Dissection of the tumor/stromal expression response to VEGF inhibition in xenograft models

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Inhibition of tumor-induced angiogenesis



VEGF (Vascular Endothelial Growth Factor) VEGFR (VEGF Receptor)

From Anthony Lama. Carmeliet and Jain (2000) Nature, Bergers and Benjamin (2003) Nat. Rev. Cancer

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VEGF inhibition in xenograft mouse models



Negative Anti VEGF Anti VEGFR

x 3 mice 72 h

Xenograft samples are heterogeneous mixtures of different cells



Adapted from Kerkar and Restifo (2012) Cancer Research

Cancer cell

Tumor (human)

Adipocyte

Leucocyte

Vascular endothelial cell

... other cell types

Stroma (mouse)

Separation of mouse and human mRNAs

- Co-alignement of reads with the mouse and human genome
- Separation based on the number of alignment mismatches



Human content

Tumor response to VEGF inhibition

B20 (anti VEGF)

- 41 DE genes
- Heatshock
- Hypoxia

DESeq2, default parameters

Axitinib (anti VEGFR)

- 0 DE genes
- No effects
- Dose too low



lacksquare

Sunitinib (Pan-RTK inh.)

• 73 DE genes

Innate immune response

Gene signature suggests contamination by muscle cells

Pearson correlation = 0.99



Tnnc2 expression (log2 RPKM)



Correlation analysis in stroma shows existence of tissue-specific genes

Pairwise gene expression Pearson correlation



Stromal composition and size factor re-estimation

- Hypotheses
 - Tissue gene distribution is similar to the overall gene distribution
 - Tissue composition is independent of treatment



Stromal composition

- Skeletal muscle
- Skin
- □ Other



Stromal response to VEGF inhibition

B20 (anti VEGF)

- 189 DE genes
- Endothelial VEGF response

Axitinib (anti VEGFR)

- 41 DE genes
- Endothelial VEGF response

DESeq2, with re-estimated size factors



Sunitinib (anti RTK)

- 378 DE genes
- Endothelial VEGF response lacksquare
- Cell cycle arrest

Conclusion

- Xenograft mouse models are hetereogeneous mixture of cells
- Method to separate stromal (mouse) from tumor (human) response
- Estimation of stromal tissue composition
- Re-estimation of size factors to sharpen differential expression analysis
- Generalizable to filter/estimate non-human fraction (bacteria, viruses...)
- To study host-pathogen interactions, virus integration, cell-cell signalling...
- Soon in Bioconductor