

## Two-step emulsion PCR to prevent formation of the chimeric molecules

E. Omelina<sup>1\*</sup>, A. Ivankin<sup>1</sup>, A. Leshchenko<sup>1,2</sup>, L. Yarinich<sup>1</sup>, M. Lebedev<sup>1,2</sup>, A. Pindyurin<sup>1</sup>

<sup>1</sup> *Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia*

<sup>2</sup> *Novosibirsk State University, Novosibirsk, Russia*

\* e-mail: [omelina@mcb.nsc.ru](mailto:omelina@mcb.nsc.ru)

**Key words:** emulsion PCR, chimeric molecules, next-generation sequencing

*Motivation and Aim:* Application of the conventional PCR method for the amplification of the random nucleotide sequence libraries often causes a formation of the undesired chimeric molecules. Invention of the water-in-oil emulsion PCR (ePCR) approach allowed to reduce the probability of the chimeric molecule formation compared to the conventional PCR. However, in the non-optimized conditions even ePCR causes the formation of the chimeric products.

*Methods and Algorithms:* We developed a step-by-step protocol for the ePCR consisting of two consequent rounds. We found that both an initial amount of the DNA template and number of amplification cycles play a critical role in the formation of the chimeric molecules. We suggest to use only  $10^6$  DNA molecule copies for the first round of ePCR.

*Results:* We analyzed a formation of the chimeric products during amplification of heterogeneous plasmid library in different conditions. To assess the percent of the formed chimers we used Illumina MiSeq platform. A proportion of chimeric molecules under optimal conditions was lower than 0.25 %. We suppose that this two-step ePCR approach may be useful for the preparation of heterogeneous sequence libraries for the next-generation sequencing and other issues which demand avoiding of the chimeric molecule formation.

*Conclusion:* ePCR approach allows to separate the DNA template molecules from each other using the water-in-oil emulsion. Our data suggest that ePCR approach is suitable for the preparation of random DNA libraries for the next-generation sequencing. However it requires additional adjustment to reduce a formation of chimeric molecules as much as possible.

*Acknowledgements:* Supported by the RSF (16-14-10288).