Cancer Biomarker Research using castPCR™ Technology

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Yun Bao, Bonnie Ching, Mokang Mouanoutoua, Yu Wang , David Keys, Toinette Hartshorne, Sejal Desai and Junko Stevens

Life Technologies, 850 Lincoln Centre Dr. Foster City, CA94404, USA

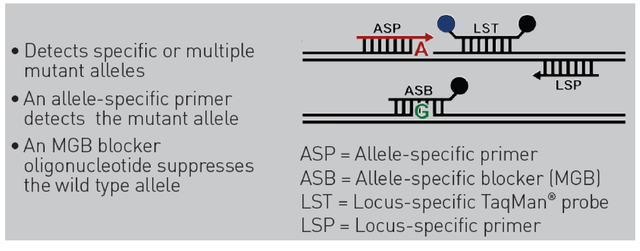
ABSTRACT

Cancer biomarkers have applications in the diagnosis, staging, prognosis and monitoring of disease progression, as well as in the predication and monitoring of drug response. Profiling and validation research tools are needed that exhibit the combined features of high sensitivity and high specificity for cancers. However, the sensitivity of molecular methods such as DNA sequencing and conventional genotyping in tumor samples is limited, typically ranging from 5-20%. We have recently developed TaqMan® Mutation Detection Assays using our competitive allele specific TaqMan® PCR (castPCR™) technology for cancer biomarker research. castPCR™ assays were tested with >300 tumor research samples (either fresh/frozen or formalin-fixed, paraffin-embedded samples) and cell lines to assess mutation status at multiple independent laboratories. The results showed that castPCR™ technology can robustly detect mutations as low as 0.1% and has >99% concordance to other technologies including PCR-based technology and sequencing. In this study, a large panel of TaqMan® Mutation Detection Assays for AKT1, BRAF, CTNNB1, HRAS, KRAS, NRAS, PIK3CA, PTEN and TP53 genes were used for investigating somatic mutations in breast tumor research samples. Initially, 4 model FFPE cell lines were used to validate the assays. Mutant DNAs were titrated in the wild type DNAs from 50% to 0.1%. Mutations were identified down to 0.1% titration with high reproducibility. No false positives were found in non-tumor samples. The results obtained by TaqMan® Mutation Detection Assays for 20 breast tumor samples (FFPE/fresh frozen) were concordant to those reported by other methods. Our data showed that castPCR™ technology provides an excellent tool for identifying cancer biomarkers or confirming potential cancer markers such as those obtained by next-generation sequencing and other technologies.

INTRODUCTION

An important but challenging part of cancer research is the identification of key biomarkers from the heterogeneous tumor samples. castPCR™ technology has provided a platform for cancer biomarker profiling, mutation detection and screening. The aim of this study was to evaluate its performance as a sensitive and accurate tool for cancer biomarker profiling in research samples.

Schematic of castPCR™ Technology



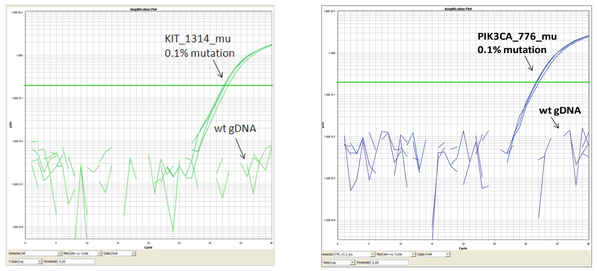
MATERIALS AND METHODS

castPCR™ was performed in 20-µL reactions comprising DNA template, 1X Genotyping Master Mix (Life Technologies) and 1X of TaqMan® Mutation Detection Assays . PCR was run on an ABI Vii A™ 7 or ABI 7900HT in 96 well or 384 well plates with the following conditions: 95 C for 10min; 5 cycles: 92ºC for 15s and 58ºC for 1min; 45 cycles: 92ºC for 15s and 60ºC for 1min. FFPE cell lines were provided by Acrometrix (a Life Technology company). DNA from fresh frozen and FFPE tumor and normal breast tumor samples were purchased from BioChain.

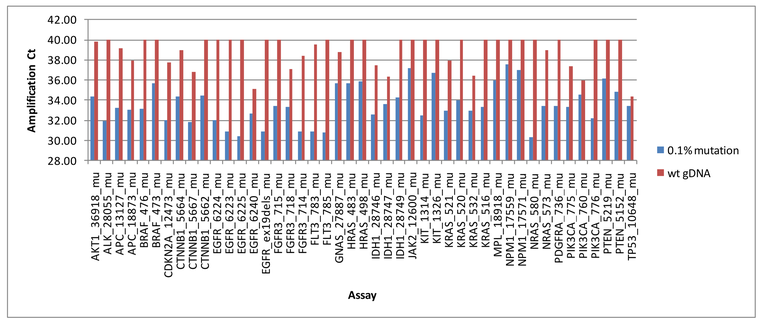
RESULTS

1. Assay Specificity and Sensitivity

Mutant allele detection is based on an allele-specific primer, while the wild type allele background is suppressed by the proprietary MGB blocker oligonucleotide. Assays can detect down to 0.1% mutant allele in the presence of wild type allele background. For each assay developed, 0.1% mutant allele samples were generated by spiking 10 copies of mutant allele synthetic templates into 10,000 copies (30 ng) of cell line wild type gDNA.



Example amplification plots for KIT_1314_mu assay and PIK3CA_776_mu assay on 0.1% mutant allele sample and wild type gDNA.



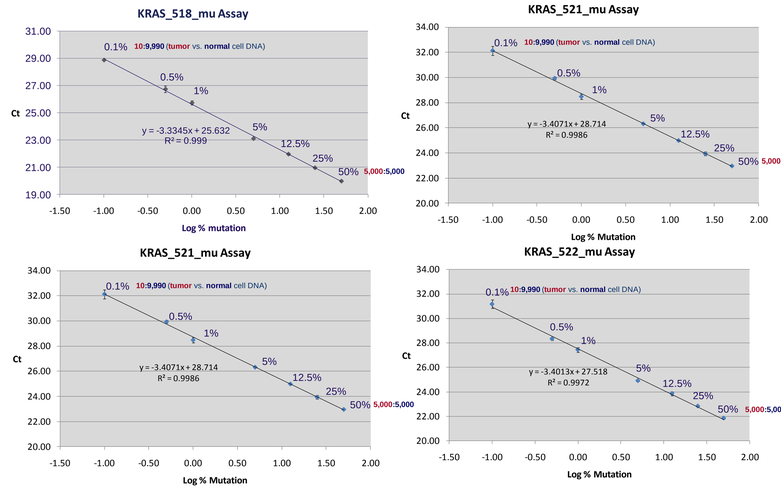
There is a significant difference in amplification Ct values between the 0.1% mutant allele sample and wild type gDNA (p-value < 0.05 for 46 out of 48 assays in the example graph).

2. FFPE Cell Line Titration Experiment

DNA extracted from 4 FFPE mutant cell lines and 1 wild type cell line were used to validate the assays. Mutated DNA was diluted in 30 ng wild type gDNA from 50% to 0.1%. Each sample was run with the corresponding mutant allele assay and gene reference assay in four replicates.

Mutant FFPE gDNA	Zygosity	Wild type FFPE gDNA	Mutation	Mutant Assay	Reference Assay
PSN-1	Heterozygous	Jurkat	KRAS G12R	KRAS_518_mu	KRAS_rf
SW480	Homozygous	Jurkat	KRAS G12V	KRAS_520_mu	KRAS_rf
PANC-1	Heterozygous	Jurkat	KRAS G12D	KRAS_521_mu	KRAS_rf
NCI-H2009	Heterozygous	Jurkat	KRAS G12A	KRAS_522_mu	KRAS_rf

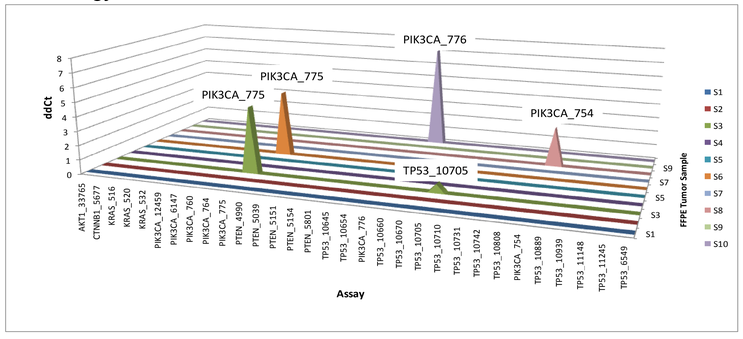
Notes



In FFPE cell lines, mutations were identified down to 0.1% titration in the background of 30 ng wild type gDNA. TaqMan® Mutation Detection Assays demonstrated excellent PCR efficiency (96-100%) and linearity (RSQ >0.997) in FFPE cell line samples.

3. Mutation Profiling of Heterogeneous FFPE/Fresh Frozen Breast Tumor Samples

A panel of 62 TaqMan® Mutation Detection Assays for AKT1, BRAF, CTNNB1, HRAS, KRAS, NRAS, PIK3CA, PTEN and TP53 genes were used for mutation profiling of FFPE or fresh frozen breast tumor research samples. 20 breast tumor samples and 10 normal breast tissue samples were used in this study. Those samples were previously uncharacterized. No false positives were found in normal breast tissue samples. The results obtained by these castPCR™ technology-based assays for 20 breast tumor samples (10 FFPE and 10 paired fresh frozen samples) were concordant to those analyzed by ARMS-PCR based technology and by Ion AmpliSeq™ Cancer Panel sequencing technology.



Mutation Profiling of FFPE breast tumor samples. 1 or 2 mutations were identified in positive samples. The dCt difference between mutant allele assay and reference assay Ct values for a given sample were compared to predetermined assay-specific detection dCt cutoff values. Detection dCt cutoff values were determined using Ct values from assays run on normal FFPE breast tissue samples, and the calculation: dCt cutoff = *[Ct(mutant allele assay) – Ct(gene reference assay)] – (3 × the standard deviation or 2 Ct, whichever is greater)*

CONCLUSIONS

- TaqMan® Mutation Detection Assays demonstrated high specificity and sensitivity/selectivity for mutation detection, capable of detecting 0.1% mutation in 10,000 copies of wild type gDNA background.
- castPCR™ technology provides a sensitive and robust method for mutation profiling in heterogeneous cancer samples.
- Results from castPCR™ technology are highly concordant to results from other technologies including sequencing using Ion AmpliSeq™ Cancer Panel.