2024 Joint Usage and Research Report

<table>
<tr><td colspan="2">Title of Research Project</td><td colspan="3">Identification and characterization of novel coding and noncoding genes regulating the innate immunity during virus infection and cancer. (The Nineth Phase)</td></tr>
<tr><td colspan="2">Status</td><td colspan="3">New / Continued</td></tr>
<tr><td rowspan="2">Applicant</td><td>Institution</td><td>Indian Institute of Science Education and Research (IISER), Bhopal, Madhya Pradesh, India</td><td>Circle if under 40</td><td>Circle if under 35</td></tr>
<tr><td>Job title and Name</td><td>Dr. (Ph.D), Professor Himanshu Kumar</td><td>Nil</td><td>Nil</td></tr>
<tr><td rowspan="4">Research collaborators
(Please add lines as appropriate)</td><td>Institution</td><td>IGM, Hokkaido University, Japan</td><td></td><td></td></tr>
<tr><td>Job title and Name</td><td>Professor
Dr. Akinori Takaoka</td><td></td><td></td></tr>
<tr><td>Institution</td><td></td><td></td><td></td></tr>
<tr><td>Job title and Name</td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Host researcher at IGM</td><td colspan="3">Prof. Akinori Takaoka</td></tr>
<tr><td colspan="2">Purpose of the Research Project (within 200 words)</td><td colspan="3">The purpose of this project is to strengthen the collaborative research to make novel fundamental and translational discoveries. The success of these project is to contribute in term of development of the diagnostic, prognostic and therapeutic for fatal infectious viral diseases or for various cancer.</td></tr>
<tr><td colspan="2">Results (including the number of web meetings; within 1,000 words)</td><td colspan="3">For over a decade, our laboratory has been dedicated to the exploration of non-coding RNAs (ncRNAs) and their roles in the regulation of host-pathogen interactions, particularly in the context of viral infections such as Influenza and Dengue virus. Non-coding RNAs, including long non-coding RNAs (lncRNAs), circular RNAs (circRNAs), and microRNAs (miRNAs), have emerged as critical regulators of gene expression, immunity, and disease progression. Our research has centered on deciphering the molecular mechanisms through which these ncRNAs influence viral replication, host immune response, and pathogenesis.

We have been particularly focused on identifying and characterizing specific lncRNAs, circRNAs, and miRNAs that are differentially expressed during viral infections. These</td></tr>
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	molecules have shown promising potential not only as biomarkers for early detection but also as targets for therapeutic intervention. By using high-throughput transcriptomic approaches, we have cataloged a wide array of ncRNAs that are significantly altered during Influenza A virus and Dengue virus infection. Through functional studies and validation, we have highlighted key candidates that modulate innate immune pathways, viral replication efficiency, and host inflammatory responses. An important extension of our work has been the search for novel ncRNAs that could serve as early diagnostic markers in body fluids such as blood, serum, or plasma. Given the non-invasive nature of such fluid-based diagnostics, identifying ncRNA signatures that correlate with disease onset or severity could provide a powerful tool in clinical settings. In particular, we are investigating whether certain circulating lncRNAs and circRNAs could predict viral infection at early stages before the onset of clinical symptoms, potentially aiding in rapid disease containment and improved patient outcomes. Our lab employs a combination of molecular biology, RNA sequencing, bioinformatics, and functional genomics tools to investigate these questions. We also integrate in vitro cell culture models and clinical samples to validate the physiological relevance of our findings. However, to further advance our studies and validate our findings in more complex systems, we are looking to collaborate with world-class research institutions that possess the necessary infrastructure and expertise. In this regard, we are particularly interested in working with Professor Takaoka at the Institute for Genetic Medicine (IGM), Hokkaido University. Professor Takaoka's laboratory is internationally renowned for its cutting-edge research in innate immunity and antiviral defense mechanisms. His team has made pioneering contributions in understanding how host immune pathways are activated during pathogen invasion and how they can be modulated. Furthermore, the IGM is equipped with state-of-the-art facilities including advanced molecular

	biology platforms, high-resolution imaging systems, and importantly, a well-established animal facility that enables in vivo experimentation. Our goal is to test a selection of our identified ncRNAs—including lncRNAs, circRNAs, and miRNAs—in both viral infection and cancer models using the facilities available at IGM. We are particularly interested in assessing how these ncRNAs behave in vivo, how they influence disease progression, and whether they hold potential for therapeutic modulation. This collaboration would allow us to translate our in vitro and bioinformatic findings into animal models, thereby providing more robust and clinically relevant insights into the role of ncRNAs in infectious disease and cancer. This proposed partnership also opens avenues for joint exploration of ncRNAs that have dual roles in viral infection and oncogenesis, given the growing evidence that certain ncRNAs can function at the intersection of immune response and tumorigenesis. We envision a synergistic research program where our expertise in ncRNA discovery and functional validation is complemented by Professor Takaoka's strengths in innate immunity and translational research. Ultimately, our long-term objective is to contribute to the development of ncRNA-based diagnostic and therapeutic tools. By leveraging the knowledge, resources, and collaborative spirit between our labs, we aim to uncover new layers of gene regulation that can be harnessed to control viral infections and cancer progression. We believe that ncRNAs represent an exciting frontier in biomedical research, and collaborative efforts such as this are key to unlocking their full potential.
Publication *Provide the details of the conferences or journals where the above work was presented or published.	【Conference, symposium, workshop etc.】 Presenter(s), presentation title, meeting name, venue, date Several hypotheses need to tested in the mouse model before presenting in Conference, symposium, workshop etc.
	【Journals】 Author(s), paper title, journal name, volume, pages, year, impact factor

	Several hypotheses need to tested in the mouse model before publication.
	【Press release】 None