Peering deep into the heart of tumor-specificity

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New sequencing technology permits us to peer deep into the tumor genomes and transcriptomes in a manner that was inconceivable even ten years ago. Our laboratory has characterized the transcriptomes of a small number of BALB/c mouse tumors, and compared the sequences of the transcripts to the normal genomic sequences. Thousand of non-synonymous mutations have been identified. A proportion of these have been predicted to form strong tumor-specific epitopes for each of the three MHCI alleles (K, D and L). These predictions have been tested experimentally in terms of the ability of these epitopes to elicit a functional CD8+ T cell response, and to modulate the kinetics of tumor growth. These results, which shed a powerful light on the identity of tumor-specific antigenic epitopes, shall be discussed. The application of this methodology to immuno-therapy of human cancers shall also be discussed.