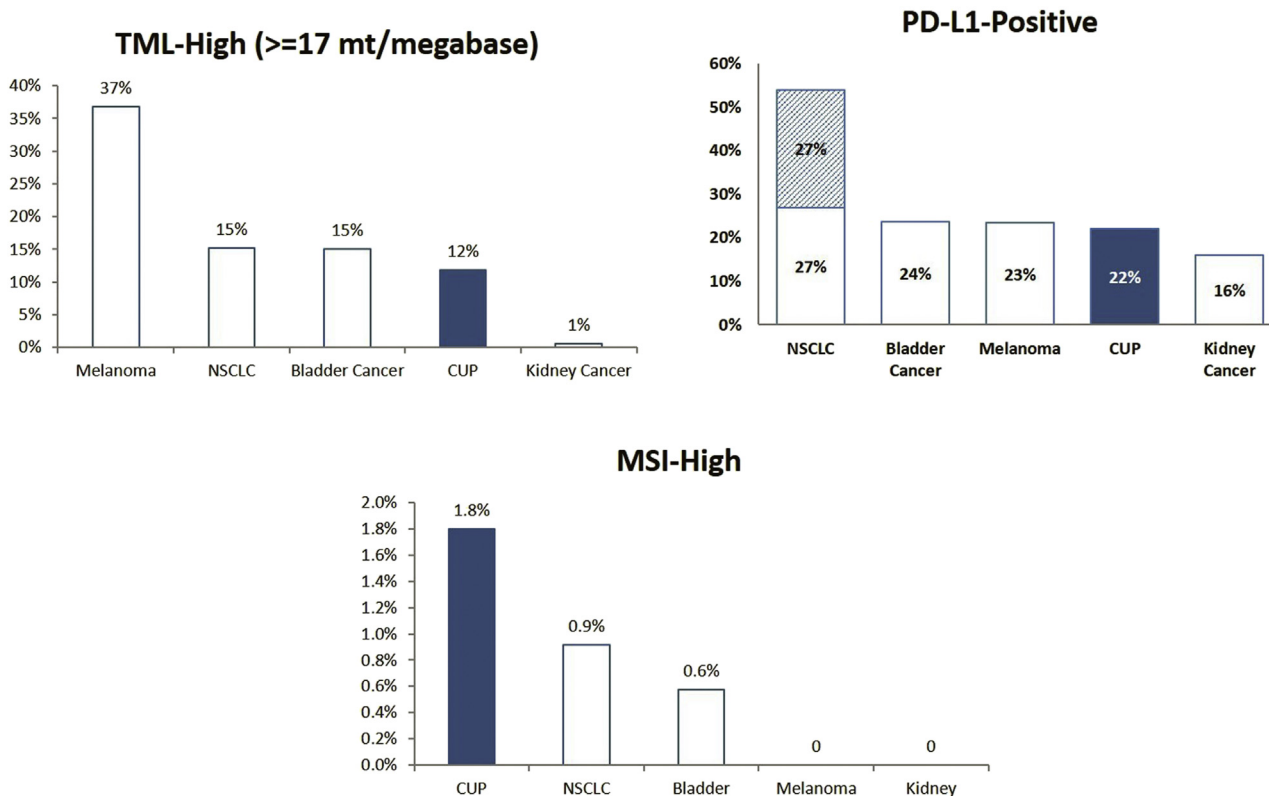


Fig. 3. Comparison between CUP and four common cancer types (non–small cell lung cancer, malignant melanoma, renal cell carcinoma and urothelial/bladder carcinoma) for three predictive biomarkers to the immune checkpoint inhibitors. The analysis was based on $n = 173$ (urothelial carcinoma), $n = 192$ (renal cell carcinoma), $n = 399$ (malignant melanoma) and $n = 2185$ (non–small cell lung carcinoma). Prevalence of PD-L1 expression in NSCLC was based on 22c3 clone (FDA-approved Companion diagnostics, DAKO) and approved thresholds (shaded bar indicates high expression: staining percentage or TPS $\geq 50\%$, while empty bar indicates low expression: TPS between 1 and 49%); for all other cancer types, PD-L1 SP142 clone (Ventana) was used with $\geq 5\%$ threshold positivity.

microsatellite loci (this threshold was established by comparing to the polymerase chain reaction–based MSI FA results from ~ 2100 cases [44,45]).

ArcherDx FusionPlex Assay (ArcherDX, Boulder, CO) was used to detect gene fusions; 52 gene targets were analysed in 156 tumours. The panel of tested gene fusions is available here: <https://www.carismoleculareintelligence.com/tumor-profiling-menu/mi-profile-usa-excluding-new-york/>.

IHC was used to detect expression of PD-L1 (SP142 antibody) and, in some cases, presence of PD-1 expressing tumour infiltrating lymphocytes (NAT105 antibody), using an automated staining platform (Ventana Medical Systems, Inc., Tucson, AZ). Tumour cells were considered positive for PD-L1 if $\geq 5\%$ of cancer cells exhibited moderate (2+) membranous positivity [6,41,46,47]. Benign tonsil samples served as a positive control for PD-L1.

In addition, IHC (Ventana) was used to assess the expression of mismatch repair proteins (MLH1, MSH2, MSH6 and PMS2) in seven MSI-H confirmed cases and 12 additional MSI-stable cases with available tissue [48].

Conflict of interest statement

Joanne Xiu, Jeff Swensen and Zoran Gatalica are all employees of Caris Life Sciences.

Semir Vranic declares no conflict of interest.

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The preliminary data from the study were presented at the ESMO 2017 Congress that was held on September 8–12, 2017 in Madrid, Spain.

Appendix A. Supplementary data

Supplementary data related to this article can be found at <https://doi.org/10.1016/j.ejca.2018.02.021>.

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