Using the Qubit[™] dsDNA HS Kit on the Eppendorf BioSpectrometer[®] fluorescence

Martin Armbrecht, Eppendorf AG, Germany

Introduction

In addition to the quantification of dsDNA samples in the Eppendorf BioSpectrometer fluorescence via the fluorescent dye PicoGreen (1,2), Qubit Assay kits by Thermo Fisher Scientific may also be used for this purpose. The UVette[®] as well as the Eppendorf μ Cuvette[®] G1.0 are ideally suited to this task. With the UVette, regression analysis of the standard curve may be carried out using a simple 2-point calibration (linear interpolation) as described in the original Qubit protocol; however, when using the μ Cuvette, it is recommended to measure 4 standards and perform a quadratic regression analysis (3).

Materials and Methods

Materials

- > BioSpectrometer fluorescence
- > UVette, Eppendorf µCuvette
- > Eppendorf Safe-Lock tubes 0.5 mL
- > MixMate[®]
- > Qubit dsDNA HS Assay kit

Preparation of samples and standards

Standards and samples are diluted 1:20 in Qubit working buffer as described in the kit protocol. The measurements can be performed in the UVette as well as in the μ Cuvette. Prior to measurement, samples and standards should be pre-incubated for a period of at least 5 minutes:

UVette

5 μL sample or standard are diluted with 95 μL of measurement buffer, respectively, directly inside the UVette ($\Sigma = 100~\mu L$), and mixed well using a pipette. This preparation is ready to be measured.

μCuvette

2 μ L sample / standard and 38 μ L buffer (Σ =40 μ L) are transferred to a 0.5 mL Safe-Lock tube and mixed well by vortexing (MixMate). Measurements performed in the μ Cuvette require only 5 μ L of the preparation (3).

Determination of sample concentration in the BioSpectrometer, with the help of the UVette, may be carried out via 2-point calibration (linear interpolation) using the standards provided in the kit (final concentrations: 0 and 500 ng/mL). In this case, no changes to the protocol need to be made, except for volume adjustments. Quadratic regression analysis is recommended when working with the μ Cuvette, which requires a minimum of 4 standards.

The two additional standards may be generated directly from standard 2 (component D: 10 μ g/mL dsDNA) of the Qubit HS kit (table 1).

Table 1: Additional standards

Standard Dilution Example: 20 µL total volume concentration	Final concentration after 1:20 dilution in Qubit working solution
10 μg/mL Standard 2 (component D undiluted) –	500 ng/mL
5 μg/mL 50 % Standard 2 + 50 % working buffer 10 μL Standard 2 + 10 μL Qubit [™] dsDNA HS	buffer 250 ng/mL
2 μg/mL20 % Standard 2 + 80 % working buffer4 μL Standard 2 + 16 μL Qubit™ dsDNA HS br	uffer 100 ng/mL
0 μg/mL Standard 1 (component C: undiluted) –	0 ng/mL

The Qubit[™] dsDNA HS buffer is included in the kit (component B). It is also used to prepare the Qubit working solution: Qubit[™] dsDNA HS reagent (component A) is diluted 1:200 in the Qubit[™] dsDNA HS buffer. The working solution is also required for sample measurement. Table 2 shows the volume of working solution required for the measurement of 20 samples, including standards.

Table 2: Volume of working solution required for 20 samples using the respective measurement systems

Measurement in the Qubit	Measurement using UVette and	Measurement in the µCuvette and
(200 μL measurement volume)	BioSpectrometer fluorescence	BioSpectrometer fluorescence
20 * 190 μL (samples) = 3800 μL	20 * 95 μL (samples) = 1900 μL	20 * 38 μL (samples) = 760 μL
2 * 190 μL (standards) = 380 μL	2 * 95 μL (standards) = 190 μL	4 * 38 μL (standards) = 152 μL
$\Sigma = 4180 \ \mu L$	$\Sigma = 2090 \ \mu L$	$\Sigma = 912 \ \mu L$

The amount of Qubit working solution (WS) that is required for X number of samples in each of the measurement systems can be calculated using the following formula:

$Vol._{WS} = (X*D) + (Y*D)$

WS = working solution

- **X** = number of samples
- $\mathbf{Y} =$ number of standards
- **D** = volume specific to the system:
 - > Qubit = 190 μ L
 - > BioSpectrometer + UVette = 95 μ L
 - > BioSpectrometer + μ Cuvette = 38 μ L

Parameter selection and measurement of standards on the BioSpectrometer fluorescence:

On the BioSpectrometer, the pre-programmed Qubit-HS method may be used (figure 1).

Method Selection			
Main Groups	Sub Groups	Methods	
Favorites	Nucleic acids	PicoGreen®	
Photometry	Proteins	PicoGreen® short	
Absorbance		OliGreen®	
Routine		OliGreen® short	
🗅 Basic		RiboGreen®	
🗅 Advanced		RiboGreen® short	
Fluorimetry		Qubit® dsDNA BR	
C Routine		🗿 Qubit® dsDNA HS	
Basic		Qubit® ssDNA	
		<new method=""></new>	
Cut Copy	Rename Delete	Paste Function	

Figure 1: Selection of the pre-programmed Qubit method

The number of standards to be measured and their respective concentrations are then defined in the area "Check Parameters" prior to measurement (figures 2A and 2B.).

Α			В	
Qubit® dsDNA HS: c	heck parameters	measure standards	Qubit® dsDNA HS: check parameters measure standards	-[]
Wavelength (em) Wavelength (ex) Unit Standards Roplicatos	520 nm 470 nm ng/mL 4	Page 1/2	Std. Conc. 1 0 ng/mL Page 2/2 Std. Conc. 2 100 ng/mL Std. Conc. 3 250 ng/mL Std. Conc. 3 250 ng/mL Std. Conc. 4 500 ng/mL	2
Decimal places	0 off	Info Edit parameters: "Edit" softkøy.	Edit parameters: "Edit" softkey.	
Edit	Page dn A	Show more parameters: "Page up" or "Page dn". bort < Back Next >	Show more parameters: "Page up" or "Page dn". Edit Page up Page dn Abort Back	>

Figures 2A and 2B: Definition of the numbers of standards and their respective concentrations:

A: The "Edit" function allows you to change the number of standards. If the μCuvette is chosen for the measurements, the 4 predetermined standards can be used as pre-programmed in the BioSpectrometer software. With the use of the UVette the number of standards to be measured may be set to "2". The number of replicates to be measured per standard may be set to "1" (red arrows).
B: When using the μCuvette, the 4 pre-determined standard concentrations may be retained, whereas standard concentrations 2 and 3 can be omitted when using the UVette (red arrows).

Measurements using the μ Cuvette can take advantage of the pre-programmed quadratic regression analysis option. If standards 2 and 3 are subsequently removed when using the UVette, the standard curve analysis will automatically adjust to linear interpolation of the standards measured. All regression analyses of standard curves may be fitted on the BioSpectrometer via "Curve Fit" (figure 3).

Qubit® dsDNA HS:	neasure sta	ndards / new	
	Conc.	Fluorescence	Quadratical regression:
	ng/mL	RFU ₅₂₀	not calculated
Standard 1	0	 X:	
Standard 2	100	 X:	
Standard 3	250	 X:	Info Measure blank:
Standard 1	500	 	"blank" key.
Last Cal Curve Fit Abort < Back			

Figure 3: Fitting of the regression analysis via "Curve Fit" (red arrow).

Results

UVette - linear interpolation

The samples are measured directly following measurement of the standards. Figure 4A shows the example of linear interpolation, resulting from the two measured standards (0 and 500 ng/mL) in the UVette. Figure 4B shows sample measurements relative to the standards. The sample results are then displayed directly in relation to the standard curve.



Figure 4: Measurement using the UVette, analyzed via 2-point calibration A: Standard curve; B: Measurement result

$\mu Cuvette-quadratic\ regression$

In contrast, quadratic regression is recommended when using the μ Cuvette. The result is shown in figure 5.



Figure 5: Measurements in the μ Cuvette, analyzed via quadratic regression A: Standard curve; B: Measurement result

Depending on which cuvette is used, it is important to remember that the path length of the μ Cuvette is 10-fold shorter than the path length of the UVette. As a result, the μ Cuvette has a higher detection limit than the UVette. As a rule of thumb, it is recommended that the sample exhibit an RFU value of at least 0.5 to be detected in the BioSpectrometer fluorescence in a reproducible manner.

This value is roughly equivalent to the following dsDNA concentrations:

A UVette: approx. 5 ng/mL B μCuvette: approx. 50 ng/mL

Conclusion

Further to the Quant-iT dsAssay kit (PicoGreen®), the Qubit dsDNA HS Assay kit offers an additional option for quantifying dsDNA samples of low concentration on the BioSpectrometer fluorescence with high specificity and sensitivity. Quantifications using the UVette require half the amount of reagent as compared to the Qubit standard protocol, and while 4 standards are recommended for measurements performed in the μ Cuvette, only 1/5 of the reagent volumes outlined in the original protocol are required.

Literature

- Armbrecht, M. Fluorimetric Determination of dsDNA Concentrations via 2-point Calibration. Eppendorf Short Protocol No. 18
- [2] Armbrecht, M, Gloe, J, Goemann, W. Determination of nucleic acid concentrations using fluorescent dyes in the Eppendorf BioSpectrometer[®] fluorescence. Eppendorf Application Note No. 271 (2013)
- [3] Armbrecht, M. Economic DNA determination in the Eppendorf BioSpectrometer[®] fluorescence using Qubit[™] Assay kits. Eppendorf Application Note No. 402 (2018)

Ordering information

Description	Order no. International	Order no. North America
Eppendorf BioSpectrometer® fluorescence 230 V/50-60 Hz, electrical plug Europe, additional electrical connection variants available 120 V/50-60 Hz, electrical plug North America	6137 000.006 6137 000.014	6137000014
Eppendorf µCuvette® G1.0, Microvolume measuring cell for Eppendorf BioPhotometer and BioSpectrometer	6138 000.018	6138000018
UVette® routine pack 220 nm – 1 600 nm Eppendorf Quality purity, resealable box, 200 pcs	0030 106.318	952010069

Your local distributor: www.eppendorf.com/contact Eppendorf AG · Barkhausenweg 1 · 22339 Hamburg · Germany eppendorf@eppendorf.com · www.eppendorf.com

www.eppendorf.com

PicoGreen[®] is a registered trademark of Molecular Probes, Inc. Corporation, Eugene, OR, USA. Qubit[™] is a trademark of Life technologies Corporation, Carlsbad, CA 92008, USA. Eppendorf[®], the Eppendorf Brand Design, Eppendorf BioSpectrometer[®], the UVette[®] and the Eppendorf µCuvette[®] are registered trademarks of Eppendorf AG, Hamburg, Germany. All rights reserved, including graphics and images. Copyright © 2018 by Eppendorf AG, Hamburg, Germany.