Solid-phase reversible immobilization beads for rDNA high-throughput sequencing library construction

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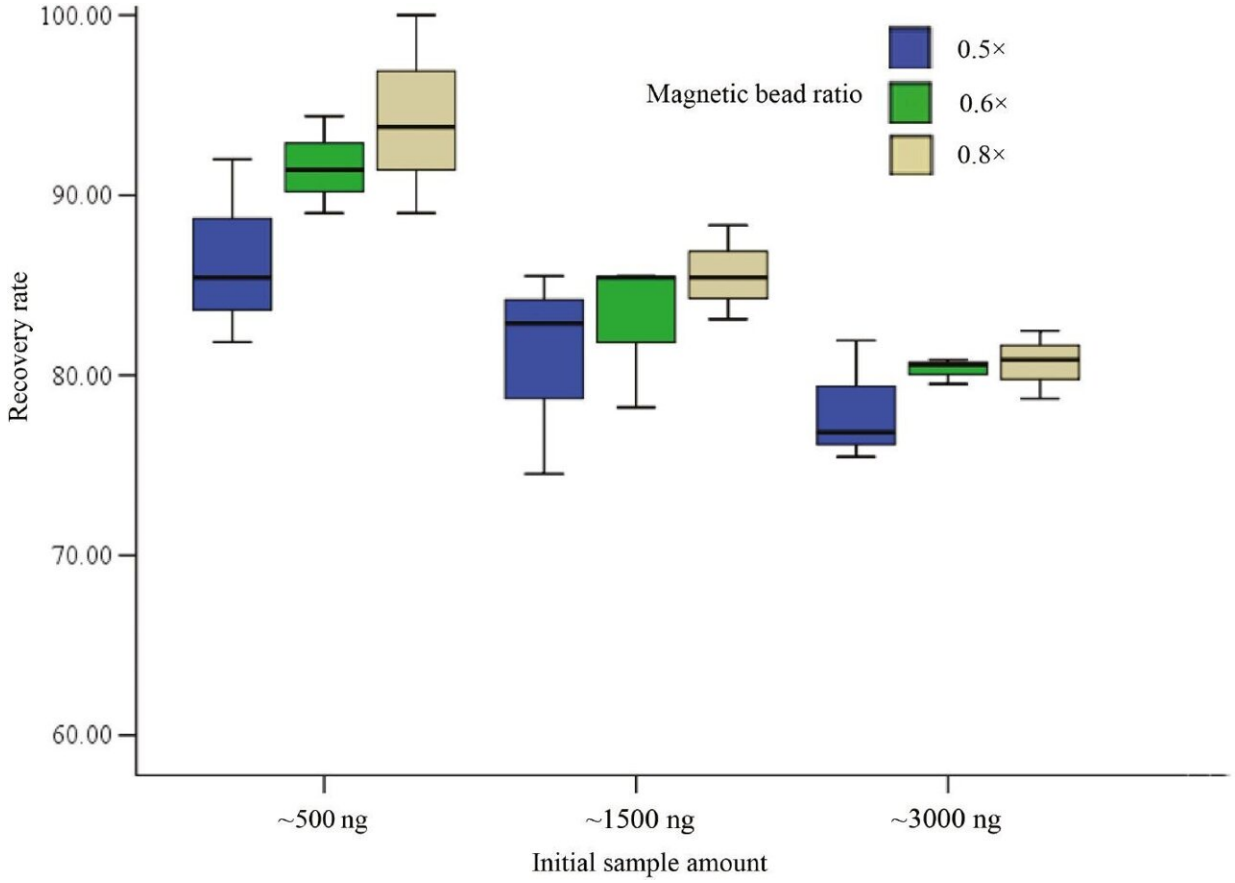

Box plot of recovery rates with different SPRI bead ratios. The x-axis represents the initial sample amount, the y-axis represents the recovery rate, and the boxes depict the recovery rate of DNA with different SPRI bead ratios, with other conditions held constant. Credit: *Zoonoses* (2023). DOI: 10.15212/ZOONOSES-2023-0007

Solid-phase reversible immobilization (SPRI) beads are widely used for high-throughput sequencing library construction to purify and recover nucleic acids. A new study published in *Zoonoses* has investigated the effects of SPRI bead ratio, incubation time, and elution time on nucleic acid recovery during full-length 16S rDNA high-throughput sequencing library construction.

The effects of different SPRI bead ratios, incubation times, and elution times were compared for three different initial sample amounts. An $L9(3^3)$ orthogonal experiment was designed to determine the optimal combination of these factors.

The incubation time of three factors including SPRI beads ratio, incubation time, and elution time had a statistically significant effect on the recovery rate for the initial sample amount of 1,500 ng and 3,000 ng. The orthogonal experiment results indicated that incubation time had the greatest impact among the three factors.

Incubation time significantly influences recovery rate in full-length 16S rDNA high-throughput sequencing library construction. The use of 0.8× SPRI beads, 15 minutes of incubation, and 10 minutes of elution resulted in the highest recovery rate. SPRI beads offer a viable method for recovering full-length 16S rDNA amplicons.

More information: Yinmei Li et al, Optimizing the Use of Solid-Phase Reversible Immobilization Beads for High-Throughput Full-Length 16S rDNA Sequencing Library Construction, *Zoonoses* (2023). DOI: 10.15212/ZOONOSES-2023-0007