Evaluation of bridge capture technology for mutation profiling in liquid biopsies of metastatic colorectal cancer patients

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Abstract

Colorectal cancer (CRC) is the second leading cause of cancer-related deaths, often presenting at an advanced stage with significant molecular heterogeneity. This is the first study to evaluate the performance of a novel next-generation sequencing (NGS)-based Bridge Capture technology for mutation profiling and minimal residual disease (MRD) detection in circulating tumor DNA (ctDNA) from metastatic colorectal cancer (mCRC) patients. Its performance was compared to digital droplet PCR (ddPCR), the Ion AmpliSeq™ Cancer Hotspot Panel v2, and the Idylla™ ctKRAS Mutation Assay. Eighty serial plasma samples from ten mCRC patients were analyzed by Bridge Capture and ddPCR, demonstrating a very strong correlation in variant allele frequency (VAF) values (rs = 0.86). The concordance of Bridge Capture with ddPCR (kappa = 0.70) and Idylla (kappa = 0.79) showed substantial agreement. A subset of samples (n = 10) was analyzed using the Ion AmpliSeq NGS-panel and both methods identified 15 driver mutations with strong correlation of VAF values (rs = 0.74). Additionally, Bridge Capture identified several oncogenic mutations beyond those detected by Ion AmpliSeq, highlighting its comprehensive profiling capability. The scalability of Bridge Capture was validated using an expanded panel and synthetic DNA targets, showing a strong linear correlation between observed and expected VAF values. This study underscores the potential of Bridge Capture to enhance mutation detection and clinical decision-making in mCRC, offering a scalable and accurate platform for comprehensive ctDNA analysis.

Do you have any conflicts of interest?

Yes, I have a conflict of interest.

I am a stakeholder and medical advisor in Genomill Health Ltd, Turku, Finland