

A novel generation of digital PCR allows fast, convenient and accurate chimerism monitoring after hematopoietic stem cell transplantation

Elise Gourri, Beat M. Frey, Stefan Meyer

Blood Transfusion Service Zurich, SRC, Department of Molecular Diagnostics (MOC), Schlieren, Switzerland.

Introduction

Monitoring of chimerism in patients after stem-cell transplantation is part of the surveillance of impending clinical relapse. Briefly, it consists of measuring the amount of stem-cell donor DNA in the blood of the receiver following transplantation. We previously established a method for chimerism monitoring based on detection of bi-allelic SNVs by Taqman™ assays on a chip-digital PCR (chdPCR) platform (Thermofisher)¹. This method enabled reliable monitoring on nearly 2,000 clinical samples. However, substantial hands-on-time renders this platform less suitable for high sample throughput. We aimed to establish an alternative system to our approved chdPCR platform providing higher sample throughput and minimal hands-on-time.

Methods

The Opal™ dPCR chip (Figure 1A) represents the larger unit of the Naica™ crystal dPCR system² (Stilla) and allows SNV detection in approximately 20,000 droplets in each of the 16 reaction chambers of the chip. Crystal dPCR combines automated droplets formation (Figure 1B) and thermocycling on a single device (Naica™ Geode). Fluorescence signal of each droplet is measured in the Naica™ Prism instrument. With up to 3 chips or 48 reactions per run, the system represents a fast and economical alternative to other dPCR platforms.

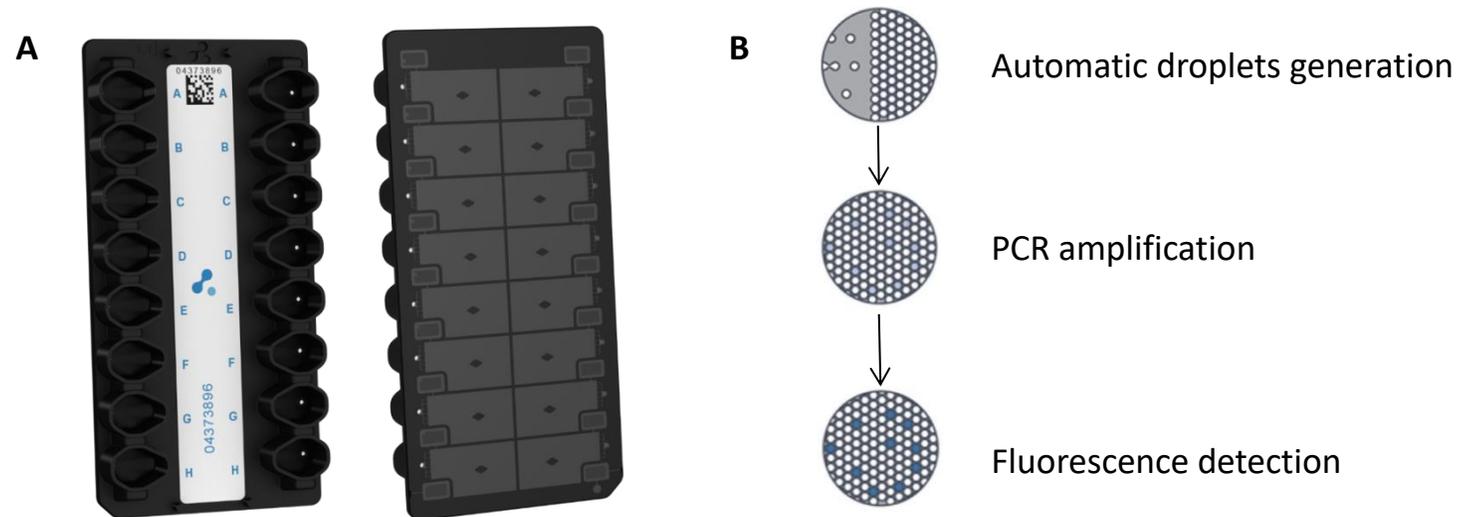


Figure 1: Opal™ dPCR microfluidic chip (Stilla). A. The larger unit of the crystal dPCR Naica™ system allows to perform up to 48 dPCR reactions simultaneously (16 per chip). B. **Crystal dPCR process.**

¹Gourri et al. DGHO Annual conference 2016.

²Madic et al. Biomol Detect Quantif. 2016.

Results 1/2

From the number of positive droplets and the total number of droplets, the crystal dPCR analysis software (Crystal Miner™) allows the calculation of the target (SNV) concentration in copies/ μ l thanks to Poisson statistics. We tested different amounts of input DNA per reaction and as foreseen, we observed an increasing amount of measured copies/ μ l with increasing amounts of input DNA. With our routine experimental setup (20 ng input DNA) around 650 copies/ μ l is expected and used as an internal quality control (Figure 2).

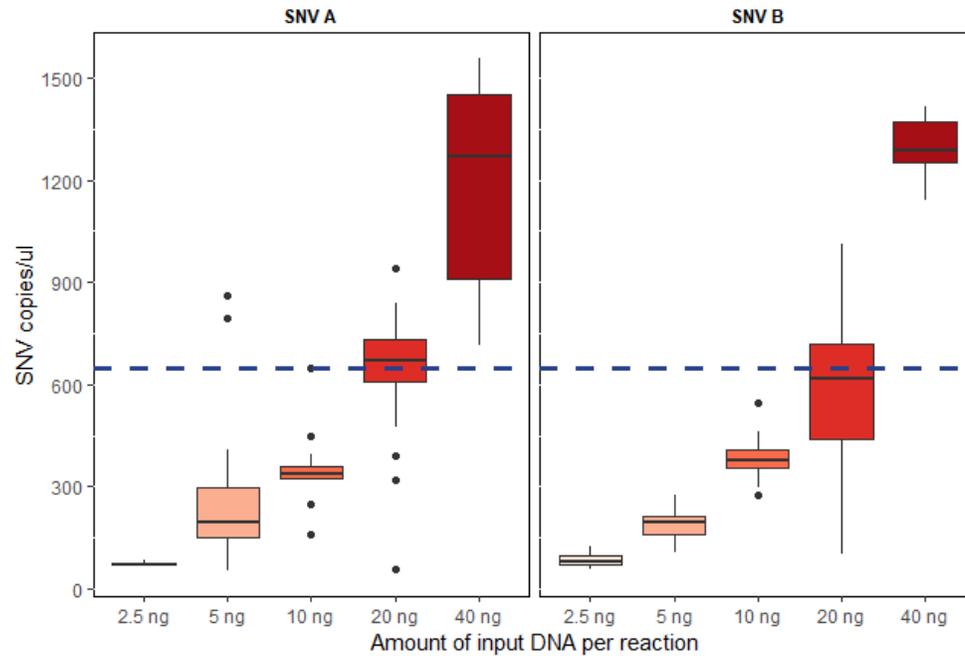
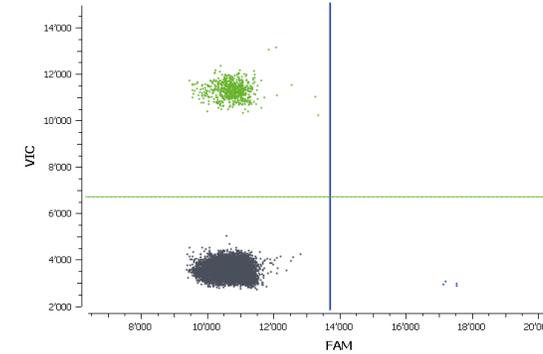


Figure 2: Total measured copies/ μ l per reaction with increasing amount of DNA per reaction. Taqman™ assays specific for 2 different SNVs were used in 16 replicates. As expected, we observed an increasing amount of detected copies/ μ l by increasing the amount of input DNA. Around 650 copies/ μ l are expected with our routine experimental setup of 20 ng input DNA per reaction.

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The analysis of artificial DNA mixes provided reproducible quantification of the minor allele, even below 0.25%. Notably, the clinically required 0.5% minor allele sensitivity was achieved with only 5 ng of input DNA per reaction (Figure 3).

A



B

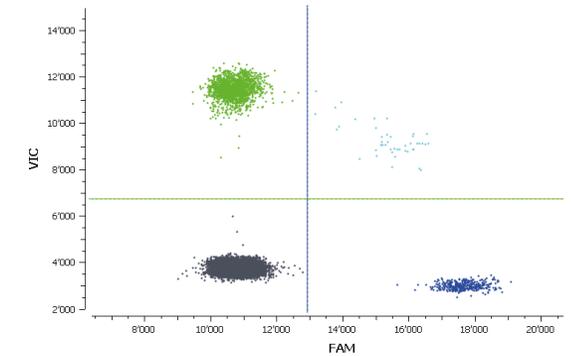


Figure 3: Crystal dPCR 2D-Plots for artificial DNA mixes. **A.** Analysis of 5ng of an artificial DNA mix: DNA A, homozygous for the allele G of the SNV rs1058396 (FAM-labelled in the specific Taqman™ assay, Thermofisher), was mixed with DNA B, homozygous for the allele A (VIC-labelled). The crystal dPCR system allowed accurate quantification of 0.5% DNA A in DNA B. **B.** Analysis of 20 ng of artificial DNA mix with 16% DNA A in 84% DNA B.

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In addition, the reliability of the crystal dPCR platform was confirmed on previously monitored patient's samples and several external proficiency testing (EQA) samples (Table 1).

Sample	Expected Value	1s-range	Crystal dPCR Result
61 a	0.00%	0.00%-0.00%	0.03%*
62 a	3.96%	3.47%-4.46%	3.96%
63 a	6.86%	5.92%-7.80%	7.12%
65 a	57.00%	54.21%-59.79%	57.41%

Sample	Expected Value	1s-range	Crystal dPCR Result
61 b	2.85%	1.64%-4.06%	2.45%
62 b	4.77%	3.16%-6.38%	4.12%
63 b	9.22%	6.59%-11.85%	9.22%
65 b	78.10%	67.60%-88.60%	75.39%

Table 1: Results of 2 EQAs from Instand e.V. Samples from 2 independent chimerism EQAs (artificial blood mixes) from 2017 (a) and 2018 (b) were analyzed in duplicate with 2 Taqman assays targeting SNVs. Results are given in percent of "receiver". Results within the 1s-range are awarded with the maximum grade. *0.03% corresponds to a negative control and would be reported as "absence of chimerism".

Conclusion

This new generation of dPCR is fully compatible with our established SNV-based chimerism monitoring and has been proven to be fast, convenient and highly accurate. In addition to minimal hands-on-time, and consumable use, the low amount of input DNA per reaction should be emphasized, opening the option of lineage specific chimerism monitoring.

References

¹Gourri et al. Chip-based dPCR: an accurate and sensitive method for routine chimerism monitoring after HSCT. DGHO Annual conference 2016.

²Madic et al. Three-color crystal dPCR. *Biomol Detect Quantif.* 2016 Dec; 10: 34–46.