10th ANNUAL CHC 2020

TRANSLATIONAL SCIENCE SESSION SUMMARIES

PRESENTED BY: DR. ROBERT KRIDEL & DR. MARCUS BUTLER

Content in this report is drawn from the presentations made by the respective speakers during the CHC 2020 virtual stream on October 2, 2020.

TOWARDS BIOLOGY-INFORMED MANAGEMENT OF B-CELL LYMPHOMA

DR. ROBERT KRIDEL / PRINCESS MARGARET CANCER CENTRE

Increased understanding of lymphoma biology provides the opportunity to refine risk-stratification and adjust therapy based on the underlying pathogenetic perturbations.

The pathological labels "diffuse large B-cell lymphoma" and "follicular lymphoma" represent collections of different molecular subtypes

Possible avenues to improve patient outcomes using enhanced understanding of lymphoma biology:

- Accurate identification of novel molecular subtypes, and precise targeting of the key aberrations underlying these subtypes
- Dynamic risk profiling, using integrated risk models that leverage the information gained from clinical risk factors, as well as radiological and molecular response

Technology that can be implemented in clinic:

- Gene expression profiling (technology: next-generation sequencing or lower resolution digital gene expression)
- Targeted DNA sequencing-tissue (technology: next-generation sequencing [or lower throughput alternatives if single gene])
- Targeted DNA sequencing-circulating tumour DNA, ctDNA (Next-generation sequencing [or lower throughput alternatives if single gene])

Refined molecular assays may allow for adaptive trial designs where treatment is changed upon early recognition of treatment failure

Looking Forward:

- The role that novel therapies, including immune therapies will play in the light of such heterogeneity needs to be elucidated
- Due to recent advances in our understanding of lymphoma biology, the value of such approaches can now be studied within clinical trials

Click here to access the slides presented by Dr. Robert Kridel

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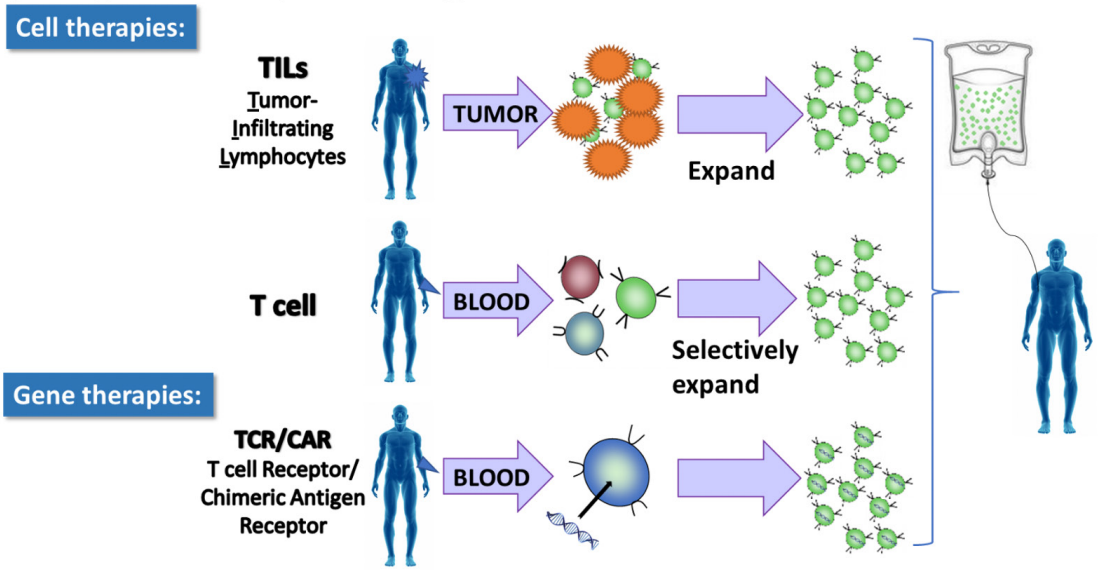
IMMUNOPROFILING FOR THE CLINICIAN: LESSONS FROM CELL THERAPY

DR. MARCUS BUTLER / PRINCESS MARGARET CANCER CENTRE

Interrogation of the tumor, blood, and host immune parameters prior to treatment can be useful in identifying biomarkers that are predictive of clinical outcomes with immunotherapy ***(Gnjatic et al. Journal for ImmunoTherapy of Cancer 2017)***

Figure 1. Approaches for adoptive T cell therapy



Tools for interrogating the immune system

- **Cytokine analysis:**
  - Multiplex assays designed for comprehensive vs focused approaches
  - Enzyme-linked immune absorbent spot (ELISPOT)- system that can measure expression of cytokines on a cellular basis
  - Metabolomics- looks at metabolites present in serum that are correlated with response to therapy
- **T cell analysis**
  - MHC-peptide multimers: Allows for sorting, clonal expansion of living cells
  - TCR sequence analysis: Vbeta families can be used to assess diversity; VDJ sequences can serve as a unique bar code for specific clones

Looking Forward:

- Understanding the relationship between pre-existing immunity and the tumour microenvironment is now more important than ever
  - New combinations and adjuvant therapies will further add a layer of complexity

Click here to access the slides presented by Dr. Marcus Butler

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