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# Role of microRNA in Molecular Detection

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## Description

MicroRNAs (miRNAs) are short non-coding RNAs that are derived from introns and exons of both protein-coding and non-coding genes. They are about 21 to 24 nucleotides long. Many miRNAs have similar sequences in distantly related animals and play important roles in development, proliferation, differentiation, metabolic and signalling pathways, chromatin structure, and apoptosis. MiRNAs can prevent their target mRNAs from being translated via partial base pairing with the 3'UTR, which usually requires a "seed" pairing of 6 to 8 nucleotides. Alternatively, in the case of perfect base complementarities, they can cause RNA interference, which is the degradation of target mRNAs via the RISC complex. MiRNAs are thought to regulate the expression of more than half of all human protein-coding genes. MiRNAs were originally connected to cancer in 2002, and in most chronic lymphocytic leukaemia patients, miR-15a and miR-16-1 were shown to be down regulated. More than half of miRNA genes are found at fragile chromosomal sites, limited regions of amplification or loss of heterozygozity, or common breakpoint regions, according to subsequent mapping of known sequences encoding miRNAs in the human genome. Many of the miRNA genes found in these vulnerable areas and cancer-related genomic regions are clustered and expressed similarly, implying polycistronic primary transcription. MiRNA expression analysis in cancer tissues has led to the discovery of miRNA "signatures" linked to tumor diagnosis, cancer staging, progression, prognosis, and therapy response. Several recent studies have described changes in circulating miRNAs in response to infectious disorders, indicating the possibility of a novel infection diagnostic tool. MicroRNAs have been found as potential biomarkers of infections caused by a variety of pathogens, including the Hendra virus, TB, malaria, and Ebola. Changes in miRNA profiles were seen early in disease initiation before the pathogen could be explicitly diagnosed and before seroconversion began in several cases. As a result, the potential for miRNA diagnostics with other respiratory viruses, such as the recent SARS-CoV-2 outbreak, should not be overlooked [1-2].

COVID-19 infections could be distinguished from other infections with similar presenting symptoms, such as influenza, rhinoviruses, or other coronaviruses, using a COVID-19 miRNA signature that has been discovered and validated. The prevalence and stability of these compounds across a wide spectrum of bodily fluids, including peripheral circulation, increases their potential utility as diagnostic biomarkers. Despite many freeze-thaw cycles or severe pH, they maintain extraordinary stability. Despite this, miRNA biomarkers would be inappropriate, ineffective, or extremely difficult to use in clinical practice for many viral disorders. The creation of these biomarkers would not aid short-term, self-limiting infections that require minimum intervention (aside from symptom relief), such as the common cold or gastroenteritis. Others, particularly those with a large impact, currently poor diagnostics, or protracted preclinical phases, would greatly benefit from the use of validated miRNA diagnostics. Before commencing on miRNA biomarker discovery, it is critical to understand the disease of interest and how miRNA biomarkers would be best utilized.

Early identification of infectious disease is important for improving patient prognosis and limiting disease transmission. As an illness progresses has an extraordinarily long asymptomatic phase of 2–3 months on average, and it is virtually invariably fatal once symptoms arise. As a result, early intervention is critical for survival. Infectious disease symptoms, treatment options often become more limited. Rabies is a classic example of a disease in which early intervention is critical; it are often non-specific (fever, malaise, headache, and lethargy) and provide little to no information regarding the causative agent when they initially arise. As a result, clinicians may misdiagnose patients, potentially leading to serious repercussions. Viral encephalitis is an example of this, with symptoms ranging from a flu-like sickness to severe neurological abnormalities such as convulsions, speech loss, confusion, and coma. Many neurotropic viruses can cause viral encephalitis, ranging from well-known agents like herpes simplex virus (HSV), varicella-zoster virus (VSV), and enteroviruses to fatal zoonotic pathogens like Japanese encephalitis virus (JEV), lyssavirus (rabies), Nipah virus (NiV), and Hendra virus (HeV).

Current diagnostic tools are insufficient for many infectious illnesses. To underlie the next generation of diagnostic tools, new biomarkers are desperately needed. MicroRNAs have a lot of potential as infection indicators, as evidenced by a growing body of research. Infections with bacteria, parasites, viruses, and even prions modify these molecules in biofluids. Use of MiRNA as diagnostic or prognostic indicators is not without difficulties; but, with rigorous analytical and validation procedures, they may be able to overcome the limitations of present assays, resulting in better patient outcomes [3- 5].

## Conflict of Interest

None.

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