

# Chemokines as predictive biomarkers for immune checkpoint inhibitor (ICI) efficacy in triple negative breast cancer (TNBC)

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## BACKGROUND

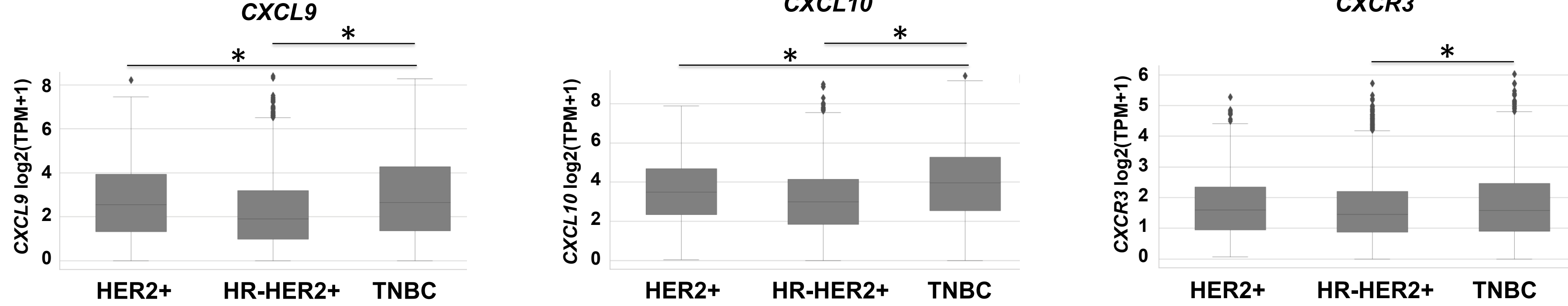
- TNBC, although an aggressive breast cancer (BC) subtype, is highly immunogenic and the only BC subtype where the ICI pembrolizumab is approved.
- However, predictive biomarkers for pembrolizumab benefit are limited.
- The chemokines *CXCL9* and *CXCL10* attract CD8 T cells into the tumor microenvironment (TME) and are associated with chemotherapy benefit, but little is known about their role in predicting pembrolizumab benefit in TNBC. We investigated the association of *CXCL9*, *CXCL10* and their cognate receptor *CXCR3* with TME and ICI efficacy.

## METHODS

- 3,038 TNBC samples were analyzed via NGS (592-gene panel, NextSeq; WES/WTS, NovaSeq; Caris Life Sciences, Phoenix, AZ).
- Tumor mutational burden (TMB) totaled somatic mutations per tumor (high > 10 mt/MB).
- CXCL9/CXCL10/CXCR3*-high (H) and -low (L) tumors were classified by RNA expression above or below the 50th percentile.
- Immune cell fractions were calculated by deconvolution of WTS: Quantiseq.
- Real-world overall survival (OS) was obtained from insurance claims and calculated from tissue collection to last contact using Kaplan-Meier estimates.
- Statistical significance was assessed using chi-square and Mann-Whitney U tests with multiple comparison adjustments ( $q < 0.05$ ).

## RESULTS

**Fig 1. *CXCL9*, *CXCL10* and *CXCR3* expression in BC subtype**



TNBC expressed higher levels of *CXCL9* and *CXCL10* (median (TPM): 2.6 and 3.9) compared to N = 1,082 HER2+ (2.5 and 3.5,  $p < 0.05$ ) and N = 4,918 HR+HER2- (1.9 and 2.9,  $p < 0.05$ ) BC. *CXCR3* expression was higher in TNBC compared to HR+HER2- (1.5 vs 1.4,  $q < 0.05$ ), but no difference when compared to HER2+ (1.5 vs 16,  $p = 0.96$ ) BC. \* $p < 0.05$

**Table 1: TNBC patients' sample demographic information**

|                    |                        | <i>CXCL9</i>      |                   | <i>CXCL10</i>     |                   | <i>CXCR3</i>      |                   |
|--------------------|------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
|                    |                        | Low               | High              | Low               | High              | Low               | High              |
| Count (N)          |                        | 1469              | 1469              | 1469              | 1469              | 1469              | 1469              |
| Median age [range] |                        | 61 (22 - >89)     | 61 (22 - >89)     | 61 (22 - >89)     | 60 (22 - >89)     | 61 (22 - >89)     | 61 (22 - >89)     |
| Race               | White                  | 59.66% (670/1123) | 62.13% (694/1117) | 60.76% (689/1134) | 61.03% (675/1106) | 57.74% (645/1117) | 64.02% (719/1123) |
|                    | Black                  | 29.83% (335/1123) | 27.93% (312/1117) | 29.28% (332/1134) | 28.48% (315/1106) | 31.96% (357/1117) | 25.82% (290/1123) |
|                    | Asian/Pacific Islander | 3.92% (44/1123)   | 4.21% (47/1117)   | 3.88% (44/1134)   | 4.25% (47/1106)   | 3.49% (39/1117)   | 4.63% (52/1123)   |
|                    | Other                  | 6.59% (74/1123)   | 5.73% (64/1117)   | 6.08% (69/1134)   | 6.24% (69/1106)   | 6.8% (76/1117)    | 5.52% (62/1123)   |
| Ethnicity          | Not Hispanic or Latino | 83.24% (884/1062) | 82.88% (881/1063) | 83.66% (896/1071) | 82.45% (869/1054) | 83.09% (870/1047) | 83.02% (895/1078) |
|                    | Hispanic or Latino     | 16.76% (178/1062) | 17.12% (182/1063) | 16.34% (175/1071) | 17.55% (185/1054) | 16.91% (177/1047) | 16.98% (183/1078) |
| Tumor site         | Primary                | 45.41% (667/1469) | 53.3% (783/1469)  | 44.38% (652/1469) | 54.32% (798/1469) | 47.99% (705/1469) | 50.71% (745/1469) |
|                    | Metastatic             | 54.59% (802/1469) | 46.7%(686/1469)   | 55.62% (817/1469) | 46.68%(671/1469)  | 52.01% (764/1469) | 49.29%(724/1469)  |

Race/ethnicity data is self-reported

**Table 2: TNBC patients' survival pembrolizumab to last contact**

| Gene          | HR   | 95% CI      | High (month)    | Low (month)     | Δ (month) | p-value |
|---------------|------|-------------|-----------------|-----------------|-----------|---------|
| <i>CXCL9</i>  | 0.65 | 0.5 - 0.84  | 26.48 (N = 363) | 15.69 (N = 189) | 10.79     | 0.001   |
| <i>CXCL10</i> | 0.74 | 0.57 - 0.95 | 25.95 (N = 341) | 20.56 (N = 211) | 5.39      | 0.02    |
| <i>CXCR3</i>  | 0.68 | 0.52 - 0.88 | 32.6 (N = 318)  | 18.32 (N = 234) | 14.27     | 0.003   |

Lowest Hazard Ratio      Highest Hazard Ratio      Shortest ΔSurvival      Longest ΔSurvival

*CXCL9/CXCL10/CXCR3*-H TNBC had higher median OS post pembrolizumab [*CXCL9*-H vs -L: 26.5 vs 15.7 months (mo), HR: 0.65 (95% CI 0.5-0.84); *CXCL10*-H vs -L: 26.0 vs 20.6 mo, HR 0.74 (0.57-0.95); *CXCR3*-H vs -L: 32.6 vs 18.3 mo, HR 0.68 (0.52-0.88), all  $p < 0.05$ ]

**Fig 2. Immune gene expression**

|               |  | Low   | High  |
|---------------|--|-------|-------|
| <i>CXCL9</i>  |  |       |       |
| CD274         |  | 2.63  | 6.89  |
| PDCD1         |  | 0.24  | 0.89  |
| PDCD1LG2      |  | 0.88  | 2.23  |
| CTLA4         |  | 0.72  | 3.15  |
| LAG3          |  | 2.10  | 6.56  |
| HAVCR2        |  | 12.74 | 26.57 |
| FOXP3         |  | 1.49  | 4.27  |
| IDO1          |  | 0.88  | 5.93  |
| TNFSF14       |  | 0.29  | 0.60  |
| TIGIT         |  | 0.49  | 2.27  |
| BTLA          |  | 0.67  | 2.88  |
| CEACAM1       |  | 22.34 | 28.27 |
| CD47          |  | 43.23 | 67.56 |
| <i>CXCL10</i> |  |       |       |
| CD274         |  | 0.65  | 1.98  |
| PDCD1         |  | 0.27  | 0.83  |
| PDCD1LG2      |  | 0.87  | 2.31  |
| CTLA4         |  | 0.79  | 3.03  |
| LAG3          |  | 1.97  | 6.87  |
| HAVCR2        |  | 11.77 | 28.02 |
| FOXP3         |  | 1.51  | 4.14  |
| IDO1          |  | 0.90  | 6.26  |
| TNFSF14       |  | 0.29  | 0.59  |
| TIGIT         |  | 0.56  | 2.15  |
| BTLA          |  | 0.77  | 2.57  |
| CEACAM1       |  | 20.62 | 29.48 |
| CD47          |  | 39.27 | 73.44 |
| <i>CXCR3</i>  |  |       |       |
| CD274         |  | 2.52  | 7.22  |
| PDCD1         |  | 0.22  | 0.99  |
| PDCD1LG2      |  | 0.86  | 2.36  |
| CTLA4         |  | 0.68  | 3.41  |
| LAG3          |  | 2.00  | 6.81  |
| HAVCR2        |  | 11.77 | 28.28 |
| FOXP3         |  | 1.38  | 4.57  |
| IDO1          |  | 0.93  | 5.59  |
| TNFSF14       |  | 0.26  | 0.65  |
| TIGIT         |  | 0.47  | 2.50  |
| BTLA          |  | 0.59  | 3.13  |
| CEACAM1       |  | 18.89 | 31.58 |
| CD47          |  | 41.42 | 69.50 |

Low TPM (Median)      High TPM (Median)

*CXCL9*-H, *CXCL10*-H and *CXCR3*-H had higher expression of immune-checkpoint genes. All  $q < 0.05$ .

**Fig 3. Immune cell infiltration**

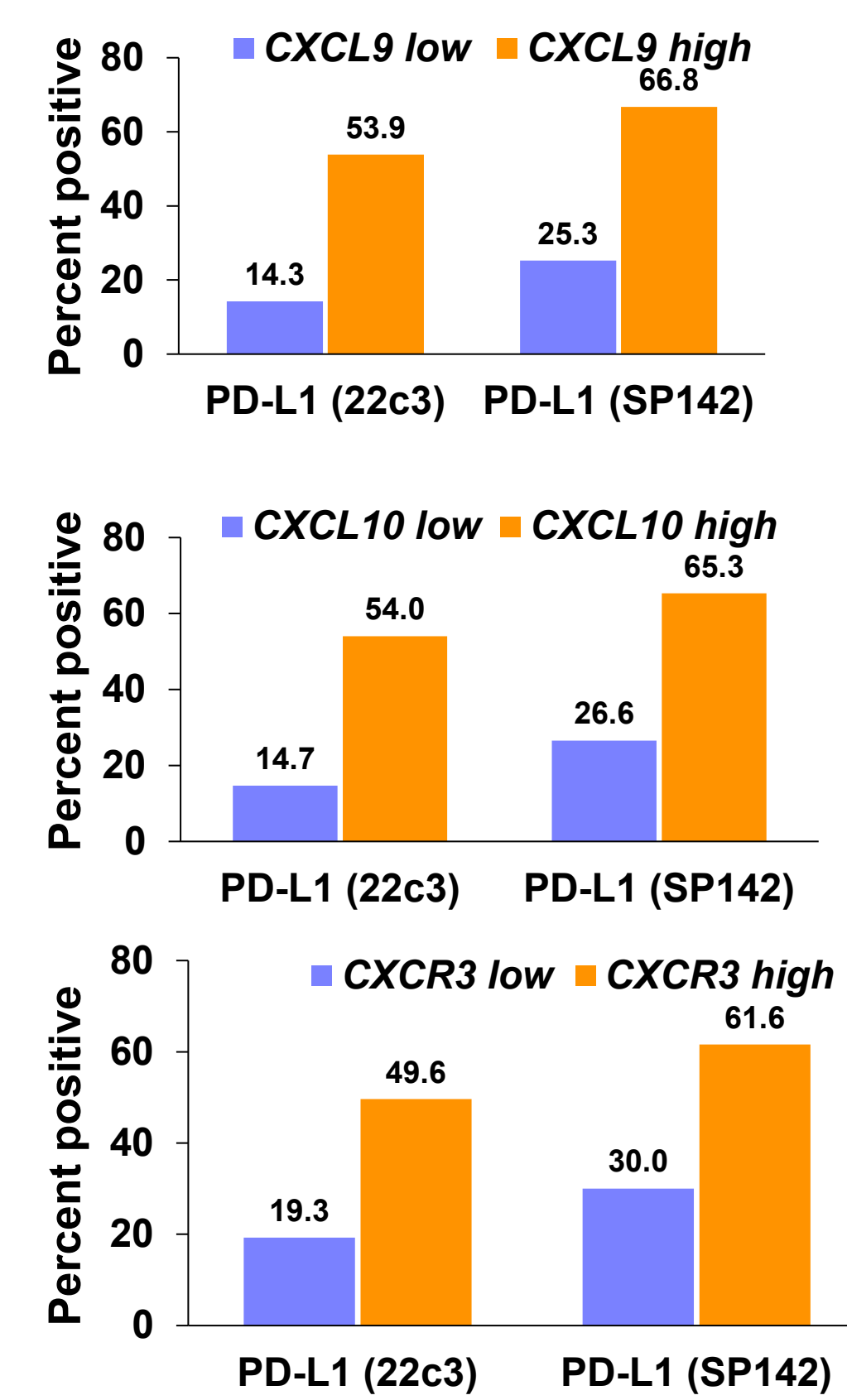
|               |  | Low  | High   |
|---------------|--|------|--------|
| <i>CXCL9</i>  |  |      |        |
| B cell        |  | 3.51 | 4.39 * |
| MΦ M1         |  | 2.4  | 3.79 * |
| MΦ M2         |  | 2.63 | 3.37 * |
| Neutrophil    |  | 4.54 | 4.15 * |
| NK cell       |  | 2.9  | 2.83   |
| DC            |  | 2.87 | 3.04   |
| T cell CD8+   |  | 0    | 1.22 * |
| Tregs         |  | 0.99 | 2.53 * |
| <i>CXCL10</i> |  |      |        |
| B cell        |  | 3.62 | 4.26 * |
| MΦ M1         |  | 2.19 | 3.99 * |
| MΦ M2         |  | 2.77 | 3.21 * |
| Neutrophil    |  | 4.39 | 4.21 * |
| NK cell       |  | 2.89 | 2.86   |
| DC            |  | 2.8  | 3.13   |
| T cell CD8+   |  | 0    | 1.04 * |
| Tregs         |  | 1.13 | 2.37 * |
| <i>CXCR3</i>  |  |      |        |
| B cell        |  | 3.36 | 4.59 * |
| MΦ M1         |  | 2.47 | 3.71 * |
| MΦ M2         |  | 2.46 | 3.52 * |
| Neutrophil    |  | 4.34 | 4.28 * |
| NK cell       |  | 2.77 | 2.95   |
| DC            |  | 2.83 | 3.06   |
| T cell CD8+   |  | 0    | 1.27 * |
| Tregs         |  | 0.99 | 2.6 *  |

Low Median%      High Median%

*CXCL9*-H, *CXCL10*-H and *CXCR3*-H elevated B cells, M1, M2 MΦ and CD8 T cells, Tregs infiltration, but not neutrophils.

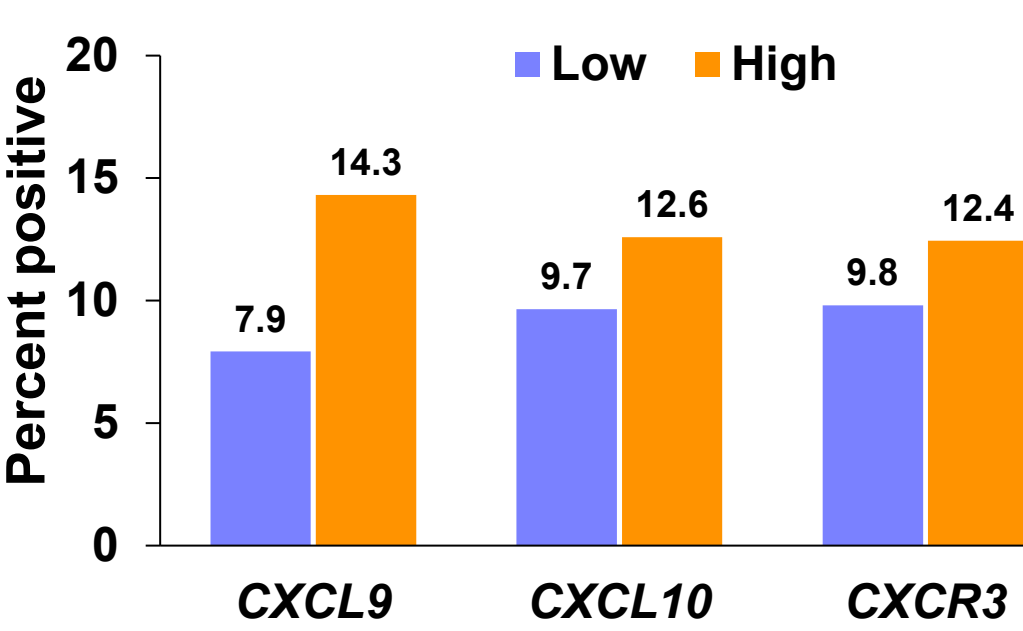
\* $q < 0.05$ .

**Fig 4. PD-L1 positivity**



*CXCL9*-H, *CXCL10*-H and *CXCR3*-H had higher PD-L1 positivity, all  $q < 0.05$

**Fig 5. TMB-high analysis**



*CXCL9*-H, *CXCL10*-H and *CXCR3*-H had TMB-high, all  $q < 0.05$

## CONCLUSIONS

High *CXCL9/CXCL10/CXCR3* expression is associated with longer survival in patients with TNBC post pembrolizumab and characterized by an immune-enriched TME. Further investigation is needed to evaluate this chemokine axis in TNBC and its potential as a therapeutic target to enhance ICI efficacy.