## Translocation

Joe Salem, Michael Escott, Emma Farrell, Joan Gordon, Matt Held, Loren Krott, Gwen MacLeod, Dan Magoon, Abbey Olsen, Bretna Parker, Stephen Pelsue, Arie Rietdyk, John Ross, Tania Spenlinhauer, Nicole Wilkinson Maine Molecular Quality Controls Inc., Saco, Maine

## Introduction

Chronic myeloid leukemia (CML) is a disease caused by a translocation between chromosomes 9 and 22, forming the truncated Philadelphia chromosome. In this translocation event the ABL1 gene on chromosome 9 is translocated to the break point cluster region (BCR gene) on chromosome 22. Expression of the BCR-ABL1 fusion genes in myeloid cells promotes aberrant proliferation, increased cel survival, and enhanced migration and invasion through the activation of ke ABL1 and exon e1 of BCR, forming a 190 kDa protein.

One method for monitoring CML treatment is measuring levels of BCR-ABL transcripts in peripheral blood by RT-PCR. The molecular response (MR) is the lo of ratio of BCR-ABL1 to ABL1 transcripts and guides treatment. A reduction of the $B C R-A B L 1$ to $A B L 1$ ratio results in a higher MR demonstrating a reduction in CML a 3 -log reduction of BCR-ABL1 transcript is defined as the major molecula response (MMR), indicating the patient is responding well to therapy. Here, we describe the development of a control panel that can be used to monitor and reports a range of p 190 BCRABL1/ABL1 levels.

## Materials and Methods

Gene segments of ABL1 and BCR were designed in silico to create DNA constructs and cloned to create stable frozen clone stocks. In vitro RNA transcripts were generated, quantified by UV spectrophotometry and formulated in a proprietary matrix that carries the RNA through extractio processes and provides stability. BCR-ABL1 a de ABy
combined to generate a panel of 5 BCR-ABL1 e1a2 levels.

| INTROL® BCR-ABL1 p190 Control Panel Component | Detection |
| :---: | :---: |
| INTROL BCR-ABLI P1900\% | Abl |
| INTROL BCR-ABL1 P1900.02\% | BCR-ABL P190 Detected [0.0259] |
| INTROL BCR-ABL1 P190 0.1\% | BCR-ABL P190 Detected [0.172\%] |
| INTROL BCR-ABL1 p190 1\% | BCR-ABL P190 Detected [1.425] |
| INTROL BCR-ABL1 P190 10\% | BCR-ABL 1900 Detected [12.8\%] |

Three lots of the panel were tested across 3 lots of the Xpert BCR-ABL Ultra Three lots of the panel were tested across 3 lots of the Xpert BCR-ABL Ultra
p190 assay, over multiple days and operators to determine the linearity and p190 assay, over

INTROL BCR-ABL1 p190 external controls are run just like patient blood samples. An overview of the sample preparation workflow is shown below:



Figure 3. Descriptive statistics of the $\mathbf{3}$ external control lots. Averages and Standard Deviations of ABL and BCR-ABL Ct figure 3. Descriptive statistics of the $\mathbf{3}$ external control lots. Averages and Standard Deviations of $A B L$ and $B C R-A B L C t$
alues: the assay reports out a $C$ for for both ABL and BCR-ABL $\operatorname{p190}$. The assay software uses the delta Ct (ABL Ct - BCR-ABL $C t$ ) values: the assay reports out a Ct for both ABL and BCR-ABL p190. The assay software uses the deta Ct ( $A B L C t-B C R-A B L C t)$
to calculate the $\%$ IS of the control sample. Out of a total 195 Xpert BCR -ABL Ultra p 190 runs, there were 3 invalid runs. Of 192 valid runs, $100 \%$ had correct results with reported $\%$ ratio values within expected limits of assays performance. The $\%$ Is ratios are manufactured by mixing ABL and BCR-ABL synthetric RNA transcripts at different ratioss. All controls have the same concentration of ABL transcript. ABL Cts and BCR-ABL Cts from all 3 control lots across 5 levels had standard deviations of <
0.75. Control lots demonstrated low variability for both ABL and BCR-ABL Cts as calculated by $\% C V$ (SD/mean Ct). The $\% C V$ of


BCR-ABIT

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190 kDa protein (p190). MMOCl's synthetic controls contain transcript sequence required for Cepheid's p190 assay

## Results

Figure 2. Linearity across 3 manufactured control lots. Lot $A(n=50$ total); $0.02 \%(n=12), 0.1 \%(n=14), 1 \%(n=12)$, 12 each $)$. Testing was performed across 3 Xpert cartridge lots which were provided by Cepheid.
$=1$

Figure 1. Gene map of ABL1 and BCR genes showing ela2 breakpoints. The
full-length human full-length human BCR activator of
RhoGEF and GTPase gene (BCR) contains 23 exons spanning $\sim 137,000$ bp on chromosome 22 ( $6,783 \mathrm{nt}$ transcript). The full-length human ABL1 gene on chromosome 9 contains 12 exons across $\sim 174,000$ bp ( $5,578 \mathrm{nt}$ transcript). The minor break point generates the e1a2 usion transcript which is tra
$\qquad$

Cts across all lots and levels was 5\% for ABL and 2.7\% for BCR-ABL p190.
ABL


| \%CV |  |  |
| :---: | :---: | :---: |
| Lot A | Lot B | Lot C |
| $5.5 \%$ | $4.9 \%$ | $5.5 \%$ |
| $4.6 \%$ | $5.1 \%$ | $5.1 \%$ |
| $6.4 \%$ | $4.7 \%$ | $3.9 \%$ |
| $5.1 \%$ | $4.0 \%$ | $6.3 \%$ |
| $5.0 \%$ | $4.7 \%$ | $4.9 \%$ |




Figure 4. Averages of \%/s values and their minimum/maximum fold-differences. The three
MMQCI control lots show average \%il values near MMQCI control lots show average
their respective targeted ranges ( $0.02,0.1,1.0$, and their respective targeted ranges $(0.02,0.1,1.0$, and
$10 \%$. Minimum and maximum \% $\%$ values observed during testing are listed within the tables and were
used to calculate the fold-differences from the used to calculate the fold-differences from the
average \%/IS. All fold differences are within 2 for 0.1 average $\%$ /s. All fold differences are within 2 for 0.1-
$10 \%$ and within 3 for $0.02 \%$. The GeneXpert reports $\%$ IS values for p190-positive samples based on the calculation below. Calculation of \%/Is by the GeneXpert system takes into account the delta Ct

| $\% 1 \mathrm{~S}=\mathrm{E}_{\text {cct }}{ }^{(4 \mathrm{Ct}} \times 100 \times$ Scaling Factor (SF) |  |
| :---: | :---: |
| \%IS | International Scale (standardizes reporting of BCR-ABL RNA levels) |
| $\Delta \mathrm{Ct}$ | ABL Ct minus BCR-ABL p190 Ct |
| $\mathrm{E}_{\text {cct }}$ | Cartridge lot-specific assay Efficiency |
| SF | Scaling Factor specific to the cartridge |

Figure 5 . Real-time stability studies demonstrate $>12$ months stability when stored at $-20^{\circ}$. Real time stability was measured for historical controls with a similar formulation. To assess stability of ABL Cts over time, samples across all \%lS levels were run in duplicate. For BCR-ABL, duplicate samples were run for all p190-positive levels. Linear regression was performed on the average Cts for all \%ols
levels for each timepoint. The criteria for rending levels for each timepoint. The criteria for trending is If two consecutive timepoints result in a
significance $f$-value <0.05 and a Ct exceeds the upper significance $f$-value $<0.05$ and a Ct exceeds the upper
bound of the $95 \%$ confidence interval. The graphs show ABL or BCR-ABL Cts over time from 0 to $\sim 19$ months post-manufacturing. Red lines show
upper/lower bounds of 4 SDs.


## Conclusions

The synthetic INTROL BCR-ABL1 p190 Control Panel (C183) demonstrated reproducible and robust performance when tested on Xpert BCR-ABL Ultra p190 assay. These controls ar BCR-ABL1 p190 controls are stable for over 1 year when stored at $-20^{\circ} \mathrm{C}$.

