ID 383

Selection of RNA Aptamers to Distinguish the V600E Mutation Status of BRAF Protein: A Potential *in silico* Approach

ND Wijesuriya[1#], AMSI Rathnayake[2], WSS Wijesundera[1] and ST Thoradeniya[1]

[1] *Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Colombo, Sri Lanka*
[2]*University of Missouri-Saint Louis, United States*

[#] wijesuriyanavoda@gmail.com

The valine to glutamate substitution at the 600th residue of B-type rapidly accelerated fibrosarcoma protein (BRAF V600E) is the most common mutation in the *BRAF* gene. Due to its high prevalence in a number of cancers, the development of efficient diagnostic and prognostic assays and therapeutics is essential for their management. Aptamers have become promising candidates in a variety of biomedical applications due to many favourable properties. However, no aptamers that can distinguish the V600E mutation status of the BRAF protein have been experimentally determined. Therefore, this study was conducted to create an initial knowledge base for *in silico* design of aptamers for wild-type and mutant (V600E) BRAF (mutant BRAF) proteins. It was achieved using molecular docking employing HADDOCK 2.4 web server. In the absence of aptamers for BRAF, five RNA aptamers targeted to the activation loop of ERK 1&2 proteins were selected for docking, considering the similarity of the 3D structure of the kinase domains of the above proteins to BRAF. Docking was done for ten protein-aptamer combinations (five aptamers with wild-type BRAF and mutant BRAF). Three complexes were selected based on the HADDOCK score and their intermolecular hydrogen bonds and salt bridges were determined. Three aptamers obtained negative HADDOCK scores signifying that they presumably target the activation loop of wild-type and mutant BRAF. Considering the total intermolecular hydrogen bonds and salt bridges, Aptamers_1 and 3 (Apta-Index IDs: 481 and 263) would preferably bind with wild-type and mutant BRAF, respectively. They have the potential to be used as starting structures in the *in-silico* aptamer modeling workflow for wild-type and mutant BRAF proteins.

Keywords: *aptamers, BRAF V600E, hydrogen bonds, molecular docking, salt bridges*