

SHERLOCK – PLATFORMA ZA OTKRIVANJE NUKLEINSKIH KISELINA

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Sažetak. Nove analitičke strategije bazirane na savremenim tehnološkim postignućima imaju znatan uticaj na modernu mikrobiološku dijagnostiku. Genetska informacija pohranjena unutar nukleinskih kiselina postala je ciljno „mjesto“ mnogih molekularnih dijagnostičkih metoda primjenjenih u cilju otkrivanja i prepoznavanja različitih mikroorganizama. Svjesnost o raznolikosti patogena koji mogu izazvati lokalne i sistemske manifestacije važna je stavka prilikom očuvanja svjetskog zdravlja stoga precizno, brzo i pouzdano razlikovanje uzročnika obezbijeduje odgovarajući odgovor. Otkriće i razumijevanje mehanizama funkcionisanja grupisanih uobičajeno isprekidanih kratkih palindromskih ponavljanja (eng. *Clustered Regularly Interspaced Short Palindromic Repeats*, CRISPR) udruženih sa Cas proteinima uveliko je omogućilo razvoj nekoliko tehnologija koje već jesu ili će biti uvrštene u kliničku primjenu. Dva Cas proteina, Cas12 i Cas13, predstavljaju glavne enzime koji se nastoje kombinovati sa metodama pre-amplifikacije nukleinskih kiselina u cilju postizanja sekvenkvencionalno-specifičnog prepoznavanja. Specifični visoko-osjetljivi enzimski reporter (eng. *Specific High Sensitivity Enzymatic Reporter UnLOCKing*, SHERLOCK) je prototip prethodno navedenog spoja. Multipleksno, ultra-osjetljivo i visoko-specifično otkrivanje RNA i DNA iz pojedinog kliničkog uzorka izvodivo je posredstvom SHERLOCK platforme u kratkom vremenskom intervalu. Daljnje istraživanje predmetne metode praćeno novim implementacijama osiguraće kontinuiran napredak mikrobiološke dijagnostike. Predmetni rad opisuje osnovne principe rada SHERLOCK platforme te naglašava mogućnosti primjene iste u kliničkoj dijagnostici.

Ključne riječi: SHERLOCK, nukleinske kiseline, detekcija

SHERLOCK – A PLATFORM FOR NUCLEIC ACID DETECTION

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Abstract. New analytic strategies based on recent technological achievements have a big impact on modern microbiology diagnostics. The genetic information stored in nucleic acids became the target of many molecular methods which are used to detect and identify different microorganisms. Awareness of the variety of pathogens that can manifest in a number of both local and systematic ways is the main concern in maintaining global health. So, the precise, rapid and reliable determination between causative agents enables an adequate response. The discovery and understanding of functioning mechanisms of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and their associated proteins (Cas) presented an enormous opportunity for developing several technologies that were and will be incorporated into clinical usage. Two of the Cas proteins, Cas12 and Cas13, nowadays are the main enzymes that tend to be combined with methods of nucleic acid pre-amplification in order to achieve sequence-specific recognition. Specific High Sensitivity Enzymatic Reporter UnLOCKing (SHERLOCK) is the prototype of the above mentioned union. Multiplexed, ultra-sensitive and highly specific detection of RNA or DNA from a particular clinical sample can be carried out with the SHERLOCK platform in a short period of time. Further research along with different implementations of this method will ensure continued improvement of analytic pathways that are an essential part of the microbial diagnostics. This paper explains main working principles of the SHERLOCK platform and point out the possibilities of its applications in clinical diagnostics.

Key words: SHERLOCK, nucleic acids, detection