PCR Protocol for Phusion™ High-Fidelity DNA Polymerase (NEB #M0530)

Materials

- $MgCl_2$ solution (NEB #B0510)
- DMSO (NEB #B0515)
- Phusion HF Buffer Pack (NEB #B0518)
- Phusion GC Buffer Pack (NEB #B0519)

Materials Required but not Supplied

Phusion™ High-Fidelity DNA Polymerase

- Deoxynucleotide (dNTP) Solution Mix (NEB #N0447)
- Nuclease-free Water (NEB #B1500)
- Template DNA
- Associated forward and reverse primers

Overview

The following guidelines are provided to ensure successful PCR using Phusion™ DNA Polymerase. These guidelines cover routine PCR. Amplification of templates with high GC content, high secondary structure, low template concentrations, or long amplicons may require further optimization. The NEB Tm calculator should be used to determine the annealing temperature when using Phusion. Please note that protocols with Phusion DNA Polymerase may differ from protocols with other standard polymerases. As such, the conditions recommended below should be used for optimal performance.

Protocol

Reaction Setup:

1. Assemble all reaction components on ice. Gently mix all the components of the reaction before use. Phusion DNA Polymerase may be diluted in 1X Phusion HF or GC Buffer just prior to use to reduce pipetting errors. Collect all liquid to the bottom of the tube with a quick spin if necessary. Overlay the sample with mineral oil if using a PCR machine without a heated lid.

2. Quickly transfer the reactions to a thermocycler preheated to the denaturation temperature (98°C).

Component	20 µl Reaction	50 µl Reaction	Final Concentration
5X Phusion HF or GC Buffer	4 µl	10 µl	1X

Component	20 µl Reaction	50 µl Reaction	Final Concentration
10 mM dNTPs	0.4 µl	1 µl	200 µM
10 µM Forward Primer	1 µl	2.5 µl	0.5 µM
10 µM Reverse Primer	1 µl	2.5 µl	0.5 µM
Template DNA	variable	variable	< 250 ng
DMSO (optional)	(0.6 µl)	(1.5 µl)	3%
Phusion DNA Polymerase	0.2 µl	0.5 µl	1.0 units/50 µl PCR
Nuclease-free water	to 20 µl	to 50 µl	

Thermocycling conditions for a routine PCR:

STEP	TEMP	TIME
Initial Denaturation	98°C	30 seconds
25-35 Cycles	98°C 45-72°C 72°C	5-10 seconds 10-30 seconds 15-30 seconds/kb
Final Extension	72°C	5-10 minutes
Hold	4-10°C	

Thermocycling conditions for a routine 2-step PCR:

STEP	TEMP	TIME
Initial Denaturation	98°C	30 seconds
25-35 Cycles	98°C 72°C	5-10 seconds 15-30 seconds/kb
Final Extension	72°C	5-10 minutes
Hold	4-10°C	

General Guidelines:

1. **Template:**
   Use of high quality, purified DNA templates greatly enhances the success of PCR. Recommended amounts of DNA template for a 50 µl reaction are as follows:

DNA	Amount
genomic	50 ng–250 ng
plasmid or viral	1 pg–10 ng

If the template DNA is obtained from a cDNA synthesis reaction, the volume added should be less than 10% of the total reaction volume.

2. **Primers:**
   Oligonucleotide primers are generally 20–40 nucleotides in length and ideally have a GC content of 40–60%. Computer programs such as Primer3 can be used to design or analyze primers. The best results are typically seen when using each primer at a final concentration of 0.5 µM in the reaction.

3. **Mg^{++} and additives:**
   Mg^{++} is critical to achieve optimal activity with Phusion DNA Polymerase. The final Mg^{++} concentration in 1X Phusion HF and GC Buffer is 1.5 mM. Excessive Mg^{++} can prevent full denaturation of DNA as well as cause non-specific binding of primers. The optimal Mg^{++} concentration is affected by dNTP concentration, the template being used, and supplements that are added to the reaction. This can also be affected by the presence of chelators (e.g. EDTA). Mg^{++} can be optimized in 0.5 mM increments using the $MgCl_2$ provided.

   Amplification of difficult targets, such as those with GC-rich sequences or secondary structure, may be improved by the use of the GC buffer and/or presence of additives such as DMSO (included). A final concentration of 3% DMSO is recommended, although concentration can be optimized in 2% increments. It is important to note that if a high concentration of DMSO is used, the annealing temperature must be lowered as it decreases the primer T_m (1). Phusion DNA polymerase is also compatible with other additives such as formamide or glycerol.

4. **Deoxynucleotides:**
   The final concentration of dNTPs is typically 200 µM of each deoxynucleotide. Phusion cannot read through or incorporate dUTP.

5. **Phusion DNA Polymerase Concentration:**
   We generally recommend using Phusion DNA Polymerase at a concentration of 20 units/ml (1.0 units/50 µl reaction). However, the optimal concentration of Phusion DNA Polymerase may vary from 10–40 units/ml (0.5–2 units/50 µl reaction) depending on amplicon length and difficulty. Do not exceed 2 units/50 µl reaction, especially for amplicons longer than 5 kb.

6. **Buffers:**
   5X Phusion HF Buffer and 5X Phusion GC Buffer are provided with the enzyme. HF buffer is recommended as the default buffer for high-fidelity amplification. For difficult templates, such as GC-rich templates or those with secondary structure, GC buffer can improve reaction performance. GC buffer should be used in experiments where HF buffer does not work.

7. **Denaturation:**
   An initial denaturation of 30 seconds at 98°C is sufficient for most amplicons from pure DNA templates. Longer denaturation times can be used (up to 3 minutes) for templates that require it.

   During thermocycling, the denaturation step should be kept to a minimum. Typically, a 5–10 second denaturation at 98°C is recommended for most templates.

8. **Annealing:**
   Annealing temperatures required for use with Phusion tend to be higher than with other PCR polymerases. The NEB **Tm calculator** should be used to determine the annealing temperature when using Phusion**.** Typically, primers greater than 20 nucleotides in length anneal for 10–30 seconds at 3°C above the T_m of the lower T_m primer. If the primer length is less than 20 nucleotides, an annealing temperature equivalent to the T_m of the lower primer should be used. A temperature gradient can also be used to optimize the annealing temperature for each primer pair, the gradient can be set as high as the extension temperature.

   For high T_m primer pairs, two-step cycling without a separate annealing step can be used.

9. **Extension:**
   The recommended extension temperature is 72°C. Extension times are dependent on amplicon length and complexity. Generally, an extension time of 15 seconds per kb can be used. For complex amplicons, such as genomic DNA, an extension time of 30 seconds per kb is recommended. Extension time can be increased to 40 seconds per kb for cDNA templates, if necessary.

10. **Cycle number:**
    Generally, 25–35 cycles yields sufficient product.

11. **2-step PCR:**
    When primers with annealing temperatures ≥ 72°C are used, a 2-step thermocycling protocol is recommended.

12. **PCR product:**
    The PCR products generated using Phusion DNA Polymerase have blunt ends; if cloning is the next step, then blunt-end cloning is recommended. If TA-cloning is preferred, then DNA should be purified prior to A-addition, as Phusion DNA Polymerase will degrade any overhangs generated.

    The Monarch® Spin PCR & DNA Cleanup Kit (5 µg) (NEB #T1130) is recommended as an efficient method for purification and concentration up to 5 µg of high-quality, double-stranded and single-stranded DNA.

    Addition of an untemplated -dA can be done with *Taq* DNA Polymerase (NEB #M0267) or Klenow exo– (NEB #M0212).

References:

1. Chester, N. and Marshak, D.R. (1993). *Analytical Biochemistry*. 209, 284-290.

Related Resources

- Tm Calculator
- PCR Troubleshooting Guide
- DNA Polymerase Selection Chart