Abstract

Aptamers are short sequences of single-stranded DNA or RNA that are able to specifically bind various molecules (drugs, lipids, sugars, proteins, etc.). These aptamers are isolated from large libraries of random oligonucleotide sequences by SELEX (Systematic Evolution of Ligands by Component Enrichment) or *in vitro* selection. Despite the success of this method, *in vitro* selection often requires more than ten rounds of affinity selection as well as optimization of selection conditions. To increase the efficiency of aptamer selection, several methods have been developed that use an increase in the number of secondary structures in random oligonucleotide libraries. These methods, based on increasing the possibility of canonical base pairing in single-stranded oligonucleotides, increased the efficiency of the *in vitro* selection method. In this work, it was tested whether increasing the probability of occurrence of G-quadruplexes, as structural motifs in random sequences, will lead to increased efficiency of aptamer selection. Four single-stranded DNA libraries with different numbers of guanine (25 %, 35 %, 45 %, 55 %) in a random sequence were used. Streptavidin was chosen as the model molecule for selection, against which several aptamers that are not rich in guanine (G) have previously been selected. Preliminary results suggest that G-rich libraries do not increase the efficiency of *in vitro* selection, at least for molecules that do not prefer G-rich aptamers.

Keywords: DNA aptamers, *in vitro* selection, G-quadruplex