High-throughput sequencing of T-cell receptors reveals a homogeneous repertoire of TILs in ovarian cancer

DECEMBER 2013

WHY IMMUNOSEQ?

The immunoSEQ Assay characterizes the distribution of TILs throughout a tumor

TILs can be tracked in peripheral blood samples using the immunoSEQ Assay
BACKGROUND

The correlation between tumor infiltrating lymphocytes (TILs) and clinical outcomes is well established, but the intratumor distribution of TILs and overlap with other tissues are not well characterized.

AIM

To characterize the basic properties of TILs in ovarian carcinoma, including:

• the spatial distribution of TILs within the tumor
• the overlap of TILs with metastases and the peripheral blood T-cell repertoire

METHODS

Primary tumor, metastases, and matched peripheral blood mononuclear cells (PBMCs) were collected from 5 patients with stage III/IV ovarian carcinoma at the time of debulking surgery:

• primary tumor
• metastatic site
• PBMCs → gDNA extraction → immunoSEQ hsTCRB

RESULTS

The intratumoral T-cell repertoire is highly homogeneous. The overlap between the primary tumor and the metastatic site is much higher than that between the tumor and paired blood samples.

Duplicate samples (from different PCR reactions) do not have systematically higher T-cell repertoire overlap than those from different tissue samples, indicating that spatial location within the tumor does not affect this value more than sampling errors.

Conclusions

• TCRB repertoire sequencing can be used to measure the intratumoral immune response
• The T-cell repertoire within ovarian carcinoma tumors is homogeneous over the mass of the tumor
• The tumor repertoire is distinct from that of peripheral blood

WHY IMMUNOSEQ?

The immunoSEQ® Assay characterizes the distribution of TILs throughout a tumor.

TILs can be tracked in peripheral blood samples using the immunoSEQ Assay.