# Quantification of bacterial DNA in blood using droplet digital PCR: a pilot study

**Running title:** ddPCR to quantify bacterial DNA

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**Key Words:** Droplet digital PCR; ddPCR; Bloodstream infections; bacteria genomic DNA quantification

## Abstract

Bloodstream infections (BSIs) caused by bacteria associated with sepsis are among the leading causes of mortality, particularly in critically ill patients [1,2]. The gold standard method for the microbiological diagnosis of BSIs is still blood culture, which is slow, cannot detect viruses, and only yield positive results in one-third of suspected BSIs and sepsis cases [1,3]. Droplet digital PCR (ddPCR) is a next-generation PCR method, with great precision and accuracy, that allows absolute quantification of target gene(s) without a standard curve and little interference from normal PCR inhibitors[4]. These characteristics make ddPCR an ideal method for the detection and quantification of pathogens directly from blood or other clinical samples [4] in patients with suspected BSI and sepsis. The aim of this work was to use genus/species specific genes ddPCR assays to detect and quantify bacterial DNA from four of the most common BSIs pathogens in blood. Here we demonstrate the quantification capacity and specificity of two duplex ddPCR assays that allow the detection and quantification of *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus* and *Enterococcus* spp directly from blood.

## Introduction

Bloodstream infections (BSIs) caused by bacteria associated with sepsis are among the leading causes of mortality, particularly in critically ill patients [1,2]. The gold standard method for the microbiological diagnosis of BSIs is still blood culture, which is slow, cannot detect viruses, and only yield positive results in one-third of suspected BSIs and sepsis cases [1,3]. Droplet digital PCR (ddPCR) is a next-generation PCR method, with great precision and accuracy, that allows absolute quantification of target gene(s) without a standard curve and little interference from normal PCR inhibitors[4]. These characteristics make ddPCR an ideal method for the detection and quantification of pathogens directly from blood or other clinical samples [4] in patients with suspected BSI and sepsis. The aim of this work was to use genus/species specific genes ddPCR assays to detect and quantify bacterial DNA from four of the most common BSIs pathogens in blood. Here we demonstrate the quantification capacity and specificity of two duplex ddPCR assays that allow the detection and quantification of *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus* and *Enterococcus* spp directly from blood.

Due to the high mortality of BSIs and sepsis, early administration of empiric broad-spectrum antimicrobials is normally the first step in the treatment of these infections, but in many occasions this it is not accurate for the actual bacterial pathogen causing BSI or sepsis, leading to therapeutic failure and death [1–3,5]. Therefore, it is imperative to identify, in a timely manner, the infectious agent causing BSI or infection leading to sepsis (bacteria, fungi, or virus) as well as possible associated antimicrobial resistances [2,4], in order to administer tailored antimicrobial therapy. Thus, it is necessary to develop rapid, sensitive, and accurate molecular diagnostic methods to

identify and quantify pathogens and their antimicrobial resistances directly in the blood [2,3]. Furthermore, time to blood culture positivity has been suggested as a surrogate marker of blood bacterial load and associated with poor clinical outcome in BSIs [6,7]. Therefore, the early identification and quantification of bacterial DNA load in blood of patients with suspected BSIs or sepsis could help to assess illness severity and further guide patient's treatment [2,4,8].

Even though the previously mentioned characteristics of ddPCR make it an attractive method for the identification and quantification of pathogens directly from blood or other clinical samples [2,4] in patients with suspected BSI and sepsis, very few studies have validated its performance to assist in BSI diagnosis. In this pilot study we aimed to demonstrate the specificity and sensitivity of ddPCR to detect and quantify bacterial DNA from *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus* and *Enterococcus* spp directly from blood.

## Material and methods

*Bacterial strains and DNA extraction.* Clinical strains, identified as belonging to the bacterial species of interest by VITEK® MS (Biomérieux, Marcy-l'Étoile, France), were recovered from de Microbiology Department of Hospital Universitario Río Hortega, Spain, from May 2019 and February 2020 (Table 1). No personal data from patients were recorded, and strains were anonymized on collection.

Strains were plated on Columbia blood agar and colonies picked and stored in 40% glycerol at -80°C. Genomic DNA from bacterial colonies was obtained using the Promega Wizard Genomic DNA Purification Kit (Promega, Madison WI, USA) and DNA concentrations measured with Nanodrop (Thermo Scientific, Waltham MA,

USA). Serial dilutions with RNase free water were done to obtain working concentrations of 10, 1, 0.1, 0.01, 0.001 and 0.0001 ng/µL. of bacterial DNA.

*Description of ddPCR assays*. Primers and probes used for ddPCR assays are listed in Table 2. All primers and probes (Integrated DNA Technologies, Coralville IA, USA) have been previously used to detect *E. coli*, *K pneumoniae, S. aureus* and *Enterococcus* spp. with either real-time PCR or ddPCR [9–11]. Probes for Gram-negative bacteria (*E. coli*, and *K pneumoniae*) were labelled with HEX and probes for Gram-positive bacteria (*S. aureus*, and *Enterococcus* spp.) were labelled with FAM.

All the assays were performed using the QX200 Droplet Digital PCR system (Bio-Rad Laboratories Inc., Pleasanton, CA, USA) according to manufacturer instructions. Template DNA (2.5µL) was added to 18.5µL of mastermix containing ddPCR Supermix for probes (no dUPTs), forward and reverse primer (0.9µM each) and probe (0.25µM). This mastermix was placed into a QX200 droplet generator in order to generate droplets. The generated droplet emulsion was transferred to a new 96-well PCR plate and amplified in a C1000 Touch Thermal Cycler (Bio-Rad Laboratories Inc., Pleasanton, CA, USA). The amplification protocol was as follows: 95ºC for 10 minutes, 40 cycles at 94ºC for 30s and 58ºC for 1 minute, and a final cycle at 98ºC for 10 minutes. After gene amplification, the plate was transferred to and read in a QX200 droplet reader (Bio-Rad Laboratories Inc., Pleasanton, CA, USA).

In order to evaluate the performance of primers and probes in the detection of the above-mentioned bacterial species, developmental ddPCR assays were first performed as simplex ddPCR and then *E. coli* and *S. aureus* were tested as duplex ddPCR and *K. pneumoniae* and *Enterococcus* (*Enterococcus faecium* and *Enterococcus faecalis*),

using one clinical strain. In the developmental assays different DNA concentrations (10, 1, 0.1, 0.01, 0.001 and 0.0001 ng/µL) were tested in triplicate.

After determining the ideal concentration to use, further clinical strains (Table 1) were used to evaluate the precision of the test in detecting the target bacteria in the clinical setting and against related isolates. To that end, isolates from the target bacteria (*E. coli*, *K. pneumoniae*, *S. aureus*, *E. faecium* and *E. faecalis*) were obtained from clinical samples. In order to evaluate primers specificity other bacteria similar to *E. coli* and *K. pneumoniae*, *S. aureus* and *Enterococcus* spp. were included (Table 1) in the assay.

*Spiked blood ddPCR assays*. One clinical strain for *E. coli*, *K. pneumoniae*, *S. aureus*, *E. faecium* and *E. faecalis* was inoculated in blood agar plate and incubated overnight at 37ºC. One colony for each bacterial species was inoculated in thioglycolate broth (Biomérieux, Marcy-l'Étoile, France) and incubated overnight at 37ºC. Each bacterial culture was serial dilute (1:10) in saline 0.9% ($1x10^8$ to 1 CFU/mL), and 20µL were plated in duplicate in blood agar plates and incubated overnight at 37ºC. Colonies were counted to calculate the CFU/mL of the initial thioglycolate broth culture. Blood was spiked with saline dilutions of $1x10^5$, $1x10^4$, $1x10^3$, $1x10^2$ and 10 CFU/mL in order to obtain blood spiked with $1x10^4$, $1x10^3$, $1x10^2$, 10 and 1 CFU/mL. DNA was extracted from spiked blood ($1x10^4$ to 1 CFU/mL) using MolYsis Basic5 DNA extraction kit (Molzym, Bremen, Germany) combined with QIAamp UCP Pathogen Mini Kit (Qiagen, Venlo, Netherlands) following manufacturer instructions. For ddPCR assays 2.5µL of each DNA extracted from spiked blood ($1x10^4$ to 1 CFU/mL) were tested in the previously described ddPCR duplex assays. The number of copies of bacterial housekeeping genes present for each bacterial genome were calculated taking into

account the number of copies each bacterial gene has in the species genome (Table 2). These experiments were performed in duplicate.

*Statistics.* Pearson correlation coefficient was used to compare the CFU/mL results obtained from bacterial cultures with copy number of those obtained from spiked blood.

**Results and discussion**

The best annealing temperature for all the simplex assays was determined to be 58ºC. In consequence, it was possible to run duplexed assays as described above, involving one Gram-Positive and one Gram-negative species each (*E. coli* + *S. aureus* and *K. pneumoniae* + *Enterococcus* spp.). These duplexed assays showed low replication variability and very low limit of detection, being able to detect DNA solutions with concentrations of 1pg/µL and in some cases 0.1pg/µL as we briefly described in Merino *et al* [4]. The very high sensitivity demonstrated by ddPCR in this study has been previously documented [4] making it an ideal method for detection and quantification of pathogens in sites were their initial load might be very small as BSIs [12].

The ddPCR assay employed to detect and quantify *E. coli* and *S. aureus* did not amplify any of the other Non-*E. coli* Enterobacteriaceae or any other species from the genus *Staphylococcus*, used to test specificity of the assay to *E. coli* and *S. aureus*, respectively. The same was true for the duplex assay for *K. pneumoniae* and *Enterococcus* spp. In this case the assay did not amplify other species from the genus *Klebsiella* or other Non-*Klebsiella* Enterobacteriaceae and *Streptococcus agalactiae*, used to test specificity of the assay to *K. pneumoniae* and *Enterococcus* spp, respectively (Table 1). These results indicate great specificity of the ddPCR assays for each of the tested genera and/species, confirming the results obtained in previous

studies using the same primers/probes set [9–11]. The high specificity demonstrated is important as it gives the analyst confidence to report the results obtained and therefore guide and improve patients' treatment.

Time from sample preparation to results was approximately 3.5h to 4h, significantly reducing the time to get actionable information (bacterial identification) compared to the gold standard blood culture technique (24h-48h). The time from sample to results we report here is similar to that reported by other pilot studies using ddPCR assays to detect BSIs [2,13].

The spiked blood experiments showed that there is an almost perfect correlation ($0.997 \leq r \leq 1.000$, $p \leq 0.001$) between the number of CFU/mL of the bacterial culture and the number of gene copies/mL detected by ddPCR in each dilution tested (Figure 1). For almost all bacterial species tested ddPCR presented gene copies/mL in the same order of magnitude as bacterial culture results (CFU/mL). These results indicate that the ddPCR assays used in this study have a limit of detection of 1-10 CFU/mL. This very low detection limit has also been found in other studies using other ddPCR assays [2,13,14] to detect bacterial pathogens in blood.

Even though these assays were designed to detect the *E. coli*, *K. pneumoniae*, *S. aureus* and *Enterococcus* spp in blood they demonstrate the high performance of ddPCR, suggesting that this technology might be used for other applications (Figure 2), as: i) diagnostic of any type of infection [4], particularly those cases with low bacterial loads or difficult access to infection site (e.g. tuberculosis, meningitis or endocarditis), or in the case of sepsis where the positivity rate of current diagnostic techniques is low; ii) detection and quantification of antimicrobial genes or point mutations leading to

antimicrobial resistance, allowing the reduction of the time from sample collection to results from at least 24-48h to a few hours, helping to guide and improve patients' treatment [2,13,14]; iii) severity stratification of the disease: high DNA loads have been associated to faster disease progression and greater mortality in patients with BSI [8,15]; iv) distinguish between colonization and infection: quantifying bacterial DNA load might help to determine whether a certain opportunistic pathogen might be just colonizing a given site or if it is causing an infection instead (e.g. intestinal infections and lung infections); v) and finally, detection and quantification of the transcriptome of bacterial toxins: the detection and quantification of mRNA of *E. coli*, *Shigella* and *Clostridioides difficile* toxins might help with the diagnosis of infections by these bacterial species and also to assess disease severity, prognosis and guide treatment. Further studies specifically designed to test the performance of ddPCR to identify and quantify bacterial genomes directly from blood samples of patients with BSI are warranted.

## Conclusions

In this study we demonstrated that ddPCR assays to detect DNA from *E. coli*, *K. pneumoniae*, *S. aureus* and *Enterococcus* spp show a very low limit of detection, high sensitivity and specificity and can be used to identify and quantify DNA from these four bacterial genus/species directly from blood samples without the need of an intermediate step of bacterial culture. This pilot study reinforces the potential of ddPCR for the diagnosis and severity stratification of BSI and sepsis.

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**Author contributions:** APT and JFBM designed the study. APT and JFBM wrote the manuscript and interpreted the data. IM, MDG and JMRE collected clinical strains used in the study. APT, IM and AO performed the assays for the detection and quantification of bacterial genomic DNA from bacterial cultures and directly from blood. All authors read and approved the final manuscript.

## Conflict of interest

The authors declare no conflicts of interest regarding this submission.

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## Tables and Figures

### Table 1. Bacterial species and number of clinical strains used in the study

| Species | No of clinical strains |
|---|---|
| ***Escherichia coli*** | **10** |
| ***Klebsiella pneumoniae*** | **12** |
| *Citrobacter braakii* | 1 |
| *Enterobacter cloacae* | 1 |
| *Klebsiella oxytoca* | 3 |
| *Morganella morganii* | 3 |
| *Proteus mirabilis* | 3 |
| ***Staphylococcus aureus*** | **10** |
| *Staphylococcus constellatus* | 1 |
| *Staphylococcus epidermidis* | 4 |
| *Staphylococcus haemolyticus* | 2 |
| *Staphylococcus hominis* | 2 |
| *Staphylococcus simulans* | 2 |
| *Staphylococcus saprophyticus* | 1 |
| ***Enterococcus faecalis*** | **6** |
| ***Enterococcus faecium*** | **4** |
| *Streptococcus agalactiae* | 8 |

## Table 2. Primers and Probes used in the study

| Bacterial Genus or Species | Gene or region amplified | Copies of the gene of the genome | Primers and Probe name | Sequence (5'-3') | Concentration (µM) | Amplicon size (bp) | ddCPR conditions | Reference |
|---|---|---|---|---|---|---|---|---|
| *E. coli* | *gad* | 2 | gad-FW | GGATATCGTCTGGGACTTCCG | 0.9 | 77 | 95ºC for 10min, 40 cycles 94ºC for 30s and 58ºC for 1min, 98ºC 10min | [9] |
| | | | gad-RV | GCGGAGCCAGACCGAATTT | 0.9 | | | |
| | | | gad-TMP | HEX-GTGAAATCGATCAGTGCTTCAGGCCA-ZEN/IBFQ | 0.25 | | | |
| *K. pneumoniae* | *khe* | 1 | khe-FW | TGGGGATCCACCACGA | 0.9 | 126 | 95ºC for 10min, 40 cycles 94ºC for 30s and 58ºC for 1min, 98ºC 10min | [9] |
| | | | khe-RV | AGAGATAGCCGTTTATCCACAC | 0.9 | | | |
| | | | khe-TMP | HEX-GAGGAAGAGTTCATCTACGTGCTGGAGG-ZEN/IBFQ | 0.25 | | | |
| *S. aureus* | SA442 | 1 | SA442-F | CAATCTTTGYCGGTACACGATATTCT | 0.9 | 112 | 95ºC for 10min, 40 cycles 94ºC for 30s and 658 for 1min, 98ºC 10min | [10] |
| | | | SA442-R | CAACGTAATGAGATTTCAGTAGATAATACAAC | 0.9 | | | |
| | | | SA442-P | FAM-CACGACTAAATARACGCTCATTCGCRATTTT-ZEN/IBFQ | 0.25 | | | |
| *Enterococcus spp* | 23S rDNA | 6 (*E. faecium*) | EnteroF1A | GAGAAATTCCAAACGAACTTG | 0.9 | 93 | 95ºC for 10min, 40 cycles 94ºC for 30s and 58ºC for 1min, 98ºC 10min | [11] |
| | | | EnteroR1 | CAGTGCTCTACCTCCATCATT | 0.9 | | | |
| | | 4 (*E. faecalis*) | GPL813TQ | FAM-TGGTTCTCTCCGAAATAGCTTTAGGGCTA-ZEN/IBFQ | 0.25 | | | |

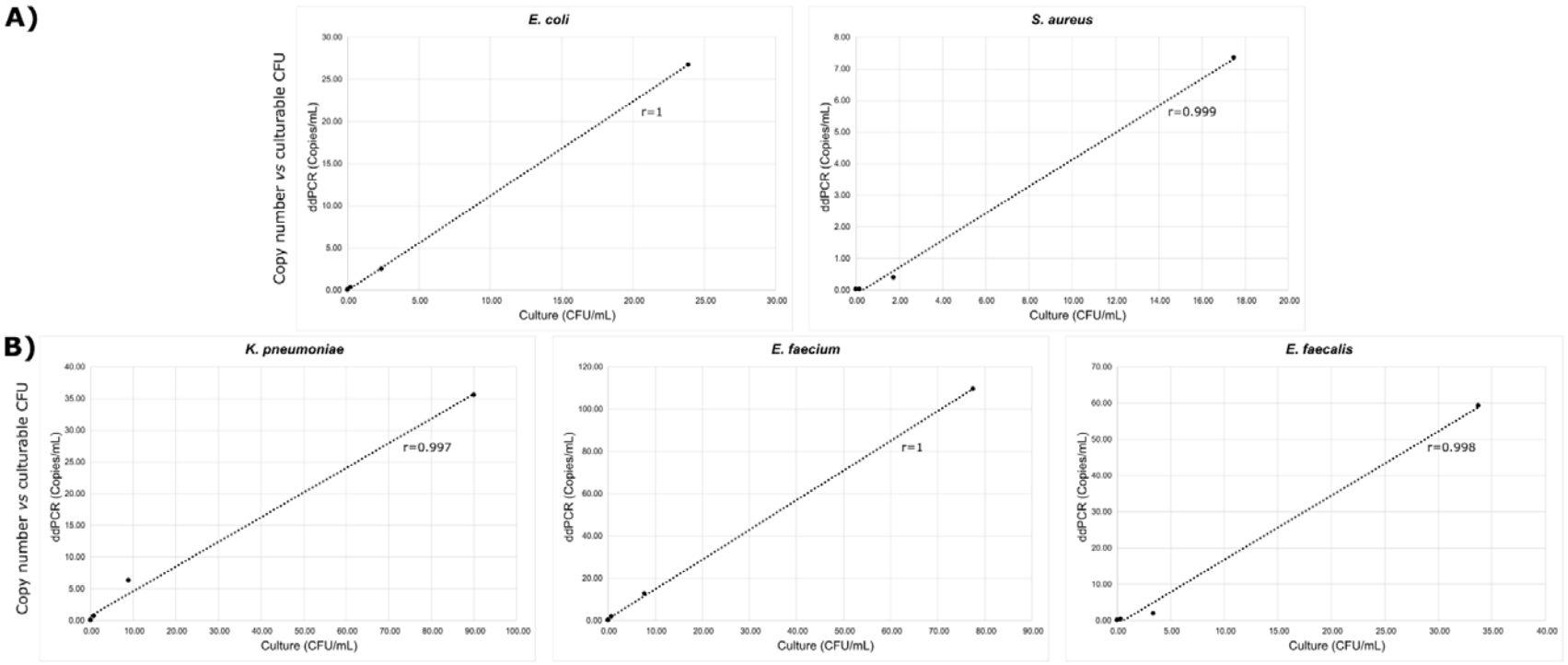


**Figure 1. Correlation between the number of CFU/mL of the bacterial culture and the number of gene copies/mL detected by ddPCR.**

A) ddPCR assay to detect and quantify *E. coli* and *S. aureus*. B) ddPCR assay to detect and quantify *K. pneumoniae* and *Enterococcus* spp.


**Figure 2. Possible applications of ddPCR for bacterial, viral and fungal infections diagnosis**