SP142 PD-L1 Scoring Shows High Interobserver and Intraobserver Agreement in Triple-negative Breast Carcinoma But Overall Low Percentage Agreement With Other PD-L1 Clones SP263 and 22C3

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Abstract: SP142 programmed cell death ligand 1 (PD-L1) status predicts response to atezolizumab in triple-negative breast carcinoma (TNBC). Prevalence of VENTANA PD-L1 (SP142) Assay positivity, concordance with the VENTANA PD-L1 (SP263) Assay and Dako PD-L1 IHC 22C3 pharmDX assay, and association with clinicopathologic features were assessed in 447 TNBCs. SP142 PD-L1 intraobserver and interobserver agreement was investigated in a subset of 60 TNBCs, with scores enriched around the 1% cutoff. The effect of a 1-hour training video on pretraining and posttraining scores was ascertained. At a 1% cutoff, 34.2% of tumors were SP142 PD-L1 positive. SP142 PD-L1 positivity was significantly associated with tumor-infiltrating lymphocytes (P < 0.01), and node negativity (P = 0.02), but not with tumor grade (P = 0.35), tumor size (P = 0.58), or BRCA mutation (P = 0.53). Overall percentage agreement (OPA) for intraobserver and interobserver agreement was 95.0% and 93.7%, respectively, among 5 pathologists trained in TNBC SP142 PD-L1 scoring. In 5 TNBC SP142 PD-L1-naive pathologists, significantly higher OPA to the reference score was provided it is properly cited. The work cannot be changed in any way or used commercially without permission from the journal.
achieved after video training (posttraining OPA 85.7%, pre-
training OPA 81.5%, P < 0.05). PD-L1 status at a 1% cutoff was
assessed by SP142 and SP263 in 420 cases, and by SP142 and
22C3 in 423 cases, with OPA of 88.1% and 85.8%, respectively.
The VENTANA PD-L1 (SP142) Assay is reproducible for
classifying TNBC PD-L1 status by trained observers; however, it
is not analytically equivalent to the VENTANA PD-L1 (SP263)
Assay and Dako PD-L1 IHC 22C3 pharmDx assay.

**Key Words:** PD-L1, SP142, triple-negative breast cancer

(Triple-negative breast carcinoma (TNBC) is an aggressive
subtype of breast carcinoma, traditionally with limited
treatment options, but is one of an increasing number of tu-
ror types that may respond to immunotherapy. As with
other tumor types treated with immunotherapy, particularly
programmed cell death protein 1 (PD-1) and programmed cell
death ligand 1 (PD-L1) inhibitors, eligibility is based on
companion diagnostic immunohistochemical assays. These
PD-L1 assays are specific to tumor type and therapeutic
agent, require specific laboratory platforms, and have specific
scoring systems and positivity thresholds for tumor and im-
mune cells or a combination thereof.1

The recently published clinical trial IMPassion130
(NCT02425891) showed significantly longer progression-
free survival and overall survival with the anti-PD-L1
antibody atezolizumab in combination with nab-paclitaxel
compared with placebo and nab-paclitaxel in SP142 PD-
L1-positive (≥1% immune cell positivity) metastatic and
locally advanced, unresectable TNBC.2 The VENTANA
PD-L1 (SP142) Assay (abbreviated to SP142) is the des-
ignated companion diagnostic test for atezolizumab,
therefore accurate assessment of this assay is essential for
identifying patients likely to benefit from atezolizumab.

However, there are limited data on interpathologist and
intrapathologist agreement for SP142 PD-L1 assessment in
TNBC. One study reported high interpathologist and intra-
pathologist agreement in the classification of SP142 PD-L1
status at a 1% cutoff in a limited number of breast carcinoma
cases (n = 30) and pathologists (n = 3),3 whereas another re-
ported an interclass correlation coefficient of 0.560 for class-
ification of SP142 PD-L1 status at a 1% cutoff in a cohort of
68 TNBCs by 19 pathologists without prior specific training
in this area.4 It is not stated whether cases in these 2 studies were
enriched around the clinically critical cutpoint of 1%, although
the latter study reports a positivity rate of 58% with a mean
score of 20% in the positive cases, suggesting a skew towards
higher scores.5 The only published study investigating SP142
PD-L1 interobserver agreement in TNBCs enriched around
the 1% cutpoint reported an interclass correlation coefficient
of 0.805 among 7 specifically trained pathologists in a limited
cohort of cases (n = 30).5
Therefore the true reproducibility by pathologists
trained in SP142 PD-L1 assessment in TNBC, and the
effect of training in determining PD-L1 positivity in cases
close to the critical decision point of 1%, remains largely
unknown.

Furthermore, there are no substantial data regarding concordance between the absolute percentages or clinical
cutpoints in comparing the different anti-PD-L1 antibody
clones and their specific instrumentation.

The existing studies addressing this issue in TNBC
have been on small case cohorts including up to 196 cases
only.3–7 There is only one study on a larger population of
the magnitude of our study (n = 420) which was the IM-
passion130 study population.8

Data on interassay concordance is essential because
in-house PD-L1 testing is likely to be impracticable for
the majority of anatomic pathology laboratories that utilize a
single immunohistochemical platform if the clones and
platforms are not interchangeable. Thus, addressing
whether PD-L1 assays currently used for other common
tumor types but not Food and Drug Administration
(FDA)-approved for TNBC, such as the VENTANA PD-
L1 (SP263) Assay (abbreviated to SP263) for urothelial
carcinoma, and Dako PD-L1 IHC 22C3 pharmDx assay
(abbreviated to 22C3) for non-small cell lung carcinoma,
gastroesophageal junction, urothelial and cervical carci-
nomas, could be substituted for the SP142 assay to de-
termine PD-L1 status in TNBC is critically important.

Therefore, the aims of this study were: (1) assess the
prevalence of SP142 PD-L1 positivity with clinicopathologic features in
the Australian TNBC population, (2) to determine the
intraobserver and interobserver agreement in pathologists
trained in TNBC SP142 PD-L1 assessment, (3) determine
the effect of training on accuracy of SP142 PD-L1 scoring
by pathologists naïve for SP142 PD-L1 scoring, and (4)
determine the concordance between the SP142, SP263,
and 22C3 PD-L1 assays in TNBC.

**MATERIALS AND METHODS**

**Tissue Samples**

Fifteen tissue microarrays (TMAs) were constructed
using a total of 1133 cores, 1 mm in diameter, from 562
previously untreated, resected primary invasive breast carci-
nomas with a triple-negative (estrogen receptor-negative,
progesterone receptor-negative, human epidermal growth
factor receptor 2-negative) phenotype. The cases were derived
from 3 hospital sites, 1 private pathology laboratory, and 1
familial cancer consortium to capture a range of TNBCs—
Peter MacCallum Cancer Centre (PMCC), TissuPath (TP)
(combined PMCC and TP, n = 286, tumors resected 2000–
2018), Concord Repatriation General Hospital (CRGH,
n = 104, tumors resected, 1997-2013), Royal Prince Alfred
Hospital (RPAH, n = 88, tumors resected, 1995-2010), and
Kathleen Cuningham Foundation Consortium for Research
into Familial Breast Cancer (kConFab) (n = 84, patients with
known BRCA mutation status, tumors resected, 1980-2008).
To achieve an adequately sized cohort, it was necessary to
include samples older than originally intended (< 10 y).
A total of 199 tumors were represented by > 1 core (2 to 6 cores)
in the TMAs.

The clinicopathologic details of the cases were ob-
tained from surgical pathology reports, and the triple-
negative phenotype of the tumors was confirmed in the CRGH, RPAH, and kConFab cohorts by repeat immunohistochemistry for estrogen receptor, progesterone receptor, and human epidermal growth factor receptor 2 before TMA construction. Tumor-infiltrating lymphocytes (TILs) were scored on whole sections and core biopsies of the tumor according to guidelines published by the International TILs Working Group, expressed as a percentage of tumor-associated stroma occupied by TILs and further categorized as 0 (virtually absent), 1 (mild, <30%), 2 (moderate, 30% to 60%), and 3 (marked, >60%).

This project was approved by the human research ethics committee of Peter MacCallum Cancer Centre (project 03/90).

**PD-L1 Immunohistochemistry**

Serial sections of the TMAs were cut at 4 μm thickness and immunohistochemistry for PD-L1 clones SP142, SP263, and 22C3 was performed at PMCC within 3 weeks of sectioning (PMCC/TP and kConFab TMAs) or within 2 months of sectioning (RPAH and CRGH TMAs). Immunohistochemistry for SP142, SP263, and 22C3 PD-L1 was performed using locked protocols for the CE-IVD PD-L1 kits on the Ventana BenchMark ULTRA Platform (SP142 and SP263) and the Dako Link 48 platform (22C3). The instrument performed the staining process by applying the appropriate reagent, monitoring the incubation time and rinsing slides between reagents. Omission of the primary antibody was used as a negative control. Tissue samples were subsequently counterstained with hematoxylin and mounted in nonaqueous, permanent mounting media. Appropriately stained external controls comprising tonsil and placenta were present on each TMA section.

**Scoring of PD-L1 Immunohistochemistry**

Full-face cores containing at least 100 invasive carcinoma cells (determined by manual counting) were required for assessment for PD-L1 status. For each PD-L1 clone, up to 15.7% and 13.2% of cores were discarded due to insufficient tumor cells or partial sections, respectively. PD-L1 scores were expressed as the percentage of tumor area occupied by positive-stained immune cells. The PD-L1 scores were categorized as tumor infiltrating immune cells (IC) 0 (<1%), IC 1 (1% to <5%), IC 2 (5% to <10%), and IC 3 (at least 10%) (Fig. 1), and dichotomized as PD-L1 negative (≤1%) or PD-L1 positive (≥1%). Scoring was performed by 2 pathologists (J.-M.B.P. and S.B.F.) who were trained and demonstrated competency in SP142 PD-L1 assessment in TNBC before assessment in clinical samples. All the cores were scored for SP142, SP263, and 22C3 PD-L1 by 1 investigator (J.-M.B.P.). Where there were multiple cores from the same tumor, the highest PD-L1 score was taken. Cores scored adjacent to the cutpoint (<1% to 5%) for SP142 PD-L1, and cores with discordant PD-L1 status between the PD-L1 assays were double scored with another pathologist (S.B.F.). Overall, 62.9% (281/452) of 22C3 PD-L1 scores were reviewed. All 60 cores included in the intraobserver and interobserver reproducibility study were scored by both pathologists to generate the reference score.

**Intraobserver and Interobserver Reproducibility and Impact of Training on SP142 PD-L1 Assessment**

The number of pathologists included in this part of the study was determined based on a statistical power calculation from an expected true overall percent agreement (OPA) of 89% for intraobserver and interobserver concordance, and it was calculated that 5 pathologists were required for each subgroup to generate 300 pairwise comparisons to ensure the lower bound of the Wilson 95% confidence interval (CI) of OPA to be >85%. The 2 subgroups of 5 pathologists each scored a cohort of 60 cases on 2 consecutive days with an overnight washout period, to generate 300 pairwise comparisons for each subgroup on each day (Fig. 2). To evaluate the reproducibility of SP142 PD-L1 status assessment in a clinically relevant manner, the 60 selected cases of the cohort were enriched around the 1% cutoff, with 29 negative samples (0% or <1%), 21 positive samples close to the 1% threshold (1% to 10%), and 10 positive samples far from the 1% threshold (>10%). The 60 TMA cores were distributed over 12 slides with 1 to 6 cores for assessment on each slide and each slide was scored in a random order. On each day, the participating pathologists assessed the same 60 SP142 PD-L1-stained tumor cores for PD-L1 status, recording scores for each case on a pro forma study response form (Supplementary Material, Supplemental Digital Content 1, http://links.lww.com/PAS/B95).

The 10 pathologists represented a range of clinical practice and experience throughout Australia. Five of the pathologists were trained and had demonstrated competency during a 1-day training course in SP142 PD-L1 assessment in TNBC 7 months before the study (subgroup 1) and 5 pathologists were selected as they were untrained in SP142 PD-L1 assessment in TNBC (subgroup 2). The subgroup 2 pathologists were only given the scoring criteria before assessment on the first day and watched a 1-hour long instructional video and received an interpretation guide on TNBC SP142 PD-L1 assessment before their assessment of the cases on the second day.

Intraobserver reproducibility was evaluated by comparing the scores obtained by subgroup 1 on days 1 and 2. Interobserver reproducibility was evaluated by comparing the scores between subgroup 1 pathologists on day 1.

The impact of training was assessed by comparing the scores obtained by the 5 previously untrained pathologists (subgroup 2) before (day 1) and after (day 2) receiving SP142 PD-L1 assessment in TNBC training.

In addition, exploratory analyses of interobserver reproducibility between 4, 6, 8, and 10 pathologists, each composed of equal numbers from subgroups 1 and 2, were also performed to assess the impact of observer numbers on interobserver agreement.
To estimate the prevalence of SP142 PD-L1-positive TNBCs to a precision of 5% (ie, the exact Clopper-Pearson 95% CI was no > ± 5%), it was determined that 369 TNBC cases were required, based on a previously reported positivity rate of ∼40% in the TNBC population. For the interobserver and intraobserver concordance study, with an expected OPA of 89% for both interobserver and intraobserver agreement, it was estimated that a total of 300 pairwise comparisons were required for both the interobserver and intraobserver assessments of agreement, for the lower limit of the Wilson 95% CI of the OPA to be > 85%. To assess analytical concordance between the different PD-L1 assays, for an OPA between 2 assays of 80% and ensuring the lower limit of the 95% CI was at least 75% using Wilson CIs, it was determined that at least 290 samples were required. Interobserver and intraobserver reproducibility was assessed using OPA, average positive agreement (APA), and average negative agreement (ANA). Cohen κ coefficient and prevalence-adjusted bias-adjusted kappa (PABAK) were calculated. Analytical concordance between the different PD-L1 assays was assessed using OPA, positive percent agreement (PPA), and negative percent agreement (NPA). 95% CIs were computed for all measurements. Association of SP142 PD-L1 status with categorical variables was assessed using the Fisher exact test and $\chi^2$ test. Statistical analyses were undertaken using SAS software, version 9.4.

RESULTS

Cohort Characteristics

The TMAs contained cores from 562 triple-negative invasive breast carcinoma cases. All the patients were
female. The clinicopathologic characteristics of the cohort are summarized in Table 1. TILs scores were available on 293 tumors, and as a continuous variable in 134 cases. Where TILs were expressed as a continuous variable, TILs ranged from 0% to 100% (median: 15%). TILs were categorized as score 0 in 20.3% of tumors, score 1 in 48.1%, score 2 in 21.7%, and score 3 in 10.0% of tumors. There was a significant difference in TILs scores between the 4 source sites, with TILs classified as virtually absent in 25.6% and 38.4% of tumors from CRGH and RPAH, respectively, compared with only 5.7% and 8.1% of cases from PMCC/TP and kConFab, respectively ($P < 0.0001$).

There was no statistically significant correlation between TIL scores and tumor grade, tumor size, lymph node status, and disease stage ($P > 0.05$, data not shown).

Prevalence of SP142 PD-L1 Positivity

Cores from 447 tumors were of sufficient quality to be scored for SP142 PD-L1. Scores ranged from 0% to 60% (median score: <1%). At a 1% cutoff, 34.2% were positive for the SP142 assay, with 60.8% of the positive cases scoring <5%. The prevalence of SP142 PD-L1 positivity, as scored by the 2 principal pathologists (J.-M.B.P., S.B.F.), varied between the source sites, 42.9%, 36.1%, 32.4%, and 25.8% of cases were positive from kConFab, PMCC/TP and RPAH, respectively, compared with only 5.7% and 8.1% of cases from PMCC/TP and kConFab, respectively ($P < 0.0001$).

There was no statistically significant correlation between TIL scores and tumor grade, tumor size, lymph node status, and disease stage ($P > 0.05$, data not shown).

**Table 1. Cohort Characteristics**

| Characteristic                                      | n (%)               |
|-----------------------------------------------------|---------------------|
| Age (n = 366), median (range) (y)                   | 59 (23-96)          |
| BRCA status (n = 84)                                |                     |
| BRCA1                                               | 42 (50.0)           |
| BRCA2                                               | 12 (14.3)           |
| BRCAX                                               | 30 (35.7)           |
| Tumor size (n = 382) (mm)                           |                     |
| ≤20                                                 | 165 (43.2)          |
| >20 to ≤50                                          | 191 (50.0)          |
| >50                                                 | 26 (6.8)            |
| Median (range) (mm)                                 | 22 (0.7-220)        |
| Tumor grade (n = 342)                               |                     |
| Grade 1                                             | 5 (1.5)             |
| Grade 2                                             | 32 (9.4)            |
| Grade 3                                             | 305 (89.2)          |
| Tumor type (n = 243)                                |                     |
| Infiltrating ductal carcinoma                       | 217 (89.3)          |
| Invasive lobular carcinoma                          | 11 (4.5)            |
| Other                                               | 10 (4.1)            |
| Carcinoma NOS; adenocarcinoma NOS (n)               | 2                   |
| Infiltrating ductal and lobular carcinoma (n)       | 2                   |
| Metaplastic carcinoma (n)                           | 1                   |
| Papillary carcinoma (n)                             | 1                   |
| Secretory carcinoma (n)                             | 1                   |
| Tubular adenocarcinoma (n)                          | 1                   |
| Apocrine carcinoma (n)                              | 1                   |
| Poorly differentiated carcinoma with neuroendocrine features (n) | 1                   |
| Nodal status (n = 335)                              |                     |
| pN0                                                 | 201 (60.0)          |
| pN1                                                 | 90 (26.9)           |
| pN2                                                 | 23 (6.9)            |
| pN3                                                 | 21 (6.3)            |

NOS indicates not otherwise specified.
demonstrating PD-L1 heterogeneity and tumors without PD-L1 heterogeneity ($P > 0.05$, data not shown).

**SP142 PD-L1 Status Is Associated With TILs and Nodal Status**

There was an increased frequency of SP142 PD-L1 positivity with increasing density of TILs ($P < 0.001$, Table 3). Node negative primary breast tumors were more frequently SP142 PD-L1 positive compared with primary tumors with lymph node metastases ($P = 0.02$, Table 3). There was no significant association between SP142 PD-L1 status and tumor grade ($P = 0.35$), tumor size ($P = 0.58$), or BRCA mutation status ($P = 0.53$) (Table 3).

**Intraobserver and Interobserver Reproducibility Among Pathologists With Specific Training in SP142 PD-L1 Assessment in TNBC Is High**

For subgroup 1 pathologists, pairwise comparisons of day 1 and day 2 results for each of the 60 evaluated samples showed excellent intraobserver agreement, with an OPA of 95.0% (95% CI: 91.9%-97.0%), APA of 95.2% (95% CI: 92.2%-97.0%), and ANA of 94.9% (95% CI: 91.7%-96.9%). Cohen $\kappa$ coefficient was 0.9 (almost perfect strength of agreement, 95% CI: 0.9-1.0) and PABAK was 0.9.

Interobserver agreement between subgroup 1 pathologists (day 1) was also excellent, with an OPA of 93.3% (95% CI: 91.1%-95.2%), APA of 93.6% (95% CI: 91.5%-95.3%), and ANA of 93.0% (95% CI: 90.6%-94.8%). Cohen $\kappa$ coefficient was 0.9 (almost perfect strength of agreement, 95% CI: 0.8-0.9) and PABAK was 0.9.

**Training in TNBC SP142 PD-L1 Assessment Improves Accuracy of Assessment**

SP142 PD-L1 scores by pathologists in subgroup 2 were compared with the reference score on day 1 (before SP142 PD-L1 assessment in TNBC training) and on day 2 (after training). Following training, there was an improvement in OPA (day 1 OPA: 81.5%, 95% CI: 76.8%-85.5%; day 2 OPA: 85.7%, 95% CI: 81.3%-89.2%, $P < 0.05$). However, OPA of day 2 scores to the reference score was still higher in subgroup 1 pathologists who had previously participated in the longer training course (OPA: 96.3%, 95% CI: 93.6%-97.9%) compared with subgroup 2 pathologists who received 1 hour of training on day 2 (OPA 85.7%, 95% CI: 81.3%-89.2%).

Subgroup 2 interpathologist agreement also improved from an OPA of 76.0% (95% CI: 72.4%-79.3%), Cohen $\kappa$ coefficient 0.5 (moderate strength of agreement, 95% CI: 0.4-0.6) on day 1 to an OPA of 81.5% (95% CI: 78.0%-84.3%), Cohen $\kappa$ coefficient 0.6 (substantial strength of agreement, 95% CI: 0.5-0.7) following training on day 2.

Exploratory analyses of interobserver reproducibility between 4, 6, 8, and 10 pathologists, each composed of equal numbers from subgroups 1 and 2, were also performed to assess the impact of observer numbers on interobserver agreement.

Interobserver agreement was consistent on each day of the study for all group sizes (day 1 OPA: 81.6%, 82.4%, 83.0%, 83.2% for 4, 6, 8, and 10 pathologists, respectively; day 2 OPA: 88.3%, 85.8%, 84.8%, 85.9% for 4, 6, 8, and 10 pathologists, respectively).

**SP142, SP263, and 22C3 PD-L1 Assays Are Not Analytically Equivalent in TNBC**

A total of 462 and 452 cases were of sufficient quality to be scored for SP263 PD-L1, and 22C3 PD-L1, respectively. PD-L1 status was available for all 3 clones in 403 cases, SP142 and SP263 in 420 cases, SP142 and 22C3 in 423 cases, and for SP263 and 22C3 in 422 cases.

At a 1% cutoff, 42.6% were positive for the SP263 assay, and 35.2 were positive for the 22C3 assay. The

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**TABLE 2. Prevalence of PD-L1 Positivity (at a 1% Cutoff) by Source Site and PD-L1 Clone**

| Source Site | SP142 | SP263 | 22C3 |
|-------------|-------|-------|------|
| PMCC/TP     | 153/447 (34.2) | 197/462 (42.5) | 159/452 (35.2) |
| kConFab     | 86/238 (36.1) | 106/241 (4.0) | 110/237 (46.4) |
| RPAH        | 21/49 (42.9) | 26/65 (40.0) | 19/50 (38.0) |
| CRGH        | 23/71 (32.4) | 31/65 (47.7) | 15/70 (21.4) |

**TABLE 3. Prevalence Of PD-L1 Positivity, n/N (%)**

| PD-L1 Clone | PMCC/TP | kConFab | RPAH | CRGH |
|-------------|---------|---------|------|------|
| SP142       | 86/238 (36.1) | 21/49 (42.9) | 23/71 (32.4) | 23/89 (25.8) |
| SP263       | 106/241 (4.0) | 26/65 (40.0) | 31/65 (47.7) | 34/91 (37.4) |
| 22C3        | 110/237 (46.4) | 19/50 (38.0) | 15/70 (21.4) | 15/95 (15.8) |

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**TABLE 3. SP142 PD-L1 Status and Tumor Features**

| Tumor grade | SP142 PD-L1 Negative | SP142 PD-L1 Positive | $P$ |
|-------------|----------------------|----------------------|-----|
| Grade 1     | 2                    | 2                     | 0.35 |
| Grade 2     | 15                   | 4                     |     |
| Grade 3     | 153                  | 85                    |     |
| Tumor size (mm) |                  |                       |     |
| ≤ 20        | 79                   | 45                    | 0.58 |
| > 20 to ≤ 50| 105                  | 50                    |     |
| > 50        | 11                   | 8                     |     |
| Nodal status |                      |                       |     |
| pN0         | 97                   | 63                    | 0.017|
| pN1-N3      | 79                   | 26                    |     |
| TILs        |                      |                       |     |
| Virtually absent | 43                 | 6                     | <0.0001|
| Mild, <30%  | 81                   | 28                    |     |
| Moderate, 30% to ≤ 60% | 22             | 26                    |     |
| Marked, > 60% | 5                    | 13                    |     |
| BRCA status |                      |                       |     |
| BRCA1       | 12                   | 12                    | 0.53 |
| BRCA2       | 4                    | 3                     |     |
| BRCAX       | 12                   | 6                     |     |
prevalence of 22C3 PD-L1 positivity varied between the source sites, ranging between 15.8% (CRGH) and 46.4% (PMCC/TP), while the prevalence of SP263 PD-L1 positivity was more constant, ranging between 37.4% and 44.0% between the cohorts (Table 2).

Comparing PD-L1 status assessed by SP142 and SP263 at a 1% cutoff (Fig. 3), OPA was 88.1% (95% CI: 85.0%-91.2%), PPA 95.2% (95% CI: 91.7%-98.7%), and NPA 84.3% (95% CI: 80.0%-88.6%). For SP142 and 22C3 (Fig. 3), OPA was 85.8% (95% CI: 82.5%-89.1%), PPA 81.4% (95% CI: 75.0%-87.7%), and NPA 88.1% (95% CI: 84.3%-91.9%).

DISCUSSION

Several studies have demonstrated significantly improved outcomes with the addition of anti-PD-L1 therapy to chemotherapy in patients with TNBC showing at least 1% SP142 PD-L1 immune cell expression, with durable effect, emphasizing the importance of accurate assessment of PD-L1 status in TNBCs. This is one of the first studies to investigate the reproducibility of PD-L1 assessment using the VENTANA PD-L1 (SP142) Assay in TNBCs and was specifically designed to have sufficient statistical power for meaningful analysis, and with samples enriched around the 1% cutoff for designation of SP142 PD-L1 positivity. Similar to other studies, SP142 PD-L1 immune cell positivity was observed in all tumor stages, and unsurprisingly was significantly associated with high stromal TILs. SP142 PD-L1 immune cell positivity in the primary tumor was significantly associated with the absence of nodal disease. In TNBCs, tumor cell PD-L1 expression has been reported to be inversely associated with lymph node involvement using the SP142 and 28-8 PD-L1 clones, and stromal SP142 PD-L1 expression at a 1% cutoff to be associated with the absence of lymphovascular space invasion. Higher prevalence of SP142 PD-L1 positivity in high-grade tumors was not observed in our cohort, possibly due to the relatively small number of non-grade 3 tumors in this study. No significant association of SP142 PD-L1 expression with BRCA1/2 mutation status was observed, similar to other published studies using the SP142 and other PD-L1 antibodies.

Overall, 34% of TNBCs in this study were PD-L1 positive as assessed by the SP142 PD-L1 assay at a 1% cutoff, less than the prevalence of 41% reported in the IMpassion130 trial. We did observe differences in prevalence of positivity for different clones in the different source cohorts, suggesting that significant differences in TILs between tumors from the source sites, as well as other possible unquantified differences in populations, age of the tumor tissue or time from sectioning to staining (the latter recognized to lead to the loss of staining in older samples), may have influenced the observed prevalence of PD-L1 positivity.
The use of TMAs in our study might have contributed to an underestimation of PD-L1-positive cases, especially where there is heterogeneity within an individual tumor. This is seen in this study at \(~50\%\) and by others at up to \(50\%\), although this might be more prevalent in metastatic sites where the overall frequency of PD-L1 positivity has been reported to be lower. Nevertheless, the use of TMAs in this study allowed standardization of staining across many samples and ensured the same area of tumor was assessed for intraobserver and interobserver reproducibility and for comparison of the PD-L1 assays. TMAs have been demonstrated to be appropriate for investigation of both PD-L1 assay concordance and PD-L1 intraobserver and interobserver concordance in breast carcinoma and other tumor types. In addition, compared with whole tissue sections, TMA cores more closely mimic the metastatic disease setting where small biopsies are the norm and PD-L1 assessment is most clinically relevant.

There was an almost perfect intraobserver and interobserver agreement and agreement to the reference score in assessment of PD-L1 status using the SP142 assay among pathologists who received specific training in SP142 PD-L1 assessment in TNBC through a day-long training seminar.

Among untrained pathologists, we observed higher agreement to the reference score and interobserver agreement than that previously reported, but below the level of agreement of \(85\%\) suggested to be acceptable for semi-quantitative assays. An hour-long training video improved SP142 PD-L1 agreement to the reference score and interpathologist agreement.

The importance of specific training in SP142 PD-L1 assessment is supported by a recent study by Reisenbichler et al which found only 38% concordance for SP142 PD-L1 status in TNBCs at a 1% cutoff among pathologists who had received minimal training before scoring, although the increased complexity of assessing SP142 PD-L1 status on whole sections, given the known heterogeneity of SP142 PD-L1 staining in TNBCs, and the use of scanned slides rather than glass slides may at least partly account for the lower interpathologist agreement. This same study also showed that the number of observers required for the interobserver agreement to plateau is inversely proportional to the robustness of the assay, and for the TNBC SP142 PD-L1 assay, interobserver agreement plateaus at 9 pathologists. In contrast, we observed consistent levels of interobserver agreement on each day of the study between 4, 6, 8, and 10 pathologists composed of equal numbers from each subgroup. This suggests that formal training and experience in TNBC SP142 PD-L1 assessment, like many other aspects of diagnostic surgical pathology, is an important determinant of interpathologist agreement rather than pathologist number alone.

The study was also designed to assess whether the different assays were interchangeable. Although SP142 is the only assay designed to identify immune cell reactivity alone, and the SP263 and 22C3 assays are not typically scored as a percentage of tumor area occupied by positive-staining inflammatory cells in their role as companion diagnostic assays in other tumor types, this scoring method was used in this study to directly compare the 3 assays. At a 1% cutoff, we observed different prevalences of PD-L1 positivity, the highest being the SP263 assay, followed by the 22C3 assay. The SP142 assay had the lowest prevalence of PD-L1 positivity. This pattern is consistent with our and others’ observations in lung cancer and with a recent meta-analysis of PD-L1 assay concordance in a range of tumor types, including non–small cell lung carcinoma, urothelial carcinoma, mesothelioma, and thymic carcinoma. In the latter study, the SP263 assay was the most sensitive of Food and Drug Administration (FDA)-approved PD-L1 assays, and the SP142 assay showed lower sensitivity compared with the 22C3 and the SP263 assays.

In our study population, PD-L1 assay substitution would result in 6.4% and 1.7% of SP142 PD-L1-positive patients being classified as PD-L1 negative by the 22C3 assay and SP263 assay, respectively. Conversely, 7.8% and 10.2% of SP142 PD-L1-negative patients would be classified as PD-L1 positive by the 22C3 and SP263 assays.

Thus, as reported in other tumor types, these findings indicate that the commercially available SP142, SP263, and 22C3 assays are not analytically equivalent in TNBCs as defined by an OPA of at least 90%. Our findings are consistent with those from the IMpassion130 study which reported OPAs of 69% for SP142 and 22C3, and 63% for SP142 and SP263, and with the lack of analytical equivalence between SP142 and SP263 PD-L1 clones observed by Reisenbichler et al and by Scott et al. and with the recent study by Noske et al which reported 10% disagreement in PD-L1 status between SP142 and 22C3 and over 20% disagreement between SP142 and SP263. This may in part due to the different epitopes targeted by the clones as 22C3 targets the extracellular domain of PD-L1, while SP142 targets an epitope on the cytoplasmic domain of PD-L1. However, SP142 and SP263 target an identical epitope, suggesting that this is not the only cause for the observed differences in PD-L1 staining.

Whether classification of PD-L1 status by the different assays results in equivalent clinical outcomes is unknown as there is a paucity of clinical trials to specifically address this question. Nevertheless, there is evidence from IMpassion130 that using the different clones 22C3 and SP263 stratified by combined positive score of 1 and IC staining at the 1% cutpoint respectively, that patients show similar differences in outcome when treated with atezolizumab, although they are not precisely the same patients.

The need for a specific PD-L1 clone, platform, and interpretation method for different tumor types presents a practical problem for many pathology laboratories but might be necessary for appropriate treatment decisions given the significant costs and potential adverse effects of immunotherapy agents. It also perhaps argues for this type of biomarker testing to be performed centrally rather than in small laboratories that might report few cases, as it is recognized that volume of reporting for many aspects of pathology significantly influences accuracy and reproducibility.

In summary, this study demonstrates the VENTANA PD-L1 (SP142) Assay to have excellent intraobserver and
interobserver reproducibility among pathologists with specific, detailed training in SP142 PD-L1 assessment in TNBC, but lower agreement among pathologists untrained or with minimal training in SP142 PD-L1 assessment in TNBC. The VENTANA PD-L1 (SP142) Assay, VENTANA PD-L1 (SP263) Assay, and Dako PD-L1 IHC 22C3 pharmDx assay are not analytically equivalent in the assessment of PD-L1 status in TNBC.

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