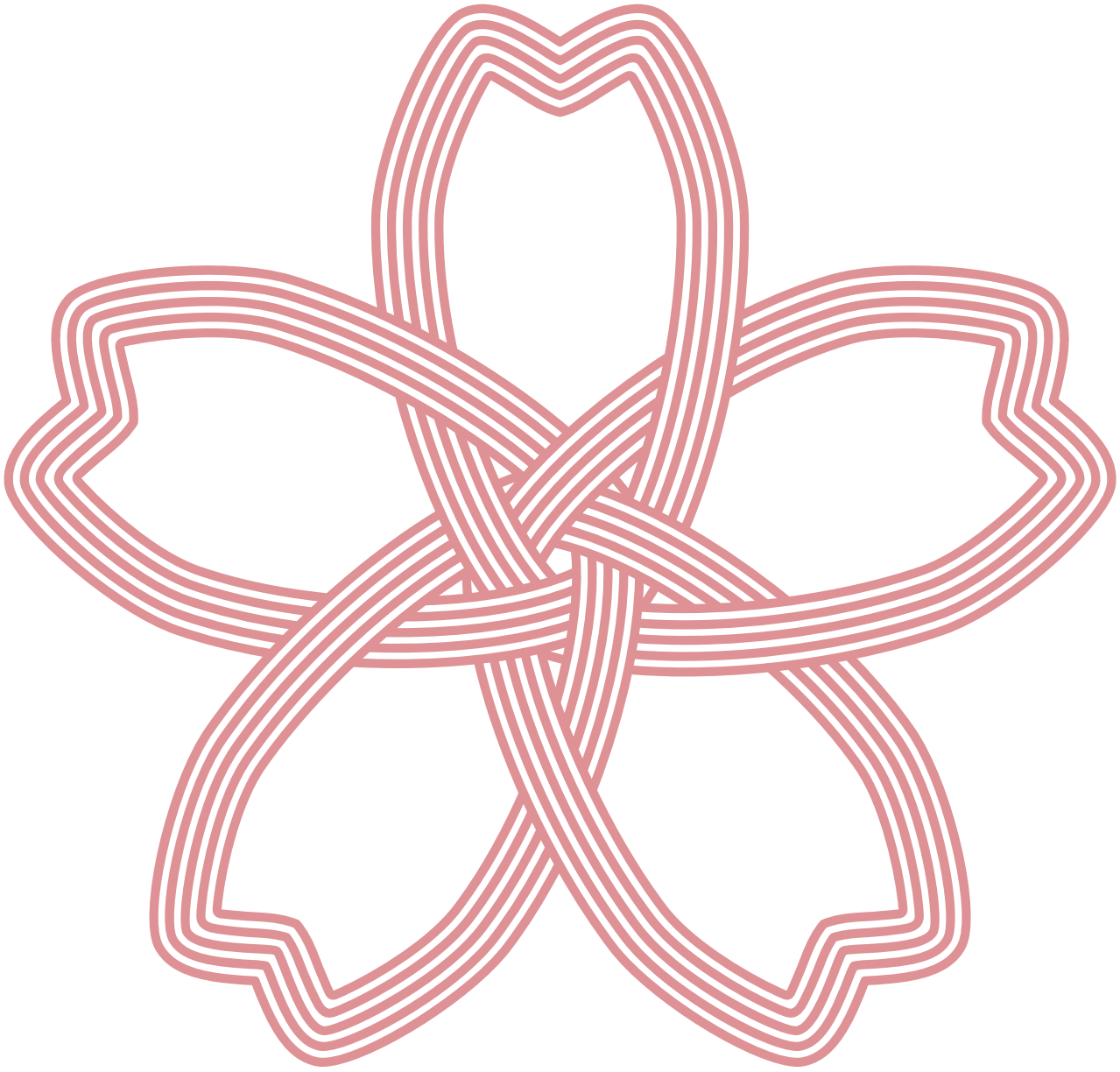


IBO2020 YEARBOOK

The 31st International Biology Olympiad 2020 Nagasaki, JAPAN

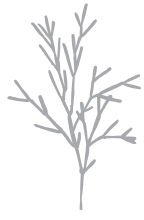
IBO Challenge 2020 (A Substitute for the 31st IBO 2020 Nagasaki, JAPAN)

Alveopora japonica

Anguilla japonica

Aspergillus japonicus

Branchiostoma japonicum



Cladophora japonica

Clypeaster japonicus

Conocephalum japonicum

Corbicula japonica

Coturnix japonica

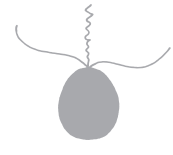
Cryptomeria japonica

Delisea japonica

Dugesia japonica

Ephebe japonica

Eutrema japonicum



Fibrocapsa japonica

Glirulus japonicus

Halichondria japonica

Hydroglyphus japonicus

Hyla japonica

Hyleoglomeris japonica

IBO2020 YEARBOOK

This book is dedicated to the participants and supporters

of the IBO Challenge 2020, who together overcame the COVID-19 crisis.

We wish them all good health.

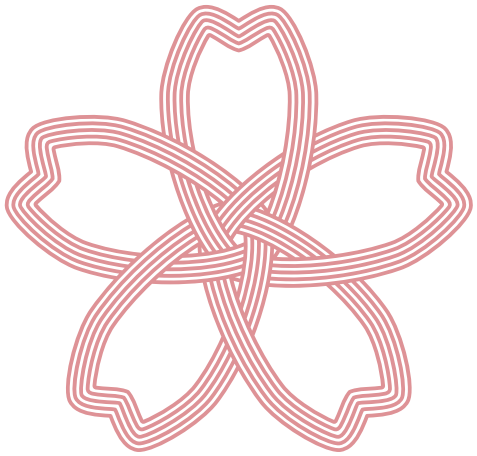
The IBO spirit never fades!

IBO2020 YEARBOOK

Printed on March 15, 2021 in Japan

Published by the Organizing Committee
of the 31st International Olympiad Biology 2020 Nagasaki, Japan

Produced & Edited by the IBO2020 Secretariat Office
Photography by Naruaki Onishi（p.34, p.37-38, p.96, p.194-195, p.204, p.206-207）
Editorial Design & DTP by Keisuke Saka
Printed by Okamura Printing Industries Co., Ltd.



IBO2020 YEARBOOK

IBO2020 YEARBOOK

Table of Contents

Introduction

IBO Challenge 2020

(A Substitute for the 31st IBO 2020 Nagasaki, JAPAN)

The 31st

IBO2020 Nagasaki, JAPAN

(Cancelled)

Enhancing the Wisdom of Youth Around the World Together

President of the IBO2020 Organizing Committee
Dr. Makoto Asashima

Emeritus Professor at the University of Tokyo
Special Research Professor at Teikyo University
Honorary Fellow of National Institute of Advanced Industrial Science and Technology (AIST)
Academic Adviser of Japan Society for the Promotion of Science (JSPS)
Foreign Academic Member of Lithuanian Academy of Science

First, I would like to express my sincere gratitude to all the people involved in the IBO Challenge 2020, who made this extremely international event possible and successful during the spread of COVID-19 worldwide. Although it was the first time for an IBO host country to organize a remote competition, we managed to successfully complete this event. I am truly appreciative for the cooperation and support of the students, jury members, and all of the other stakeholders. Despite our initial concerns, 53 countries and regions participated in the competition, far exceeding our original expectations for an event like this. We were also pleased that the students attended from various parts of the world.

We were able to successfully finish the practical exams on August 11th and the theoretical exam on August 12th without any major issues. On the 24th of the same month, we announced the names of the gold, silver and bronze medalists and their countries on our website without any specific rankings. After the event, we received emails and videos from many countries around the world about this remotely held international contest. Each of them was filled with joy and compliments about the event, which made us extremely happy.

Although the remote nature of the event limited us in most ways, it also pushed us to bring a new and unique activity to the IBO community: the International Group Project. Consisting of 4 students from different countries and a project facilitator, each group selected a topic from: (1) infectious diseases, (2) biodiversity and oceans, (3) genome editing, and (4) evolution. They then discussed their topic for more than two months and created their deliverables. This time, we asked IBO alumni and former volunteers, an extremely experienced, knowledgeable, and passionate group of youth, to be project facilitators for this event.

Within the Organizing Committee, the International Group Project was always considered to be as important as the examinations – that was how much this project meant to us. We could present a new opportunity for young people across the world to imagine, discuss, and propose something on a global scale. I believe that we succeeded in preparing students to be the next generation of world leaders who will lead the world with a new set of social, scientific, and biological issues. All the project posters that were submitted were wonderful despite various challenges that included the COVID-19 global pandemic, time zone differences, and poor internet connections.

In addition, I'd like to thank all of the organizing members who worked together from preparation to realization for nearly five years until the contest concluded, particularly the Secretariat Office and Ms. Mitsuko Kudo and Mr. Taiga Araki. I would also like to express my sincere gratitude to all of the companies and individuals who donated funds or sponsored us, as well as many other stakeholders such as the Japan Science and Technology Agency (JST) and the Japan Science Foundation (JSF).

Although our remote event was a success, I'm sure it made all of us miss the on-site IBO competition at the same time. It's a pity that the students and the international jury members didn't get to see the wonderful culture and nature of Japan this year, but I would like them to still come to Japan in the future. Thank you very much again to all of the people who are related to this IBO Challenge 2020. See you all in Portugal next year in 2021!

Message from the Governor of Nagasaki

I would like to extend my sincerest congratulations on the holding of the 31st International Biology Olympiad in Nagasaki, Japan (IBO Challenge) with 202 participating students from 53 different countries and regions. It is unfortunate that the competition could not be held in Nagasaki and had to be conducted remotely due to the COVID-19 global pandemic. I believe, however, that the primary objectives of the competition have been fulfilled, as high school students from all around the world have been furnished with an opportunity to showcase their wits and compete in a test of biological knowledge on an international stage.

Although we did not have the chance to welcome you to Nagasaki this time, Nagasaki prefecture is blessed with extraordinary biodiversity. Nagasaki has many diverse ecosystems fostered by complex geography such as its remote islands, the Saikai National Park in Sasebo which possesses the Kujukushima or the "Ninety-Nine Islands," and Mount Fugen on Shimabara Peninsula. Nagasaki also has many organisms that are born into rich, natural environments. I look forward to welcoming you all to Nagasaki in the near future so that you can explore its abundant charms.

I have high expectations that the competitors will play active roles as world leaders based on the experience they gained in this contest competing against their global counterparts in the field of biology. I pray for the continued good health and success of all those who have made this event possible.

Houdou Nakamura

Message from the Mayor of Sasebo

Sasebo City, Nagasaki Prefecture, located at the westernmost part of mainland Japan, is a port town with the beautiful scenery of the Saikai National Park "Kujukushima" archipelago. Kujukushima and its exceptional beauty are recognized amongst other internationally distinguished sceneries by the association of "The Most Beautiful Bays in the World" and has been deeply cherished and treasured by citizens. Its rich ecosystem has been formed corresponding with its complex topography, and its sea area is a cradle of life that contains various rare species. You can also enjoy huge bird migrations in the season. Sasebo City also contains various heritage sites such as the Hidden Christian site, which is designated as a World Cultural Heritage site, and the important military ruins of the Sasebo Naval District that is deeply involved with history of Sasebo.

The outbreak of COVID-19 has had a big impact all over the world and it was very unfortunate that the International Biology Olympiad 2020 Nagasaki had to be cancelled. However, I hope this extraordinary experience was a chance to be thankful for the "ordinary days" and to reaffirm your determination towards biology.

I hope you will work and learn hard, and that it will lead you to big success in your life. I also hope that IBO2020 will be an opportunity to lead you to Sasebo one day.

Norio Tomonaga

Message from the President of Nagasaki International University

To our regret, the 31st International Biology Olympiad in Nagasaki, Japan could not be held because of the worldwide COVID-19 infection. We prepared to welcome many students with hospitality who had a mind for biological research from all over world for more than 1 year. Fortunately, we are very glad to hear that the modified 'IBO in Nagasaki' was held on August 11 and 12 remotely, and that the results were announced on August 25. With drastic weather and environmental changes worldwide, the wave of students interested in biology should increase. We appreciate the help and various activities of the Organizing Committee and the participants.

Yukio Ando M.D. Ph.D.

Nagasaki International University — Event Venue

Located in Sasebo City, Nagasaki Prefecture, Nagasaki International University (NIU) is a private university founded in 2000. Since its foundation, the university has grown into a comprehensive university with four undergraduate departments (International Tourism, Social Work, Health and Nutrition, and Pharmacy) as well as three graduate schools. To this day, NIU cherishes its founding principle of "respect for human beings" and its motto of "always with humanity, always from the heart." The university is also known for its extensive incorporation of cultural education into its curriculum, such as the traditional tea ceremony.

IBO2020 Committee Members at NIU

Dr. Yoshinori Ohsumi

Dr. Yoshinori Ohsumi was born in Fukuoka in 1945. In 1963, he entered the University of Tokyo and chose to study molecular biology due to the influence of Prof. K. Imahori. As a graduate student, he enrolled in Rockefeller University to study under Dr. G. M. Edelman in 1974. He returned to the University of Tokyo as an assistant professor under Prof. Y. Anraku at the end of 1977. In 1988, he opened up his own small lab and started to work on the lytic function of the vacuole, and then found yeast autophagy by light and electron microscopy. After leaving the University of Tokyo he continued his research at the National Institute for Basic Biology at Okazaki. Then he moved to the Tokyo Institute of Technology in 2009 and received the Nobel Prize in Physiology or Medicine in 2016 for elucidating the mechanisms for autophagy.

Message from Yoshinori Ohsumi to the next generation of biologists

It's very unfortunate that the International Biology Olympiad must be held online this year, preventing us from discussing biology in person.

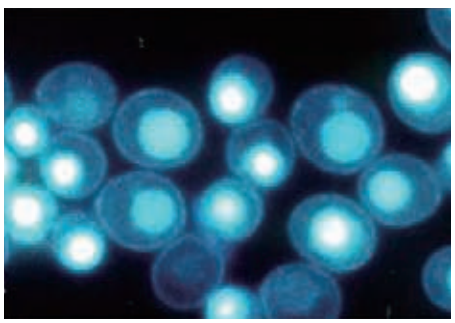
I'd like to send a message to the young generation of biologists.

Developments in our understanding of biology are truly striking. The establishment of foundational principles in molecular biology last century are the bedrock of this progress. In addition, rapid advances in the technologies available to researchers have also spurred on research. Contact between the fields of biology and medicine have become productive, with the fruits of biological research allowing us to overcome many diseases and improve human health in a direct and tangible way. These are without a doubt wonderful achievements. However, I believe that focusing on the practical application of biological knowledge alone is dangerous to the healthy development of biological research.

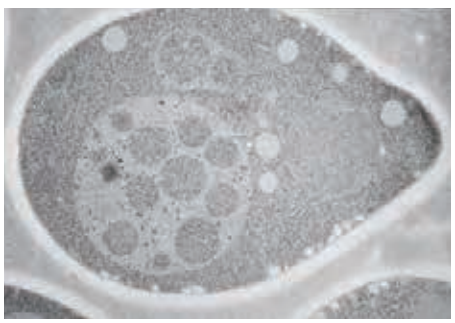
It is now clear that the activities of humans are having a strong impact on the natural environment and ecosystems. The ongoing COVID-19 pandemic is one example. Global warming is growing increasingly serious, and every year there are more and more natural disasters. Limits in the earth's resources are becoming ever more apparent.

Meanwhile, great technological progress has ushered in an information age, and we are now faced with an overwhelming supply of information. While the COVID-19 pandemic continues to bring major changes to people's lives, we must now address problems never before faced by humanity. As future scientists, I believe that how you challenge these problems will have a direct effect on the future of our species.

I'd like to talk briefly about my research career. I began with an interest in a yeast vacuole. At the time, the vacuole was thought of as the place where cellular rubbish was collected, but I showed that the vacuole is able to transport amino acids and ions and has a V-ATPase, indicating it plays much more intricate roles in the cell. When I first started my own lab at the age of 43, I assumed that the vacuole is involved in intracellular degradation and set out to study the process of degradation. I discovered that yeast cells undergo massive self-degradation during starvation and showed that this was the same as previously observed autophagy. Then my group identified the genes required for autophagy and used these to unravel the molecular mechanism of this process. When I launched into this problem, the word 'autophagy' was virtually unheard of among biologists. Now that autophagy is such a major field of research, I feel like we are in a completely different age. As we discovered that the autophagy genes we identified are broadly conserved in animals and plants, autophagy research was revolutionized. The role of autophagy in a range of species, tissues, organs and individual organisms became clear, and we came to understand the amazing diversity of autophagy functions. When one considers that life is, essentially, a balance between synthesis and degradation, it is perhaps obvious to think that degradation is involved in every biological phenomenon, but this was overlooked for many years. Nowadays, many researchers are focusing on the involvement of autophagy in cancer and neurodegenerative diseases, as well as its higher-order functions such as longevity.



Fluorescence image of yeast vacuoles



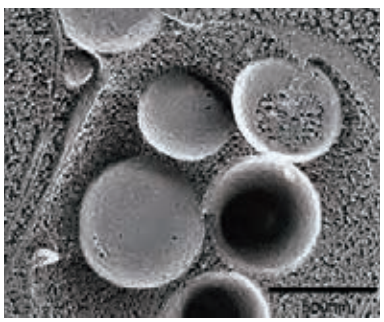
Electron microscopic image of a vacuolar proteinase-deficient cell under nitrogen-starvation conditions. The vacuole shows several autophagic bodies which contain a portion of cytoplasm.

I didn't set out on my scientific journey expecting that my research could be used to treat diseases. Most basic research begins instead with curiosity. This year's Nobel Prize in Chemistry for the development of gene editing technologies also recognized achievements at the forefront of microbial immunity. I chose to study the vacuole due to my interest in turnover, but also because it was overlooked by other researchers. Rather than taking part in fashionable areas of research that have already attracted a lot of attention, I think it's easier to make important progress without the distraction of competition by focusing on your own unique research topic.

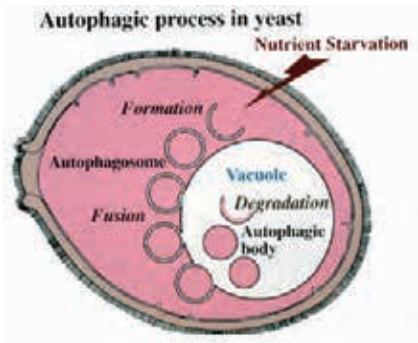
The most important thing in science is not simply the speed at which you are able to answer a question that is put to you. Today's answers can be rewritten by tomorrow's research. What is more important is identifying new questions that require answers. My hope is that young researchers can begin with scientific questions to which they can return throughout their career, rather than problems with immediate solutions. Paradigm shifts do not begin with questions that have direct and foreseeable answers.

While research is conducted by individuals, it is not a process that you should conduct alone. Big discoveries do not occur suddenly in isolation. Scientific research is ultimately a social activity, and it is important to work collaboratively with others. It's particularly important to discuss your research with people with a range of perspectives and who use different approaches to solve problems and even members of the public.

Finally, as future scientists, you should ensure that you experience the natural world as much as possible, and that you never forget that humans are only one form of life on earth. Draw inspiration from nature, discover new questions and allow yourself to be moved by the joy of discovery.



The very moment that an autophagosome fuses with the vacuole. Several autophagic bodies are also observed by freeze-fracture electron microscopic imaging.



Upon nutrient starvation, a membrane sac appears, expands and forms a double membrane bound structure, autophagosome, which contains a portion of the cytoplasm.

The outer membrane of the autophagosome fuses with the vacuolar membrane, releasing an inner membrane vesicle into the vacuolar lumen. The autophagic bodies are immediately degraded in wild type cells.

IBO Challenge 2020 (A Substitute for the 31st IBO 2020 Nagasaki, JAPAN)

From an On-site to Online Event

As we started hearing more and more news about the worldwide COVID-19 outbreak in February, we found ourselves in an increasingly difficult situation.

At first, we started evaluating multiple possibilities as precautionary measures, such as shortening the event's duration, postponement, and hosting it remotely. Many people from around the world, from country coordinators to selected competitors, started inquiring with us about the status of the event, which made us realize how high the stakes were. Whichever possibility we leaned toward, our biggest concern was that it seemed likely that we would have to alter or take away the once-in-a-lifetime opportunity that IBO provides its students, from testing their abilities in biology to interacting with like-minded youth from around the world.

As the pandemic grew bigger around the world, Japan halted all school activities in March. The nationwide state of emergency was issued in Japan in the following month. Even though we could no longer meet in person, the IBO2020 Organizing Committee kept the discussion going. Although we first assessed the possibility of hosting an on-site event with limited capacity, this was rejected as a result of the growing severity of the pandemic.

In the end, we concluded that changing the event to a remote competition was the best bet for us. Though not ideal, we thought it was a way to provide the IBO experience to as many students as possible in the world of lockdown and travel restrictions. Some raised concerns about the fairness of the examinations. We tackled this issue by awarding medals without releasing participant rankings, in addition to issuing exam operational guidelines against cheating. At the same time, we tried to give as much flexibility in exam operations as possible in order to accommodate all participating countries with varying situations. For example, each country could set their own exam timetables and exam venue (i.e., competitors gathered in one place or from their home). The International Group Project was also planned so that we could provide competitors with an opportunity to interact with each other online.

Although we received some criticism, almost all countries kindly and actively supported this new attempt. Thanks to the cooperation of the IBO community, we managed to host a successful event with 53 participating countries and regions.

Overview

Schedule

Phase	Event/Task	Date
Registration	Country/Personal Registration	31 July, 2020
	Exam Info Registration	5 August
Part 1 Examination	Practical Exams	11 August
	Theoretical Exam	12 August
	Results Released	24 August
Part 2 International Group Project	Group Project	3 August – 31 October
	Results Released	20 December

General Data

Part 1: Exams	
Participating Countries / Regions	47 + 3 Observers
Competitors	186
Jury Members	202
Exam Supervisors* *Non-jury people who oversaw the exams	45

- All questions were approved at the online jury meeting.
- All participating countries/regions conducted exams based on their own exam timetables. Announcements from the organizers were issued according to their local time zones.
- Competitors were permitted to take the exam from their home, as long as their countries/regions could set up a proper supervising environment. Out of the 47 participating countries/regions, seven conducted the exam completely online, nine incorporated some online examination, and 31 of them offered on-site supervision to all of their competitors.
- While optional, 31 countries/regions provided a link to their online supervision (Zoom, Skype, etc.).

Part 2: International Group Project	
Participating Countries / Regions	52
Competitors	202
Group Project Facilitators	37
Initial Number of Group Project Teams • Some competitors dropped out due to their academic responsibilities, vacations, time difference, connection issues, etc. • By the end of August, three teams were merged into other teams (46 remaining). 20 competitors had dropped out in that period.	49
Teams that successfully submitted the final deliverables by the deadline (November 5th)	39
Competitors who finished the group project	approx.130
Competitors who did not participate / quit halfway* *Due to illness, time difference, conflicted responsibilities, etc.	approx.70

Pre-Event Important Dates

2020 5 March	Announced that the event status of IBO2020 would be linked to the status of the Tokyo 2020 Olympic Games
24 March	Postponement of the Tokyo 2020 Olympic Games announced
25 March	Cancellation of IBO2020 Nagasaki (on-site event) and hosting of IBO Challenge 2020 (remote event) was approved by the IBO Steering Committee
26 March	Cancellation and the possibility of IBO Challenge 2020 announced on the website
30 March	IBO Challenge 2020 initial proposal submitted to the IBO Steering Committee
9 April	Discussion of the event details at an IBO Steering Committee meeting
20 April	General overview of the IBO Challenge 2020 finalized
27 April	Overview of the IBO Challenge 2020 announced to IBO member countries
7 May	Supplemental document released
1 June	Exam Operation Guidelines (version 1) released
10 June	International Group Project overview released
15 June	Practical Exam 2 (Bioinformatics) demo application released to all member countries
16 June	Participation poll started (deadline: June 21)
24 June	Country/Personal Registration started (deadline: July 31)
7 July	International Group Project facilitator registration started (deadline: July 20)
15 July	Exam Info Registration started (deadline: August 6)
16 July	Answer sheets distributed
30 July	Exam Operation Timetable and Instructions released
1 August	Subgroup Meeting
3 August	International Group Project grouping determined

IBO Challenge 2020

PART 1

Examination

Practical Exams

Theoretical Exam

Exam Timeline

Date	Event	
1-7 August	Online Subgroup Meeting	
7-11 August	Online Jury Meeting • 7 Aug: Exam questions revealed (English & Russian) • 8 Aug: Voting deadline to accept/reject each question • 10 Aug: English Official published & Translation deadline • 11 Aug: Certified questions distributed to all countries	Conducted based on each country's time zone (GMT +10 to GMT -6)
11-12 August	Exams • 11 Aug: Practical Exams Animal Physiology 3 hrs. & Bioinformatics 1.5 hrs. • 12 Aug: Theoretical Exam (3 hrs x 2 parts)	
13 August	Deadline to submit answer sheets / exam cover pages	
24 August	Results released on the website at 5 PM JST (Medal and special award recipients; no rankings)	

Thoughts Behind the Exam

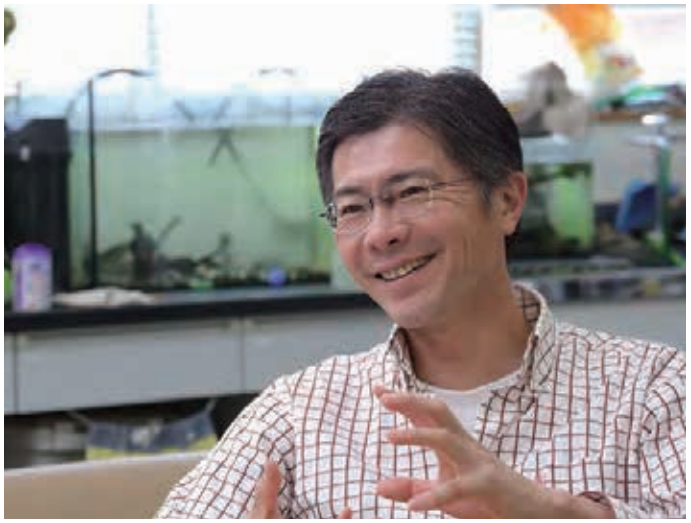
Chief of the Practical Exams

Inspiring and Encouraging Young Talents

Hiroshi Wada (University of Tsukuba)

Usually in the IBO, students take four slots of practical exams of 90 minutes each. After the exams, students often say that they did not have enough time to complete the exams. It is a pity that most students do not even touch the prepared materials. After hearing about these experiences, one doubt hit me: Do our practical exams truly test the students for the abilities that are expected of good scientists? Sometimes it seems to me that the exams test for abilities found in good technicians, such as extracting DNA from cells as quickly as possible. Perhaps science is not an activity to compete in the speed of performance, but rather to compete, if we must compete, in originality or creativity. Thus, in the practical exam of IBO2020, I wanted to give students multiple chances to do trial-and-error. Yes, I wanted to give students the chance to make errors and to learn from those errors. As a trial case, we set up one practical exam to be twice as long as the usual exams (i.e., three hours).

I also like to refer back to the spirit of IBO that our activities are not for ranking students, but for inspiring and encouraging young talents in biology. Our practical exams should intend to show the new world of biology through the exams. In order to achieve this, I asked the scientists to include some messages in each exam. What do you want to show students through the exams? I hope students got the message and were inspired from the exams.



Photography by Tsuyoshi Asano

Chief of the Theoretical Exam

Finding Ways to Improve the World Through Biology

Tatsuhiko Noguchi (National Defense Medical College)

People who contributed to prepare the theoretical exams of the IBO Challenge 2020 are researchers who are currently active in many different fields of biology. I asked each author to freely create questions on biological topics that they considered most important. As a result, we were able to provide competitors with a diverse collection of problems covering a wide range of biological fields. We would be happy if they enjoyed answering our questions.

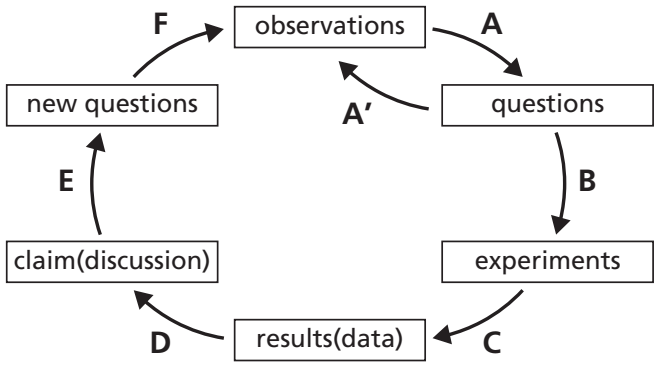
Here is a message from us to all of our competitors with great potential; in order for you to play an active role as social leaders, it is essential to acquire broad knowledge and wisdom from nature. This is true whether you become a scientific researcher or not. As nature and human society change faster than ever before, future leaders must have deeper understanding of various emerging challenges and choose the right solutions scientifically. By studying biology extensively, you will realize how wonderful the mechanisms of life are, and through the process, you should be able to find hints for solving many challenges humankind is or will be facing. So, please continue to study biology.

Practical Exam 1

Animal Physiology Team

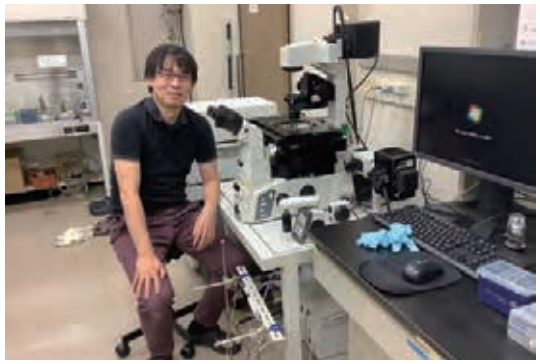
Kimiko Fukuda

For the practical exam in the original IBO2020, the Scientific Committee members decided to test the participants' abilities as future biologists.

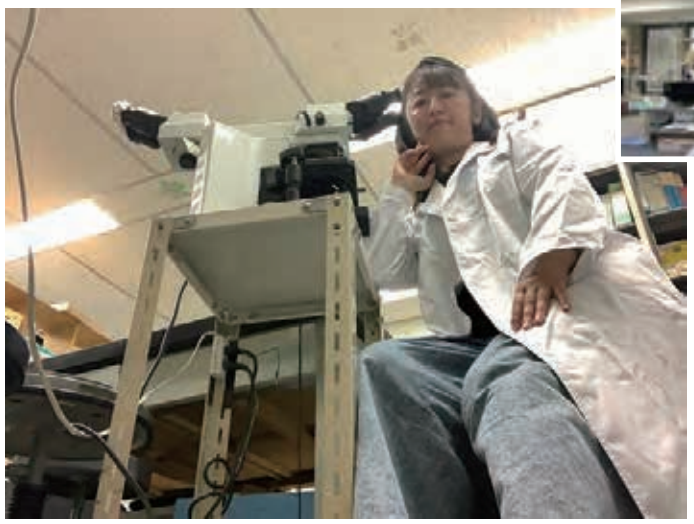


This diagram shows the cycle of scientific research. Researchers need to be able to do all of these seven processes, but typical practical exercises often test the participants' ability to perform mainly process C (as illustrated in the diagram). However, the IBO Challenge 2020 is remote, so it is impossible to conduct actual experiments. Therefore, we asked ourselves which competencies to test. The most important ability as a researcher is the process of deriving a question from observations. Researchers must be original. Originality is directly related to how deep the observation is and how interesting the questions are. Unfortunately, the thing that you don't train for during your high school education is how to observe deeply. In biological research, this "observation" includes not only observation with the eyes, but also many other means such as the modification of proteins, gene expression, exchange of substances, cell behavior, and the number of individuals. In this exam, we decided to have the participants observe the subject deeply and thoroughly with their naked eyes and express them. Instead of being unable to experiment, we also asked participants to design experiments to solve the question. At that time, you went back to the observation again (process A'). I would like to invite all of the participants to make deep observations of various subjects. It is a pleasure for researchers to solve the original questions from deep observations and produce their own results. I would like to meet the participants who are doing original research in the near future.

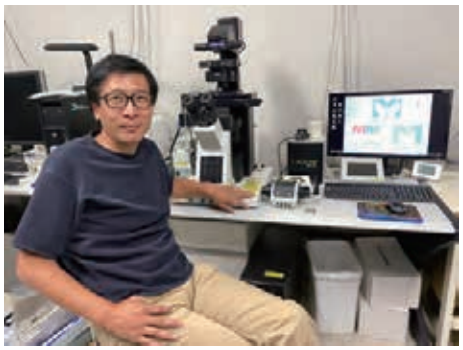
Iwao Koga
(Kamigoto High School)



Naoshi Takatori
(Tokyo Metropolitan University)



Kimiko Fukuda
(Tokyo Metropolitan University)



Guojun Sheng
(Kumamoto University)

Kyoko Fujimoto
(Nagasaki International University)

Practical Exam 2

Bioinformatics Team

Takeshi Kawashima

Sharing the Joy of Research Through Simulating the Research Process

What we cared the most about when creating the bioinformatics exam for this event was to only use actual biological data. We didn't want to simplify the content by using artificial sequence data. We thought that the students' true biology talent would be best reflected in the way they analyze the real data. Because of this, we created questions recreating the actual research process of bioinformaticians.

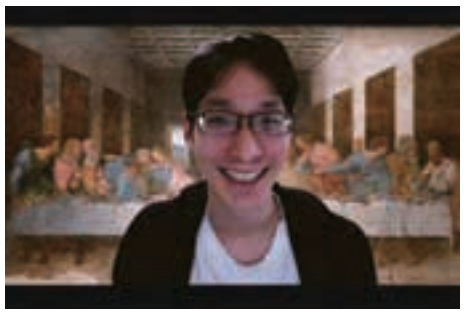
Bioinformatics is a field of science that has been most active in the use and analysis of databases of DNA and amino-acid sequences. In modern science, there is a massive effort to replace real-world observations with digital information. In other words, bioinformatics is the field that analyzes such digitally replaced biological data.

Therefore, considering the historical context of bioinformatics, we set the three essential abilities required for bioinformaticians as: 1) replacing observations with digital data (database), 2) approximating real life phenomena with equations (modeling), and 3) properly processing and analyzing the first two using a computer (computer science). Then, we planned to test these three abilities through our exam.

The most challenging part for us was making sure that there was one clear-cut answer for each question. The use of bubble sheets for answering greatly limited our flexibility, since we couldn't provide any open-ended questions to the competitors.

Another challenge for us was the IBO syllabus. In Campbell Biology, there is little mention of bioinformatics- the section about gene databases is about the only one. This forced us to begin every question with an explanation of the required background knowledge, which inevitably made the questions lengthy. We tried our best until the very last moment to create informative yet concise question sentences. Thanks to the generous cooperation of many people, we managed to make our questions into a web application that could be accessed from any device and implemented it on the internet.

In our exam, competitors started with some simple genome sequence data in hand. However, as they went through the questions, they could simulate the research process of gradually adding interpretations to the raw data using some computer programs. While anybody could reach the correct answers by simply trying all possible patterns, it required a series of educational guesses based on extensive biological knowledge to answer them correctly in a limited amount of time. We are greatly pleased if, through the exam, our competitors could experience the joy of biological research.



Haruka Ozaki
(University of Tsukuba)

Takeshi Kawashima
(National Institute of Genetics)

Josephine Galipon
(Keio University)

Tatsusada Yoshida
(Nagasaki International University)

Miho Totoki
(Sasebo Kita High School)

Practical Exam 3

Plant Physiology Biochemistry Plant Morphology Team

Koichiro Awai

If somebody asks you to name Japanese food you know, most of you would answer sushi first. Have you eaten sushi before? Unless you are completely new to sushi, you would know there are some green spicy paste between rice and raw fish; it's called Wasabi. Wasabi is an original spice of Japan and is produced by grinding the plant roots of *Eutrema japonicum*. This year, we planned to make the practical examination about Wasabi.

The exam included three topics: 1. Phylogenetic analysis of Wasabi by comparing the detailed structure of leaves among phylogenetically different kinds of plants, 2. Biochemical analysis of the enzyme responsible for producing spiciness of Wasabi by using fresh roots of *Eutrema japonicum*, and 3. Histochemical analysis of Wasabi to understand physiological role of the spiciness of Wasabi. It is widely believed that the purpose of Wasabi in sushi is to erase fishy smell of raw fish, but there is another and more important purpose: Wasabi can keep bacteria and fungi away from raw fish. Wasabi is, in fact, a traditional preservative.

Wasabi's spiciness is similar to the spiciness of radish or mustard, rather than red pepper. If you have a chance to eat sushi, please search for Wasabi and remember why it is good for sushi. Enjoy!

Koichiro Awai
(Shizuoka University)

Shinichi Inoue
(Isahaya High School)

Takuhiro Uto
(Nagasaki International University)

Kiyohiko Igarashi
(The University of Tokyo)

Shinichiro Sawa
(Kumamoto University)

Yoshihisa Kotake
(Saitama University)

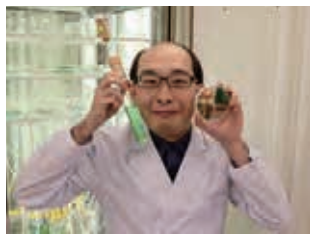
Theoretical Team 1

Biochemistry Team

Masahiko Ikeuchi

Science is a study of elucidating functions from mechanisms. In order to understand the functions of living organisms, it is important to learn underlying mechanisms that drive every biological function. The most fundamental part of biology is biochemistry, which deals with biological molecules and structures. If we could thoroughly understand their behaviors at the molecular level, we should be able to understand and predict cellular functions at higher levels, eventually all life phenomena, with further possible applications to medicine, industry, ecology, etc.

Masahiko Ikeuchi
(The University of Tokyo)



Kaisei Maeda
(Tokyo University of Agriculture)

Theoretical Team 2

Cell Biology Team

Shinji Kamimura and Tetsuro Mimura

Cells are the basic units that make up life forms. The same is true even for humans that are placed at the very tip of eukaryotic twigs in the evolutionary tree. In this respect, understanding the structures and functions of cells leads to the basic understanding of universal principles that are common to all other organisms, including bacteria, animals, plants and us, human beings. Considering such universality in the field of cell biology, we tried to prepare our questions to cover the whole field of cell biology and asked not only textbook knowledge but also your deeper understanding of biological principles based on physics and chemistry.

Shinji Kamimura
(Chuo University)

Tetsuro Mimura
(Kobe University)

Kimitsune Ishizaki
(Kobe University)

Yuta Otsuka
(The University of Tokyo)
IBO2011 Former Competitor

Hidehiro Fukaki
(Kobe University)

Takashi Osanai
(Meiji University)

Harushi Nakajima
(Meiji University)

Theoretical Team 3

Genetics Team

Harushi Nakajima

In the field of genetics, we created questions which required the ability to think logically and calculate accurately. Therefore, there are more problems based on fictitious experimental results and observations than problems based on actual academic papers. This type of question can be answered without any special knowledge as long as you read the question sentences carefully, but it is still difficult for examinees to solve because of the long sentences and heavy calculations. Despite some concerns, we believe that the competitors who participated in the IBO Challenge 2020 could compete well. We hope they enjoyed the problems.

Masahiko Kato
(Meiji University)

Tomohiro Shimada
(Meiji University)

Yoshiya Seto
(Meiji University)

Theoretical Team 4

Plant Biology Team

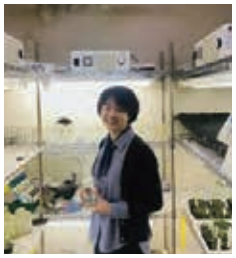
Munetaka Sugiyama

Plants represent a large group of multicellular eukaryotes of which structure, development, metabolisms, and physiological processes are quite different from those of animals in many aspects. By struggling with our questions of plant anatomy and physiology, we wanted the competitors to better understand the logics and mechanisms of underlying plant-specific forms and lifestyles, to get familiar with research in this field, and to become much more interested in the plant's world.

Left: Akihito Mamiya
(The University of Tokyo)
Right: Munetaka Sugiyama
(The University of Tokyo)

Kenji Nagata
(The University of Tokyo)

Yuta Otsuka
(The University of Tokyo)
IBO2011 Former Competitor



Hatsune Morinaka
(The University of Tokyo)

Takaaki Yonekura
(Nara Institute of Science and Technology)

Theoretical Team 5

Animal Biology Team

Tatsuo Michiue

There are more than one million species of animals living on Earth. Each animal has various shapes and characteristics, and lives in a variety of natural environments. There is no doubt that we, humans, are also animals. Once we think about our own bodies, we can easily understand that the body has so many function. We take food, move, breathe, support our body, supply oxygen throughout the body, and sometimes prepare for invasion from the outside. For thousands of years, human being has clarified how animals achieve these functions through observations and experiments. We prepared the exam questions with the hope that you would reconsider the splendor of animals through answering them.

Tatsuo Michiue
(The University of Tokyo)

Takayoshi Yamamoto
(The University of Tokyo)

Tatsuhiko Noguchi
(National Defense Medical College)

Masafumi Inui
(Meiji University)

Shinji Kamimura
(Chuo University)

Manabu Yoshida
(The University of Tokyo)

Hideki Abe
(Nagoya University)

Thoughts Behind the Exam

Theoretical Team 6

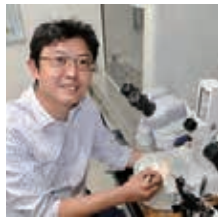
Evolution Team

Masato Nikaido

Knowing the evolution and the diversity of living things are directly linked to the idea of protecting the global environment. Please be aware that all living organisms are connected in the time of evolution; do not focus solely on the current research on mice and humans, but also have wider perspectives including the past, present, and future. Indeed, our questions covered a variety of organisms, including whales, mice, fish, insects and even algae. In addition, we prepared larger-scale questions that included extinct fossil animals as well as extant animals. We hope that solving our questions provided a good opportunity to consider the processes and mechanisms of biological diversification.

Masato Nikaido
(Tokyo Institute of Technology)

Takushi Kishida
(Museum of Natural and Environmental History, Shizuoka)



Masafumi Nozawa
(Tokyo Metropolitan University)

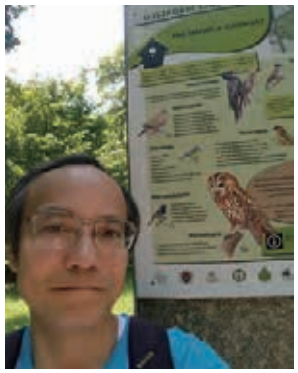
Koji Fujimura
(Niigata University)

Theoretical Team 7

Ecology Team

Tadashi Miyashita

Ecology is a field of science that deals with interactions between organisms and the environment, with an emphasis on exploring how ecosystems work. More specifically, ecology tries to identify the mechanisms of how the number of individuals and species richness are determined in nature, and how materials and energy flows in an ecosystem are controlled. Ecology also helps solve global issues, such as biodiversity conservation and sustainable use of ecosystem services. In recent years, reducing the risk of zoonotic diseases is becoming an urgent issue. Integration of ecology with other fields of biology as well as social sciences may be the key to achieve the long-term, harmonious coexistence of human society with nature.



Tadashi Miyashita
(The University of Tokyo)

Akira Mori
(Yokohama National University)

Yuya Fukano
(The University of Tokyo)

International Subgroup Meeting

Special Thanks to the Subgroup Members

It is since IBO2009 in Japan that the host country of IBO holds a subgroup meeting to shape up the exams prior to the jury meeting. For this IBO Challenge, we had two days of online subgroup meetings for both the practical and theoretical exams. Ten members of the subgroup devotedly spent four days reading the exams carefully. Thanks to their extremely constructive comments, our questions were brushed up to completion. We felt very happy when no question was rejected during the jury meeting.

Because we spent such an intense time together throughout the subgroup meeting, we felt like we already knew each other very closely, even though we just communicated over the comment function of Word files. I now feel it quite a pity that we couldn't see each other face-to-face. I hope we, including the scientists who made the questions, of course, can see each other in future IBOs.

My heartful thanks to all of the subgroup "family".

Chief, the IBO2020 Scientific Committee
Hiroshi Wada

Anindya Rana Sinha
(India)

Christiane Mühle
(Germany)

Gayane Ghukasyan
(Armenia)

José Matos
(Portugal)

Joshua Hodgson
(UK)

Mary Oliver
(UK/Australia)

Poonpipope Kasemsap
(Thailand)

Saman Hosseinkhani
(Iran)

Vasili Pankratov
(Belarus)

Exam Operations

IBO Challenge 2020 was the first attempt for an IBO host country to coordinate examinations remotely. Due to the COVID-19 pandemic, the participating countries were in vastly different situations, which made our operations challenging. Although there were numerous challenges and limitations this year, we tried to build the best operational structure and methods for fair examinations. As a result, we managed to coordinate the exams with five staff members, only using existing services and platforms for nearly all operations.

1 Online Subgroup Meeting and Jury Meeting

- Exam questions for International Biology Olympiad, originally made by the host country, are first reviewed and edited by the international subgroup members appointed by the host. After that, the questions are released to the jury members of all participating countries. The jury members also review the questions and, if they find an objectionable part, a vote by all jury members is conducted to determine whether to keep, reject, or modify the part. Some jury members translate the questions during the meeting as well. After this whole process, the official IBO examinations are finally created.
- Just like the examinations, we had no choice but to organize subgroup and jury meetings completely online for the IBO Challenge 2020. Since it was logistically too difficult to host a real-time online meeting with around 50 countries that have different time zones, internet environments, and COVID-19 statuses, we utilized emails and cloud platforms like Google Drive for communication and an online form service (i.e., Cognito Forms) for voting.

2 Supporting Exam Operations Within Each Country

- Prior to the event, we published two essential documents for all participating countries: "Exam Operation Guidelines" for specific rules and recommendations to ensure fair examinations, and "Exam Operation Timetables and Instructions" for each country's daily to-dos and step-by-step instructions for every task.
- During the event, the IBO2020 Secretariat Office sent a "daily reminder" email every day to remind them of the tasks and deadlines of that day.

3 Online Resources for the Practical Exams

- For the practical exams (animal physiology and bioinformatics), we required competitors to access online applications (i.e., webpages) to answer some of the questions. In order to avoid slow connections or server failures caused by access concentration, we prepared multiple servers (26 for the animal physiology exam and 33 for the bioinformatics exam) and placed them across the globe according to the geographical locations of the participating countries. We used Amazon Web Services for this operation. Although some minor issues were detected, we successfully managed the servers from the beginning of the jury meeting until the end of the practical exams. The online applications were developed for this event.

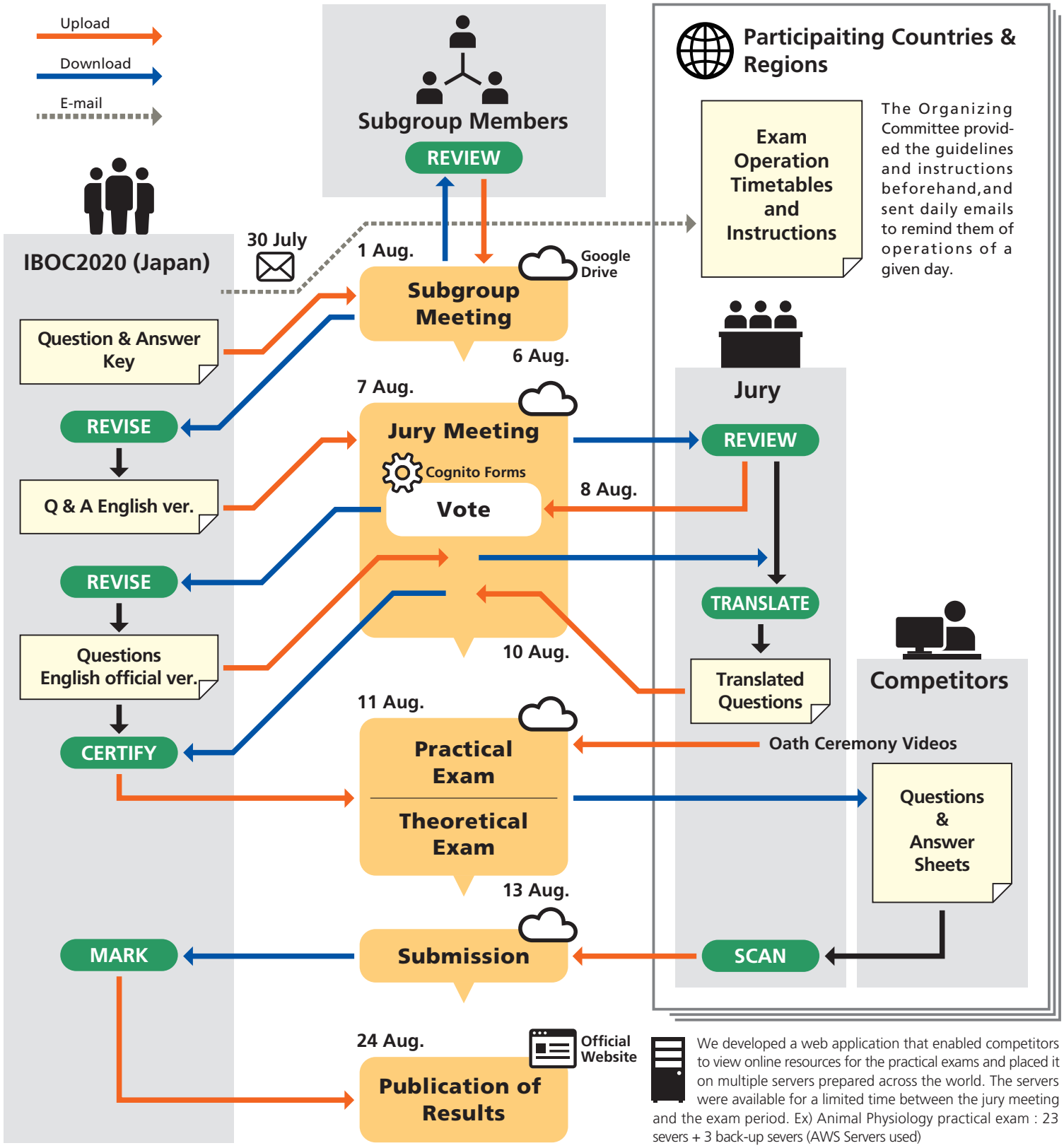
4 Cheating Prevention

- In order to minimize the risk of cheating, we announced various exam-related rules and recommended operational methods prior to the event. For instance, the participating countries had to film an oath ceremony before the exam (both competitors and jury) and upload it to a designated Google Drive folder. We also recommended countries to share an online supervision link (Zoom, Skype, etc.) with us so that we could randomly join their exam supervision for higher transparency.

5 Accommodating All Countries

- Throughout the event, from the beginning of the jury meeting until the end of the exams, we coordinated nearly everything based on each country's local time zone instead of Japanese Standard Time. This was to ensure all participating countries had an equal amount of time to review and translate the questions, and to accommodate each country's unique situations and challenges during the COVID-19 pandemic.

(Kentaroh Honda, IBO2007 Former Competitor)



We developed a web application that enabled competitors to view online resources for the practical exams and placed it on multiple servers prepared across the world. The servers were available for a limited time between the jury meeting and the exam period. Ex) Animal Physiology practical exam : 23 severs + 3 back-up severs (AWS Servers used)

Exam Results

Gold

Country/Region	Name
Thailand	Chaisrisawatsuk, Bhumpanya
Chinese Taipei	Chen, Chien-Yi
Vietnam	Duc, Ho Viet
South Korea	In, Heewon
Czech Republic	Janoušek, Jiří
Germany	Kessels, Fynn
Netherlands	Kooter, Berit
Russia	Kovalev, Maksim
USA	Lam, Judson
Singapore	Lin, Ziwei, Dewey
Azerbaijan	Muradli, Matin
Russia	Nagimov, Ruslan
Russia	Nikolaev, Nikolai
USA	Parsan, Nithin
China	Shao, Chengjun
Japan	Suematsu, Mahiro
Uzbekistan	Valijonova, Saida Atabekovna
China	Xu, Runtian
Chinese Taipei	Yang, Cheng-Chun
China	Yao, Qian
USA	Zhang, Albert

Silver

Country/Region	Name
Turkey	Ateş, Yiğit Can
Netherlands	Bosgoed, Dante
Hungary	Buzafalvi, Denes
Chinese Taipei	Chang, Hsiang-Chun
Latvia	Ekmanis, Toms
Azerbaijan	Gafarov, Sadiyar
UK	Grodzinski, Noah Joseph Baker
Germany	Groß, Damian
Azerbaijan	Gurbanov, Ranal
Vietnam	Ha, Dong Ngoc
Iran	Hassani, Arian
Chinese Taipei	Huang, Chi-Sheng
China	Jia, Hongzhe
Japan	Kanehisa, Ren
Uzbekistan	Karimov, Ravshanbek Mirgolib ugli
Japan	Kawamoto, Seita
South Korea	Kim, Geono
Russia	Kuzmenko, Oleg
Poland	Kwiatkowski, Jakub Krzysztof
USA	Liang, Derrick
Latvia	Lopatko, Rolands
Singapore	Lu, Kate
Indonesia	Marsetyo, Farrel Alfaza
Japan	Matsufusa, Manami
Lithuania	Melaika, Simonas
Iran	Moheimani, Nazgol
UK	Mulford, John
Indonesia	Nadia, Joan
Czech Republic	Pelánek, Ondřej
Turkey	Polat, Gencay Kaan
Singapore	Qiu, Xinzhi
Estonia	Rahe, Martin
Netherlands	Ruiten, Xanta van
Iran	Sabbaghi Lalimi, Mohammadamin
Singapore	Tan, Cheng Yat
Uzbekistan	Tojiboev, Sardor Eshqul ugli
Hong Kong, China	Tsang, Hoi Yeung
Hungary	Tusnady, Simon
Turkey	Yilmaz, Anil Deniz
South Korea	Yoon, Jae Won
Azerbaijan	Ziyaddinov, Asiman
Poland	Zurowski, Maciej Mateusz

Bronze

Country/Region	Name
Sri Lanka	Abbinanthan, Arulanantham
Latvia	Apsitis, Martins
Australia	Bahra, Priya Kaur
Latvia	Berzins, Mairis
Poland	Borak, Martyna Aneta
Poland	Buchalska, Barbara Anna
Australia	Bui, Nicholas Man Dac Vo
Hong Kong, China	Chan, Tsz Ching
Hungary	Czako, Balint Laszlo
Lithuania	Dapšys, Povilas
Sri Lanka	Dhanapala, Dhanapala Mudiyanselage Nilushi Navodya
Bulgaria	Dimitrov, Nikola Milenov
Lithuania	Duchovskytė, Marija
Luxembourg	Furlano, Jean-Marc Raffaello Matteo
Luxembourg	Gerhards, Frédéric
Bulgaria	Gilin, Viktor Dimitrov
Hungary	Gulacsi, Mate Mihaly
Denmark	Hansen, Tobias Spliid
Hong Kong, China	Ho, Ka Chun
Germany	Jaschinski, Ilka
South Korea	Kim, Dale
Armenia	Kurghinyan, Mher
Bulgaria	Kutrovski, Dimitar Marinov
Switzerland	Lanz, Kaspar Merlin
UK	Leung, William Henry Ty
Vietnam	Linh, Ha Vu Huyen
Sri Lanka	Malavige, Sauni Ruwanima
Luxembourg	Marth, Raffaël
Finland	Marttinen, Harri Ensio
Indonesia	Maulana, Achmad Rizky
Czech Republic	Maxerová, Tereza
Slovenia	Mežnar, Anamarija
UK	Mousavi, Seyed Sepehr
Syria	Nasra, Majd
Philippines	Ng, Jeremy Ace Feliciano
Netherlands	Osenbruggen, Lucas van
Thailand	Piyanirun, Kantawich
Slovenia	Prelog, Ivo
Bangladesh	Raayan, Rafsan Rahman
Thailand	Rattanawannachai, Kittitach
Estonia	Remm, Mari
Switzerland	Salud, Anna
Nepal	Sapkota, Awahan
Germany	Sauer, David
Iran	Shahsavand Davoudi, Amirhossein
Bangladesh	Sharar, Raad
Thailand	Sima-Aree, Arthitaya
Kazakhstan	Taimanov, Adam
Estonia	Tamm, Johan
Indonesia	Tjandra, Nathanael
Bulgaria	Toshev, Kiril Teodorov
Belgium	Toussaint, Marie
Czech Republic	Tulis, Jan
Turkey	Tüney, Ali Berdan
Tajikistan	Vatanshoevich, Shams Davlyatbekov
Finland	Vuorela, Teemu Toivo Viljami

Certificate of Merit

Country/Region	Name
Armenia	Avanesyan, Gevorg
Kyrgyzstan	Azhybaev, Baktynur
Kazakhstan	Bissembayev, Arman
Turkmenistan	Hallayev, Hoshgeldi
Estonia	Haug, Sofia Marlene
Sri Lanka	Munasinghe, Samidhi Manthilani
Kazakhstan	Muratov, Yerassyl
Vietnam	Nga, Nguyen Thi Thu
Belgium	Van Roy, Mander
Hong Kong, China	Wong, Lok San
Australia	Zhou, Angie Jie

Special Awards

The 3D Reconstruction Award (Practical Exam 1: Animal Physiology)

Thailand	Chaisrisawatsuk, Bhumpanya

The Intron=Exon Boundary Award (Practical Exam 2: Bioinformatics)

Russia	Kovalev, Maksim
Russia	Nagimov, Ruslan
Indonesia	Nadia, Joan

The Champions of the Theoretical Exams (Theoretical Exam 1 & 2)

China	Shao, Chengjun
China	Yao, Qian

The Champions of Hard Questions (Theoretical Exam 1 & 2)

Chinese Taipei	Chang, Hsiang-Chun
Chinese Taipei	Huang, Chi-Sheng
Germany	Kessels, Fynn

About Medals

Gold	Kamuysaurus japonicus Read more on the next page
Silver	Nipponia nippon is an ibis of the order Pelecaniformes that can reach a length of 75 cm and a wingspan of 130 cm. They have white feathers with salmon-pink coloration under their wings and a bare, red face. The birds feed on amphibians, fish, and insects found in rice paddies. The crested ibis was once widespread in China, Japan, Korea, and eastern Russia. However, habitat destruction and pesticide use decimated ibis populations until they could only be found in Shaanxi Province, China. In 2008, joint Chinese-Japanese conservation efforts led to the reintroduction of crested ibises on Sado Island in Japan.
Bronze	Camellia japonica is a shrub or small tree species that grows to heights of 3-5 meters and is native to southern Japan and China. It is widely planted as an ornamental species around the world, with over 2,000 different cultivars in existence. This species is iconic for its beautiful white, pink, or red flowers that appear from late winter to early spring as well as its thick, glossy, and evergreen leaves. Its flowers produce a sweet nectar that is popular with several bird species and the monkeys of Yakushima island in southern Japan.

About Kamuysaurus

Dr. Yoshitsugu Kobayashi
Professor at the Hokkaido University Museum

Excavated skeleton of **Kamuysaurus japonicus**.

Kamuysaurus japonicus, newly named in 2019, is the best preserved and most complete large dinosaur skeleton from Japan. The genus name "Kamuy" refers to a mythological deity of the Ainu, the indigenous people of Hokkaido Island of Japan. "Saurus" and "japon" mean "reptile" and "Japan", respectively, so *"Kamuysaurus japonicus"* has a meaning of "the god of Japanese dinosaurs". The skeleton of *Kamuysaurus* was discovered from Cretaceous rock, dated as 72 million years ago, in Hobetsu area of Mukawa Town in Hokkaido Prefecture. This dinosaur was at least 12 years old at the time of death with a body length of approximately 8 meters and body mass of about 4.3 to 5 tons. *Kamuysaurus* is a duck-billed dinosaur, or hadrosaurid, which was common plant-eating dinosaurs during the Cretaceous. This discovery is not only significant for the people of Hokkaido and all of Japan, but it has global significance because this dinosaur shows us how the world has been connected through time. *Kamuysaurus* is closely related to dinosaurs from USA and Canada, *Edmontosaurus*, a duck-billed dinosaur found throughout much of western North America. Because these dinosaurs are so closely related, they provide evidence that long ago, Asia and North America were connected.

The initial discovery of the fossils came in April 2003 when a local resident unearthed 13 articulated vertebrae in the Upper Cretaceous Hakobuchi Formation in Hobetsu area of Mukawa Town. The vertebrae were initially considered to be a part of marine reptile plesiosaur, but were later identified as a partial tail of a dinosaur in 2011. Joint expeditions, held in the summers of 2013 and 2014, were launched to find the remaining parts of the dinosaur. In 2013, while exploring the same hill where the original

About Kamuysaurus

Left: Excavation of **Kamuysaurus japonicus** in Hobetsu area of Mukawa Town.
Above: Reconstruction of **Kamuysaurus japonicus** at the beach.

fossils were found, the paleontologists excavated multiple skeletal elements including isolated teeth. During the excavation in 2014, a large amount of rocks, containing dinosaur bones and parts of skull elements were excavated, and the dinosaur was considered to be a nearly complete skeleton. Preparation of the dinosaur took nearly 10 years with the help of many volunteers. The prepared fossils clearly demonstrate that this is a nearly complete skeleton including multiple cranial elements, nearly complete series of vertebrae, and nearly complete fore- and hind-limbs. It turns out that it was the biggest discovery of Japan ever.

The study of dinosaurs is not about studying monsters. It is about discovering the fascinating and incredible evolution of animals. Some dinosaurs evolved into strange figures. Good examples are long and large horns on a head like *Triceratops*, one-meter-long bony plates on a back like *Stegosaurus,* and a snorkel-like crest on the top of the head like *Parasaurolophus*. This diversity in shapes shows how successful dinosaurs were back in time. Other dinosaurs competed how big they could be. About 150 million years ago, a large meat-eating dinosaur, *Allosaurus*, conquered a niche in North America, where sympatric plant-eating dinosaurs, sauropods with body size of over 30 meters, became larger than predators for protection. Lastly, some dinosaurs challenged to fly and evolved into birds. This evolution was revolutionary because they had to adapt to a completely new habitat in the air. Innovative dinosaur research in recent years has revealed the evolutionary process from reptiles to birds, which gives us better understanding of how animals in ancient time evolved to animals in modern world and how all organisms are related and connected to each other.

I love what I do. I am always fascinated with dinosaurs. Dinosaurs tell us so many things we don't know. I wish you have a thing that you are interested in like I do. I hope you love what you do. I want you to be always curious, because it is a strong driving force and creates a bright future. If you're not interested in anything right now, dinosaurs might be the first step for you!

About IBOC2020 Goods

Official IBOC2020 T-Shirt

Traditional Round Fan (Uchiwa)

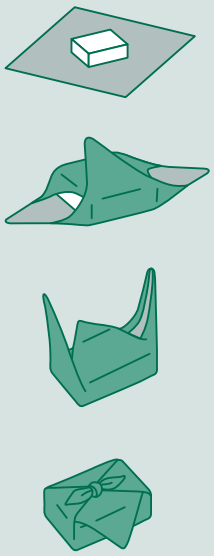
One of the two Japanese traditional gifts from IBO2020 is uchiwa, a round fan that is made from the wood of sustainably harvested Japanese cedar trees (*Cryptomeria japonica*). We hope you enjoy the scent of *Cryptomeria japonica*, a very distinctly Japanese aroma.

About IBOC2020 Goods

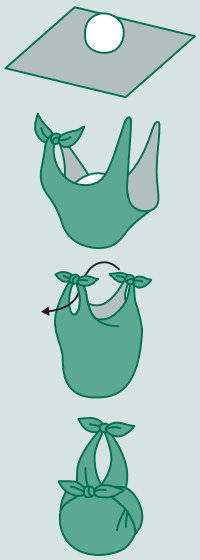
Traditional Cloth (Furoshiki)

The other Japanese traditional gift is furoshiki, a traditional Japanese wrapping cloth. Depending on how you fold the cloth, it can transform from a bag or purse to a cover that secures important items. If you search for furoshiki on the internet, you can find many folding patterns for this cloth that you can try. Some examples are shown on the next page.

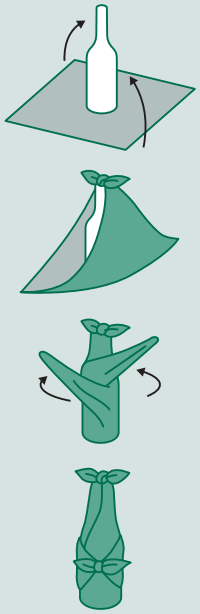
Otsukai Tsutsumi
(Basic Carry Wrap)



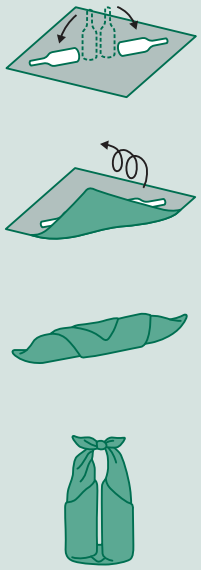
Suika Tsutsumi
(Watermelon Carry Wrap)



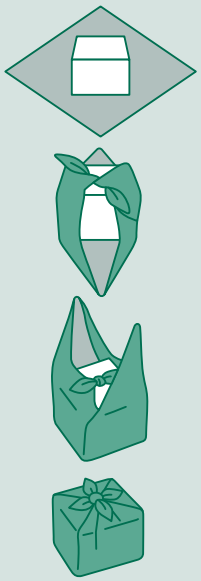
Bin Tsutsumi 1
(Bottle Carry Wrap 1)



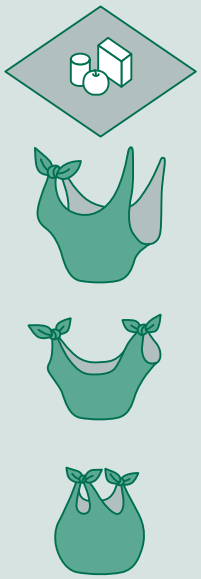
Bin Tsutsumi 2
(Bottle Carry Wrap 2)



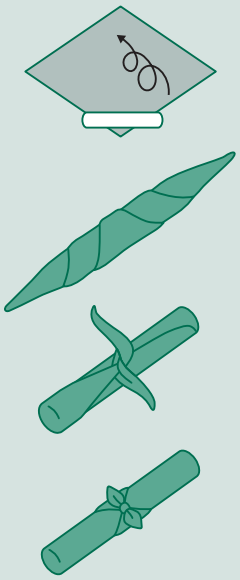
Yotsu Musubi
(4 Tie Wrap)



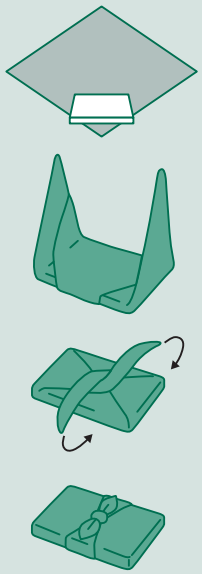
Tesage Bukuro
(Hand Carry Wrap)



Entou Tsutsumi
(Long Object Wrap)



Sao Tsutsumi
(Podding Carry Wrap)



Armenia

Competitors


Mher Kurghinyan


Ani Harutyunyan


Gevorg Avanesyan


Naeiri Sohrabian

Jury


Gayane Ghukasyan

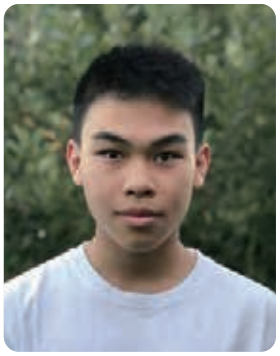

Arman Simonyan


Aren Petrosyan


Seda Marutyan

Australia

Competitors



Nicholas Man Dac Vo Bui

Angie Jie Zhou

Priya Kaur Bahra

Hamish Brodie Walker

Jury

Julie Cooke

Juliey Beckman

Supervisors

Nathan Bui / Nikki Mcdonald / Paul Mitchell

Azerbaijan

Competitors


Matin Muradli


Sadiyar Gafarov


Asiman Ziyaddinov


Ranal Gurbanov

Jury


Rashad Salimov


Tural Javadzade


Hasan Hasanov


Elvin Abdullayev


Anar Gojayev


Elvin Huseynov


Ramil Khammadov


Nargiz Mammadli

Bangladesh

Competitors

Tasnim Binte Zulfiqar

Rafsan Rahman Raayan

Raad Sharar

Abrar Jamil

Jury

Md Samiul Alam Rajib

Saumitra Chakravarty

Rakha Hari Sarker

Md Habibur Rahman

Supervisors

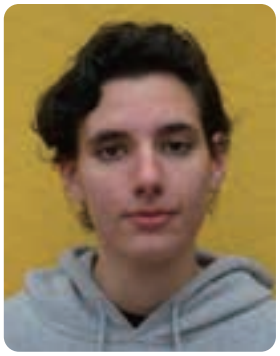
Muhammad Tarik Arafat / Saif Bin Salam Bondhon / Talukder Galib Shahriar Prince
Md. Minu Islam Khan / Samiha Sayeed / Md. Sahadat Hossain / Mahdi Hasan

Belgium

Competitors

Milan Roelens

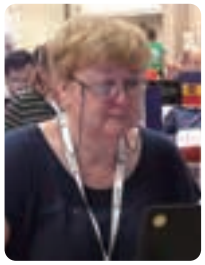
Mander Van Roy



Marie Toussaint

Sébastien Laurent

Jury



Marleen Caroline Van Strydonck

Hugo Paul Vandendries

Gérard Marie Cobut

Michaël Carmelo Terzo

Bulgaria

Competitors

Kiril Teodorov Toshev

Nikola Milenov Dimitrov

Dimitar Marinov Kutrovski

Viktor Dimitrov Gilin

Jury

Albena Georgieva Jordanova

Radoslav Aleksandrov Aleksandrov

Snezhanka Borisova Tomova-Gogova

China

Competitors

Qian Yao

Runtian Xu

Chengjun Shao

Hongzhe Jia

Jury

Yibo Hu

Xiangjun Tong

Dong Liu

Jinglan Wang

Yanyun Zhang

Xin Liang

Ruoting Tao

Supervisors

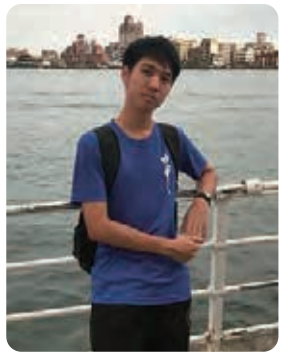
Fuwen Wei / Yongwen Zhang

Chinese Taipei／Republic of China

Competitors

Hsiang-Chun Chang

Chien-Yi Chen



Chi-Sheng Huang

Cheng-Chun Yang

Jury

Ying Wang

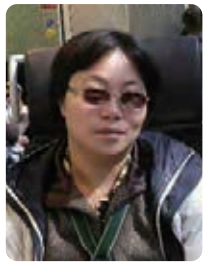
Chiu-Hsin Chu

Yu-Chung Chiang

Shu-Chuan Hsiao

Shen-Horn Yen

Jong-Kang Liu



Yi-Ling Yang

Jiin-Tsuey Cheng

Kuei-Shu Tung

Chih-Wei Shin

Fang-Lin Chu

Supervisors

Sheng-Pao Chen / Zi-I Song / Yu-Chi Chiu / Feng-Li Tsai

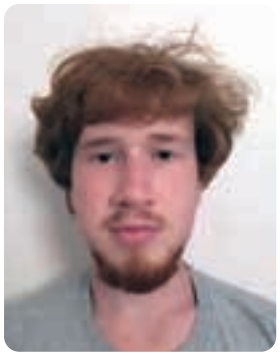
Czech Republic

Competitors

Ondřej Pelánek

Jan Tulis

Tereza Maxerová



JiříJanoušek

Jury

Lenka Libusová

Jan Černý

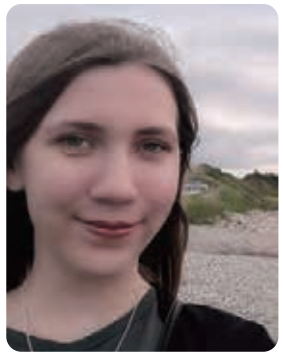
Antonín Reiter

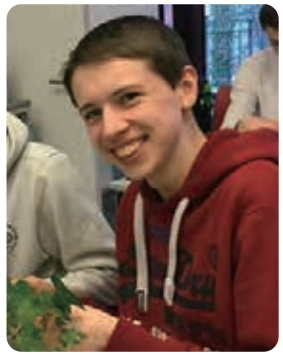
Denmark

Competitors


Tobias Spliid Hansen


Josefine Møgelvang


Sofie Buur Beck


Jonatan Høhne

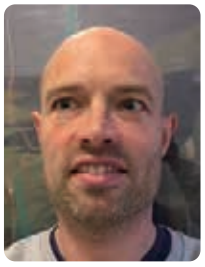
Jury


Kirsten Wøldike


Birthe Zimmermann


Vibeke Birkmann


Karen Helmig


Morten Eskildsen


Simon Albrechtsen

Estonia

Competitors


Sofia Marlene Haug


Mari Remm


Martin Rahe


Johan Tamm

Jury


Ando Vaan


Karl Jürgenstein


Uku-Laur Tali

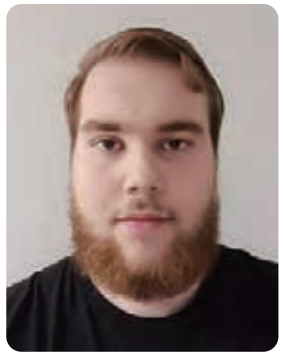

Sulev Kuuse

Finland

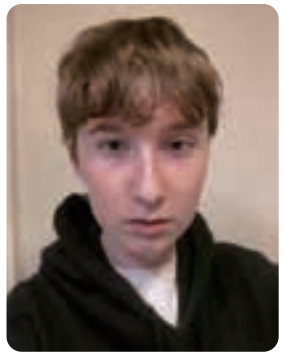
Competitors

Harri Ensio Marttinen

Suvi Linnea Laitinen



Teemu Toivo Viljami Vuorela



Oona Elina Charlotta Kurola

Jury

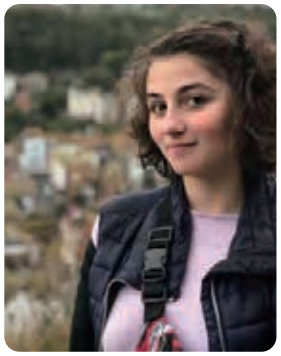
Niko Rainer Johansson

Tuomas Juha Eero Aivelo

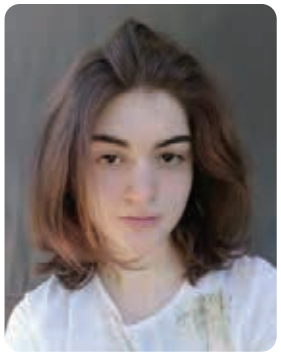
Jakke Sameli Neiro

Georgia

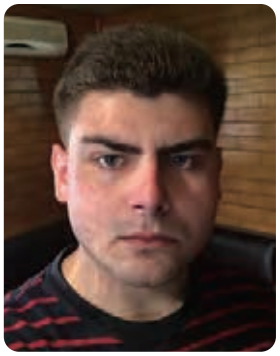
Competitors



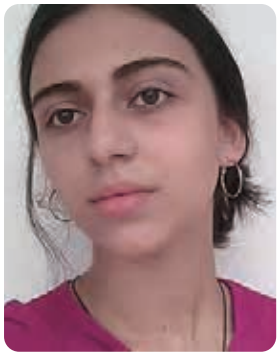
Elene Meskhi



Khatia Nadiradze



Gega Karanadze



Tinatini Morchadze

Jury

Ekaterine Bakuradze

Irina Modebadze

Nana Barnaveli

Ekaterine Mitaishvili

Germany

Competitors


Damian Groß


Ilka Jaschinski


Fynn Kessels


David Sauer

Jury


Burkhard Schroeter


Dennis Kappei


Toni Gossmann


Christiane Mühle


Patricia Scholz


Cedric Cappel

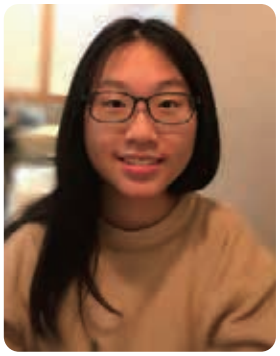

Jan Krieghoff

Hong Kong, China

Competitors

Lok San Wong

Ka Chun Ho



Hoi Yeung Tsang

Tsz Ching Chan

Jury

Ka Hoi Lau

Pui Yan Cecilia Yau

Hungary

Competitors


Balint Laszlo Czako


Denes Buzafalvi


Simon Tusnady


Mate Mihaly Gulacsi

Jury


Sandor Ban


Viktoria Gal


Zsolt Eros-Honti


Andrea Borbola

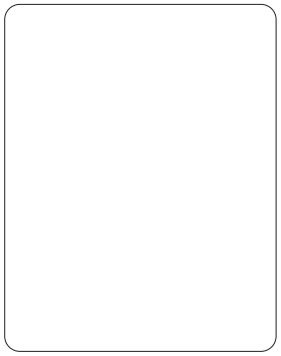

Adam Zoltan Seres

Supervisors

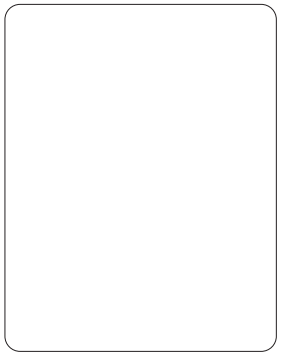
Eniko Gulyas / Anna Regina Krizsan

Iceland

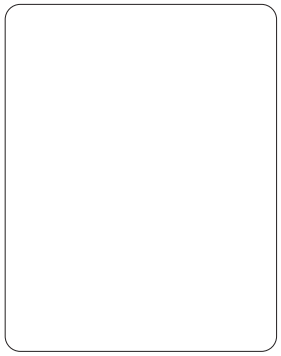
Competitors



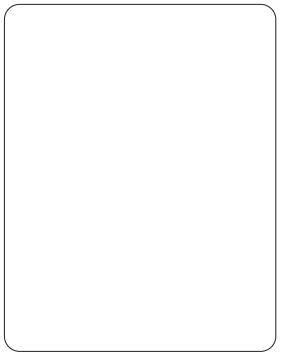
Katla Rut Robertsdottir Kluvers



Vitor Logi Þórisson

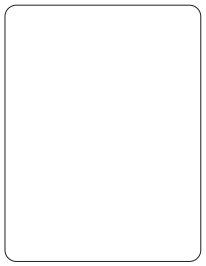


Kjartan Kristjánsson

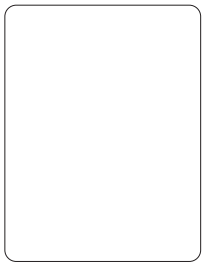


María Guðjónsdóttir

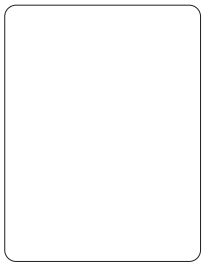
Jury



Þórhallur Halldórsson



Ólafur Patrick Ólafsson



Arnór Bjarki Svarfdal

Indonesia

Competitors

Achmad Rizky Maulana

Farrel Alfaza Marsetyo

Joan Nadia

Nathanael Tjandra

Jury

Ahmad Faizal

Agus Dana Permana

Ida Bagus Made Artadana

Husna Nugrahapraja

Titis Setiyobudi

Syailendra Karuna Sugito

Iran

Competitors

Amirhossein Shahsavand Davoudi

Nazgol Moheimani

Mohammadamin Sabbaghi Lalimi

Arian Hassani

Jury

Alireza Majd

Amirhossein Zare Mohazabiyeh

Alireza Tanoori

Mohammad Ebrahim Katebi

Ali Yazdizadeh Kharrazi

Maryam Gholami Gharatappeh

Saman Hosseinkhani

Supervisor

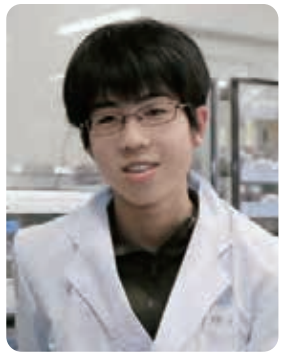
Mohammad Karamudini

Japan

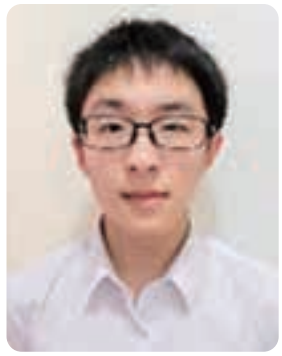
Competitors

Manami Matsufusa

Seita Kawamoto



Mahiro Suematsu

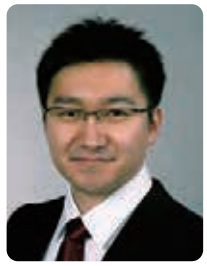


Ren Kanehisa

Jury

Junichi Saito

Ryo Iwama



Daisuke Takahashi

Masayuki Hatta

Gaku Takimoto

Supervisors

Hiroko Hasegawa / Akari Soma / Jun Yatsu

Kazakhstan

Competitors

Arman Bissembayev


Dinmukhammed Urazbayev


Adam Taimanov


Yerassyl Muratov

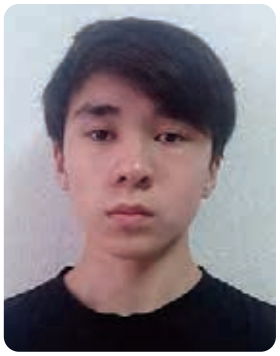
Jury


Adlet Sagintayev

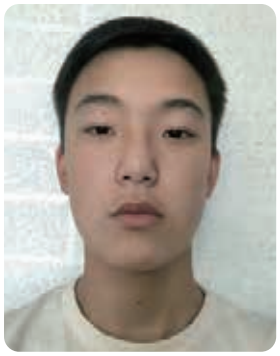

Ilyas Sakimov

Kyrgyzstan

Competitors



Azim Chyngozhoev



Aiatbek Kubanov

Baktynur Azhybaev

Aibek Medetbekov

Jury

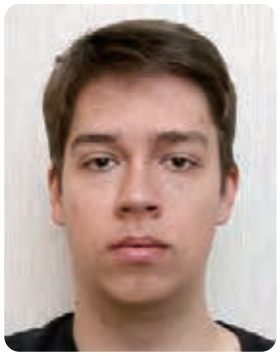
Elbrus Tazhibaev

Supervisor

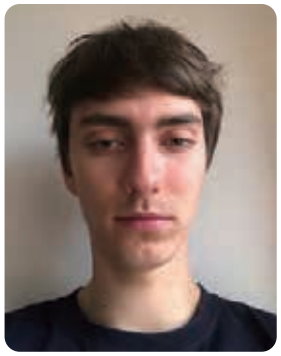
So Ho Kim

Latvia

Competitors



Toms Ekmanis



Martins Apsitis

Rolands Lopatko

Mairis Berzins

Jury

Janis Liepins

Agnese Kokina

Gunda Zvīgule Neidere

Katrina Daila Neiburga

Valdis Pirsko

Supervisors

Jana Kasaliete / Anitra Zile

Lithuania

Competitors

Povilas Dapšys

Marija Duchovskytė

Simonas Melaika

Edgaras Zaboras

Jury

Andrius Petrašiūnas

Rasa Sabaliauskaitė

Julius Juodakis

Dominykas Murza

Supervisor

Miglė Čiurinskaitė

Luxembourg

Competitors

Jean-Marc Raffaello Matteo Furlano

Raffaël Marth

Frédéric Gerhards

Jury

Thierry Marx

Alexandre Salsmann

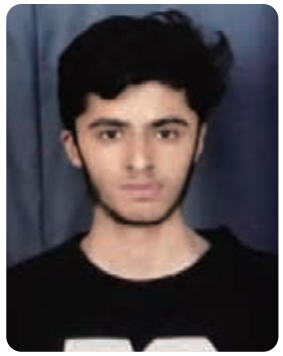
Sabrina Rodrigues Freitas

Nepal

Competitors

Garima Rokaya

Divya Prakash Yadav



Awahan Sapkota

Aadim Nepal

Jury

Surgeon BC

Dilip Bhattarai

Netherlands

Competitors

Berit Kooter

Dante Bosgoed

Lucas van Osenbruggen

Xanta van Ruiten

Jury

Ange Taminiau

Christine Moene

Leonie Cazemier

Nienke Nobel

Roel Baars

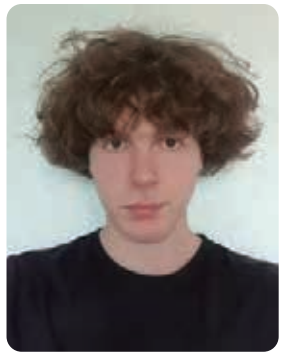
North Macedonia

Competitors

Stevan Bogdanov

Jovana Stojcheska

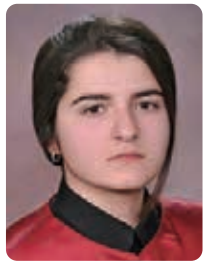
Verica Gjeorgieva



Filip Petrovski

Jury

Lozenka Ivanova



Elena Rafailovska

Nikola Hadji Petrushev

Supervisors

Aleksandra Cvetkovska-Gjorgjievska / Biljana Miova / Cvetanka Cvetkoska / Maja Mladenova
Slavcho Hristovski / Oliver Tushevski / Sara Cvetanoska / Marija Trencheva

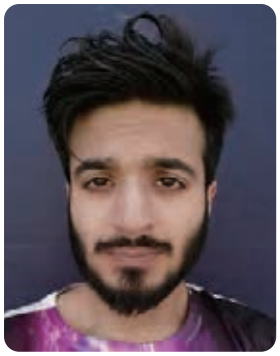
Pakistan

Competitors

Ahmed Kashif

Musa Salar

Umar Jamshad



Muneeb Waqas

Jury

Asma Imran

Asma Rehman

Philippines

Competitors

Sean Red Cruz Mendoza

Jeremy Ace Feliciano Ng

Elizabeth Rae Santiago Peralta

Jury

Ronald Allan Lopez Cruz

Poland

Competitors

Martyna Aneta Borak

Barbara Anna Buchalska

Jakub Krzysztof Kwiatkowski

Maciej Mateusz Zurowski

Jury

Takao Ishikawa

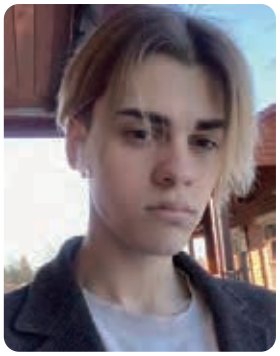
Lukasz Banasiak

Jakub Baczynski

Piotr Bernatowicz

Russia

Competitors



Oleg Kuzmenko

Maksim Kovalev

Ruslan Nagimov

Nikolai Nikolaev

Jury

Alexander M. Rubtsov

Calina Beliakova

Evgenii Shilov

Viktoriia Lavrenova

Saudi Arabia

Competitors

Zainab Al-Alawi

Maryam Ghalib Alhashim

Basil Habiballah

Omar Banjar

Jury

Yousef M. Al-Shahrani

Singapore

Competitors

Kate Lu

Cheng Yat Tan

Ziwei, Dewey Lin

Xinzhi Qiu

Jury

Dominic Jian Chien Heng

Beverly Pi Lee Goh

Ngan Kee Ng

Izavel Shu Yih Lee

Supervisors

Keene Lee / Renata Triani

Slovenia

Competitors

Ivo Prelog

Matic Smolič

Anamarija Mežnar

Dominik Primožič

Jury

Katja Ota

Mojca Ota

South Korea

Competitors

Dale Kim

Geono Kim

Jae Won Yoon

Heewon In

Jury

Jae Geun Kim

Kyoung Sang Cho

Kwang Pum Lee

Yong-Hwan Moon

Sri Lanka

Competitors

Sauni Ruwanima Malavige

Dhanapala Mudiyanselage Nilushi Navodya Dhanapala

Samidhi Manthilani Munasinghe

Arulanantham Abbinanthan

Jury

Hiran Samarasinghe Amarasekera

Nissanka Kolitha De Silva

Jayantha Wijeyaratne

Switzerland

Competitors

Anna Salud

Orna Tabea Frohnert

Kaspar Merlin Lanz

Kalila Hörler

Jury

Thomas Schneeberger

Lorenz Widmer

Sarah Hilfiker

Linus Meier

Andrea Audétat

Nina Kathe

Alain Fauquex

Syria

Competitors

Majd Nasra

Aows Dayoub

Basel Alkanjo

Batoul Amraya

Jury

Abdul Qader Abbady

Nazir Khalil

Abdulsamie Hanano

Antonious Aldaoude

Mohamad Bashir Arnous

Chadi Soukkarieh

Supervisors

Razan Arour / Dania Kabbani

Tajikistan

Competitors

Munisa Pulatova
Muminjonovna

Shams Davlyatbekov
Vatanshoevich

Zokirjon Mamadjonov
Suhrobovich

Akramzoda Nazira
Jamshed

Jury

Iskandar Ghayurov
Sayvalievich

Dilovar Turaev
Avrotovich

Thailand

Competitors


Arthitaya Sima-Aree


Bhumpanya Chaisrisawatsuk


Kantawich Piyanirun


Kittitach Rattanawannachai

Jury


Supachitra Chadchawan


Sittiporn Pattaradilokrat


Chatchawan Jantasuriyarat


Chatchawan Chaisuekul


Kittikhun Wangkanont

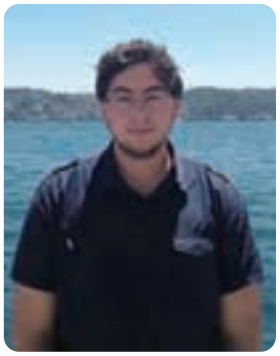

Panick Weingchai

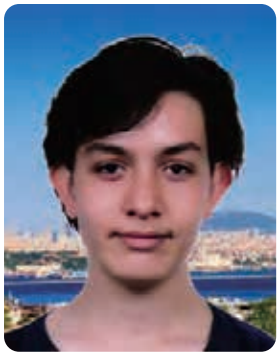
Supervisors

Charoensak Mueangkaew / Worachet Promruk

Turkey

Competitors


Yiğit Can Ateş


Anıl Deniz Yılmaz


Ali Berdan Tüney


Gencay Kaan Polat

Jury


Leyla Açık


Yusuf Menemen


Batuhan Karakuş


Ismail Hakkı Dur


Atahan Durbaş

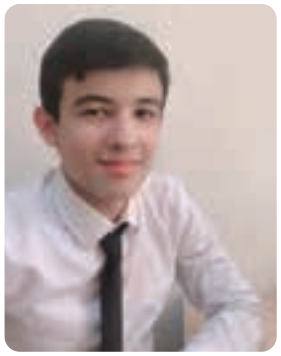

Sezgin Er


Ahmet Umur Topçu

Turkmenistan

Competitors

Abdullah Deryayev



Azat Meredow

Rahym Rahymov

Hoshgeldi Hallayev

Jury

Atajan Rahmanov

Supervisor

Berdimyrat Yazhanov

United Kingdom

Competitors

Noah Joseph Baker Grodzinski

John Mulford

Seyed Sepehr Mousavi

William Henry Ty Leung

Jury

Andrew Treharne

Matthew Johnston

Jiaqi Chen

Rebecca Peel

Katherine Lister

United States of America

Competitors

Nithin Parsan

Derrick Liang

Albert Zhang

Judson Lam

Jury

Kathy Frame

Michelle King

Uzbekistan

Competitors

Barno Kuranboy Qizi Rustamova

Sardor Eshqul ugli Tojiboev

Saida Atabekovna Valijonova

Ravshanbek Mirgolib ugli Karimov

Jury

Davron Dilmurot ugli Tukhtaev

Nodirbek Islom ugli Kholikulov

Supervisor

Oybek Rustamboyevich Abdullaev

Vietnam

Competitors


Dong Ngoc Ha


Ha Vu Huyen Linh


Nguyen Thi Thu Nga


Ho Viet Duc

Jury


Mai Sy Tuan


Nguyen Quang Huy


Dinh Doan Long


Trieu Anh Trung


Le Thi Phuong Hoa


Nguyen Thi Hong Van


Le Ngoc Hoan


Vu Thi Thu


Le Hong Diep

Supervisors

Tran Duc Long / Bui Phuong Thao

Afghanistan

Competitors

Tania Shams

Anara Hussaini

Rozina Haidary

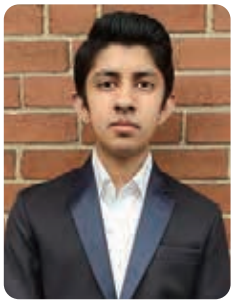
Jury

Nizamuddin Mohibi

Qurban Ali Waezi

Canada

Competitors



Param Patel

Jia Ni Jenny Wu

Jessica Yu

Jury

Jiashen Jayson Tian

Sylvie Bardin

Croatia

Competitors

Ema Moskatelo

Olga Jerkovic Peric

Mihaela Simunic

Jury

Andreja Lucic

France

Competitors

Rayan Pierquet

Eilone Nahon

Isaure Berard

Eve Rouquette

Jury

Jacques Chanteloup

Norway

Competitor

Heidi Berg

Jury

Malin Benum Roe

El Salvador / Ibero-American Countries

Jury

Huilhuinic Angel Orantes

Abizaí Clemente Chinchilla

Fátima Alejandra Hernández

IBO Challenge 2020

PART 2

International Group Project

International Group Project Timeline

Date	Event
25 July, 2020	**Deadline to apply for Project Facilitators** (Invitation sent to all accepted IBO2020 Nagasaki volunteers)
31 July	**Competitors: deadline to submit their topic preferences**
3 August	**Grouping of competitors finalized** (All competitors were assigned to a group of their first choice)
8-9 August	**Grouping announced to Project Facilitators**
13 August	**The International Group Project begins** • Slack used for communication between facilitators and organizers • Facilitators were asked to submit Progress Check Sheet every two weeks to be reviewed by Supporting Faculty Members
Early October	**Project Facilitators recorded their meeting for archiving**
31 October	**Deadline to submit project deliverables**
20 December	**Results announced on the website**

*"**Imagine, discuss,** and **propose** the future of biology through current worldwide biological challenges."*

General Data

Participating Countries / Regions	52
Competitors	202
Group Project Facilitators	37
Initial Number of Group Project Teams • Some competitors dropped out due to their academic responsibilities, vacations, time difference, connection issues, etc. • By the end of August, three teams were merged into other teams (46 remaining). 20 competitors had dropped out in that period.	49
Teams that successfully submitted the final deliverables by the deadline (November 5th)	39
Competitors who finished the group project	approx.130
Competitors who did not participate / quit halfway*	approx.70

*Due to illness, time difference, conflicted responsibilities, etc.

IBO Challenge 2020

International Group Project

Human beings in the 21st century are facing various challenges that are more global and interdisciplinary than ever in history. We believe that biology is a key academic field in resolving these highly complicated issues and sustainably developing our society, as it deeply encompasses both knowing ourselves and knowing our surroundings.

Through the IBO Challenge 2020 International Group Project, we aimed to provide students with valuable opportunities to imagine, discuss, and propose the future of biology together with fellow young biologists across the world. Even during the COVID-19 pandemic, students had a chance to form life-long relationships with other IBO community members and obtain professional feedback on their deliverables.

Group Structure

Each group initially consisted of a maximum of five students, all representing different countries. Utilizing online communication tools (emails, messages, video calls, etc.), each group tackled a unique project that focused on a task and topic of their choice (see Tasks and Topics).

Project Facilitators, selected from accepted IBO2020 volunteers, oversaw the project in each group. They also worked as a bridge between the students and the IBO2020 Organizing Committee (organizer).

Tasks and Topics

Prior to the event, each student selected a) the task they would like to carry out and b) what topic area they would like to focus on. Based on these preferences, we matched students with others interested in the same tasks and topic areas.

Tasks (Choose One)

A. Plan and propose a creative experiment on a selected topic.
B. Discuss and propose how biology can address a selected topic.

Topics (Choose One)

1. Infectious Diseases
2. Biodiversity and Oceans
3. Genome Editing
4. Evolution

Project Deliverables

At the end of the project, all groups were asked to create and digitally submit their proposal in either of the following two forms. We purposefully didn't specify any layout or format requirements- the participants had the freedom to design their own work.

- PowerPoint: maximum 4 pages
- Poster (in PDF format): maximum 1 sheet

While groups could include photos or other static visual aids in their proposal, they were not allowed to include videos.

Awards

Top Groups:
After multiple evaluation sessions by professional scientists, we awarded 11 groups with top performances with some special prizes.

All Groups:
Submitted deliverables are available on our official website (password required). In addition, all groups received professional feedback on their works.

Co-host

The Ocean Policy Research Institute (OPRI), The Sasakawa Peace Foundation

Covering 70% of the surface of the earth, the oceans are a treasure shared among all of humanity, and one on which we depend for our survival. The Ocean Policy Research Institute (OPRI) thus aspires to become a "think-and-do-tank," to address the many challenges to the ocean and thereby achieve the mission of the Sasakawa Peace Foundation to establish a new system of ocean governance. To do so, we will expand our research and advocacy activities, disseminate relevant information, facilitate necessary measures, and promote networking opportunities. Japan cannot solve all the ocean's problems on its own, however, which must be tackled from a global perspective through initiatives that are based on international discussion. We therefore sincerely wish to collaborate ever more closely with like-minded stakeholders who are also concerned about the oceans.

Feedback to the Participants

First, I would like to thank everybody who participated in the IBO Challenge 2020 International Group Project. Despite various difficulties, a lot of students worked very hard on their own project. As a head of this project, I'm very happy and honored to have been able to provide this opportunity of intercultural exchange through biology, which is one of the very important missions of the IBO.

As many of you know, our original plan was to host the group project at a beautiful beach in Sasebo city, Nagasaki. While we tried to provide students with the similar experiences through this remotely-hosted group project, it is not hard to imagine that a lot of students and country coordinators were confused by some big differences between the two. Since we hosted the project for a much longer period, some students were forced to drop out in order to prioritize their academic responsibilities. Reading the post-event questionnaires, we also found out that many groups had difficulties with time-zone difference, internet connection, or personal and nationwide issues. Even during this completely-remote event, we felt the negative effects of the COVID-19 pandemic everywhere. I expect that those valuable feedback will be carefully analyzed and utilized for the future IBO events.

Throughout the project, I was amazed by the students' enthusiasm and hard work on their topic, selected from (1) infectious diseases, (2) biodiversity and oceans, (3) genome editing, and (4) evolution. Even though it was not a smooth-sailing for most groups, I could easily see how hard they worked on their research and final deliverables. Some strongly reflected the students' cultural backgrounds. Some were at the level of a graduate school or even an academic conference. We enjoyed reading and evaluating every single one of them. If I need to say one thing, however, I believe that a lot of deliverables could have been more concise with less text. While I understand that they wanted to put everything they learned in a limited space, this is something to keep in mind in the future.

When we first planned this project, we were expecting some deliverables to be wild and eccentric while staying logically-sound, just like a thing we see in a good Sci-Fi movie. However, against our expectations, almost all deliverables were both realistic and feasible. Eccentric ideas, such as an idea that creates a huge breakthrough (Task A) or an idea that defines the perfect (but a bit unrealistic) state of the world (Task B), are always essential for the advancement of science. For example, genome editing techniques are products of these eccentric ideas. I believe it is young and talented students like the IBO participants who are expected to provide more "eccentricity" into the world.

Finally, I would like to thank all the project facilitators, mainly IBO alumni, who volunteered and supported the students during the project. After the event, a lot of students expressed that they could enjoy this difficult and demanding process because of the presence of the facilitators. I hope the competitors this year will also stay involved in the IBO just like them. (Akira Katoh)

Topic 1

Kazuhisa Ota

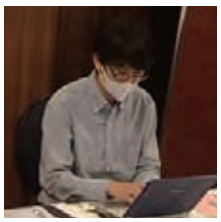
Topic 1 (infectious diseases) had 14 deliverable submissions; six from Task A and eight from Task B. Due to the current COVID-19 pandemic, six groups focused on the coronavirus as their target disease. On the other hand, their discussions were extremely diverse, from a disease model simulation to an effect of climate change. While the wide range of content made the evaluation quite challenging, we could enjoy the process from the beginning to the end because of that.

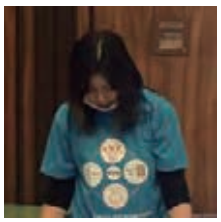
Picking a discussion theme for the Topic 1 might have been easy for most groups, as there are countless numbers of news related to infectious diseases and the demand of society is clear. On the contrary, I could tell that a lot of groups struggled to properly understand the current research or to find a creative solution, because the field is extremely competitive and there are almost too many articles you could base your discussion on. Nonetheless, I could see the students' hard work, passion, and talent in a lot of deliverables, which deserves our sincere applause.

Not only infectious diseases, but a lot of fields are now in need of decision-making and actions on a global scale. I expect all participants to take advantage of this experience and play an important role globally in the future.

Topic 2

Ko Tomikawa





Junko Toyoshima

For themes in Topic 2 (biodiversity and oceans), most groups chose problems that are recently becoming serious on a global scale, such as climate change, microplastics, and biodiversity. Each group explored solutions to the selected problem using their own original approaches along with some previous studies, and I'm proud to say that the quality of deliverables was very high. Additionally, all deliverables were well designed and composed, making their hard work attractive. The reviewers enjoyed reading them. While the feasibility of the proposed experiments and analyses were uncertain in part, we are excited about their work and looking forward to seeing their future improvement.

Feedback to the Participants

Topic 3

Akira Katoh

As you can see from this year's Nobel Prize in Chemistry on CRISPR-Cas9, genome editing (Topic 3) might have been the hottest and most familiar topic for the IBO participants. This topic attracted the largest number of participants, creating 19 groups to start with. Amongst them, 14 teams successfully submitted the final deliverables, which were all well-researched. Some had a great design, and others strongly reflected group members' diverse cultural background. We enjoyed evaluating them a lot.

For the Task A submissions, we primarily focused on the uniqueness in their viewpoint. While realistic and well-constructed, most of the deliverables were, unfortunately, not unique or creative enough to blowing our experts' mind. However, some groups took a step deeper and discussed the improvement of technique itself, which impressed the reviewers greatly.

For the Task B submissions, we valued their discussion section the most. All groups did a great job on analyzing the current issues, but not a lot of them used the analyses for creative discussions. Many groups could have had much higher evaluation if they had deeper and more creative discussions.

Even though genome editing is a relatively new tool for genetic engineering, a lot of research have already been done at this point. Society is waiting for the next techniques. I hope this event's participants will soon play a main role in discovering and developing the next research areas and techniques.

Topic 4

Shinichiro Sawa

Koichiro Awai

Topic 4 (evolution) had five deliverable submissions; two in the Task A, and three in the Task B. Focusing on animals like humans or birds, they discussed various topics such as problems related to behavioral ecology, effect of microwaves, and evolution of microbiota and diseases. All of them were well thought-out and discussed.

Since students had to either propose a creative experiment on evolution (Task A) or address an issue within evolution (Task B), we were concerned that the topic would be too difficult for students from the beginning to the end. We were expecting something simple because of those concerns, but they all betrayed us in a good way. All deliverables were well-constructed, and made us re-confirm where the field of evolution stands in the context of biology.

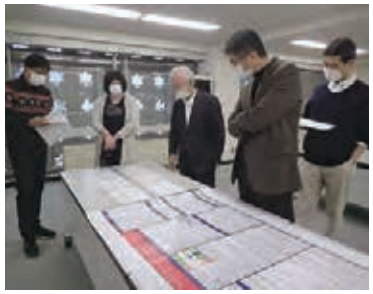
I believe the students will play an active and important role in society in the future. Even if that role is not related to biology, I wish that they will keep this evolutionary viewpoint somewhere in their mind.

IGP Results

The Awards of Excellence

Given to groups with the best performance in each topic.

Topic1:	1A01	page 106
	1B02+1A04	page 120
Topic2:	2A02	page 136
Topic3:	3A01	page 146
	3A03	page 150
Topic4:	4B03	page 180



The Ocean Policy Research Institute Award

Given to one Topic 2 group with outstanding performance.

2B03 page 142

The IBO2020 President Award

Awarded by the president of the IBO2020 Organizing Committee, Dr. Makoto Asashima, to his choice of an outstanding group.

3B01 page 162

The "Beyond Bio" Award

Awarded for the group's creative solution beyond biology.

2B05 page 144

The Uniqueness Award

Awarded by Dr. Shinichiro Sawa, for the group's unique approach toward the project.

4A02 page 174

The "Making Great Sense" Award

Awarded by Dr. Akira Katoh, for the group's innovative idea related to the biosensor.

3A07+3B05 page 156

About Participation Prizes

We have prepared participation prizes for everybody who took part in the International Group Project. After some discussion about what would be the best gift, we decided to give out handcraft resin-embedded specimens of two East Asian species.

Japanese goose barnacle

Scientific name:
Capitulum mitella (Arthropoda: Crustacea)
Distribution:
The western Pacific from the Japanese Archipelago to the Malay Archipelago.
Notes:
The Japanese goose barnacle, which looks like a shellfish, actually belongs to Crustacea. They have appendages which correspond to the legs of shrimps inside the hard shell. This species is also used for food in Japan. The specimen is designed to show both the external hard shell and the internal appendages.

Japanese maple

Scientific name:
Acer palmatum (Angiosperms: Sapindaceae)
Distribution:
East Asia from Japan to China.
Notes:
This species is the most common maple species in Japan and is representative of Japanese autumn leaves. In autumn, the leaves of the Japanese maple trees turn Japanese mountains red. This species has winged seeds, which are dispersed by wind. The specimen is designed to show the leaf and the seeds.

Questionnaire Summary

We asked both competitors and project facilitators to submit a post-event questionnaire within two weeks after the conclusion of the project. We collected responses from all but one of the facilitators and 76 out of 202 competitors.

According to the facilitator's responses, approximately 130 students successfully finished the project. The rest of the competitors, about 70, didn't participate in the project from the beginning or dropped out halfway. We started the project in mid-August with 49 groups, but had to restructure some groups and reduce the total count to 46 in September because of the increasing number of competitors dropping out from those groups. At the end, 39 groups submitted the final deliverables.

Even though the advancement of technology enabled us to hold this type of event virtually, most groups faced some major difficulties, such as time zone differences and internet connection issues, especially when they tried to schedule online meetings. Moreover, many groups also struggled with competitors' conflicting academic responsibilities or maintaining their motivation after the IBO exams. These factors must be carefully considered for future events.

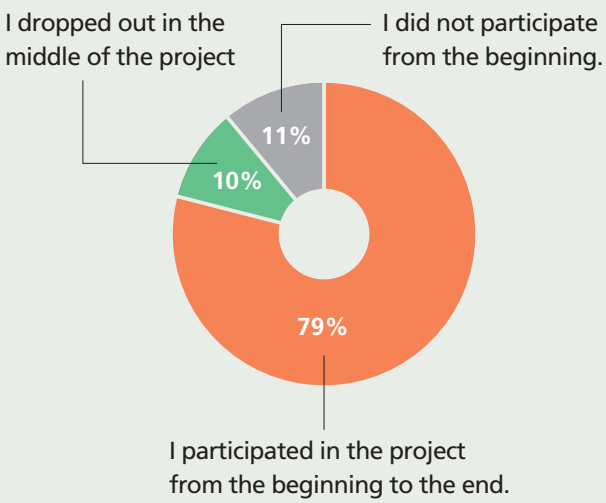
Nonetheless, a lot of competitors and facilitators commented that this project was a valuable opportunity for them, where they could interact and form friendships with like-minded people from around the world in the midst of lockdowns and travel restrictions.

We hope that this project could provide passionate and talented youth from around the world with a platform to express their creativity and to form meaningful friendships.

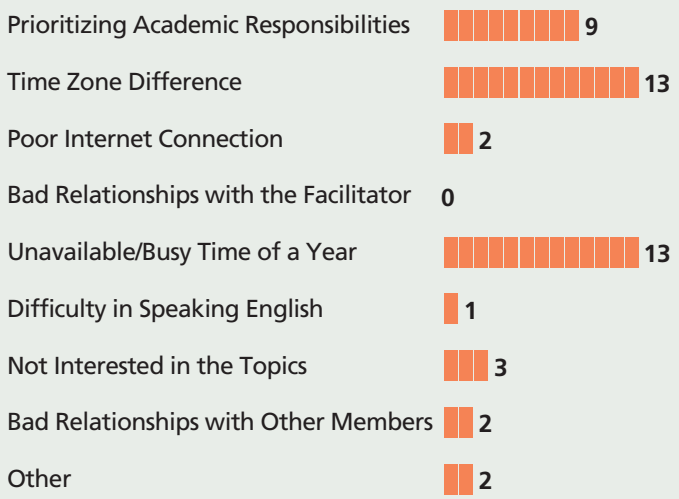
(Ryoko Utsumi)

Competitors

Your Participation Status

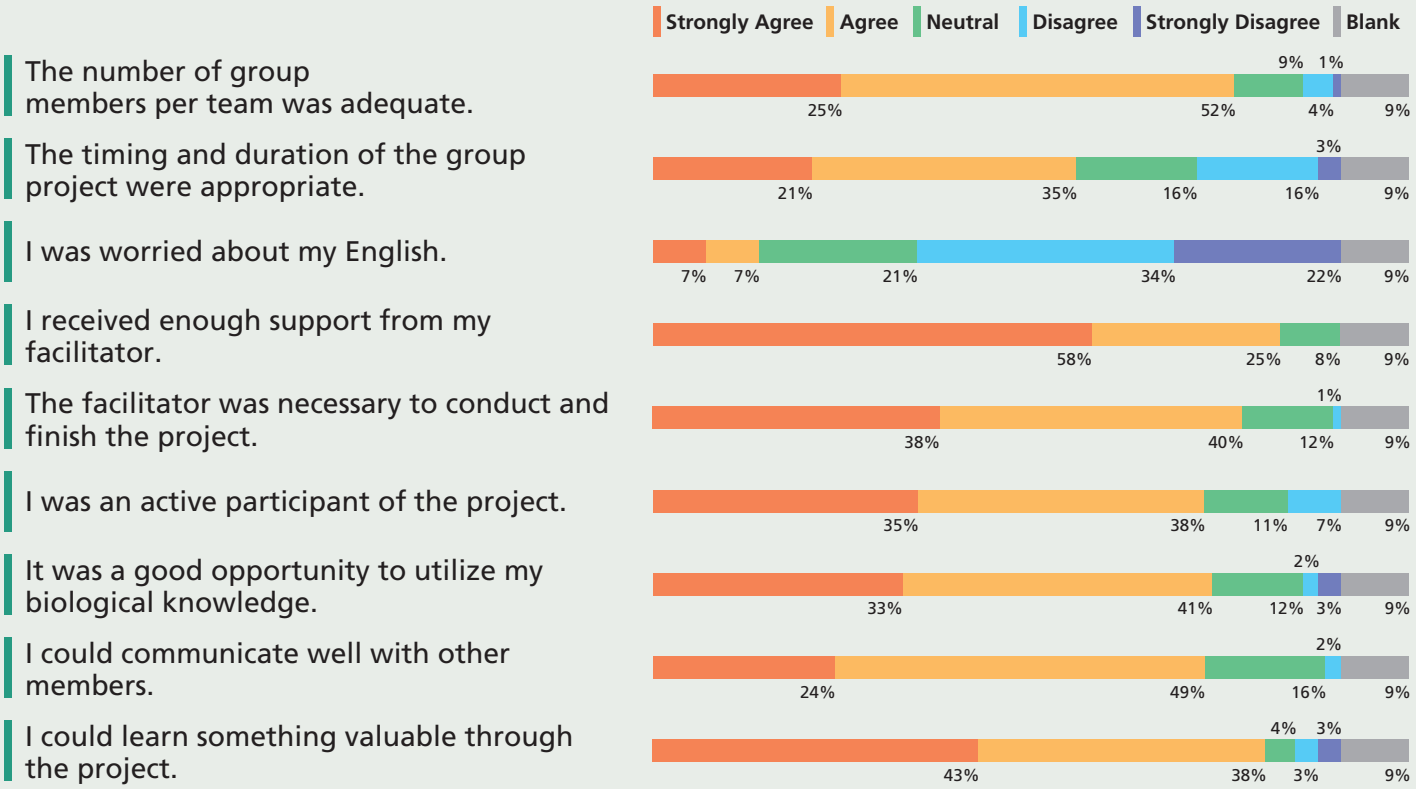


Please tell us the reason(s) why you did not participate / dropped out.



Questionnaire Summary

Competitors



Which factor(s) influenced your participation level?

Which factor(s) influenced your communication level with other members?

Comments

It was a wonderful experience to learn from other team members while staying safe during this pandemic.

It was an amazing opportunity and I really learned so much from this experience. I specifically enjoyed being able to talk to students who were ambitious and passionate about biology all over the world, connect, and make a project together. Thank you so much for organizing such an event amidst the COVID-19 crisis.

I believe the internet connection did influence the communication level negatively with one of our team members, as the team member did not have access to a stable internet, which made it impossible to hear the team member. However, we solved this by using the chat function on Zoom. The time zone differences were no problem at all.

All in all, I really liked and enjoyed this concept of an International Group Project. I hope it is a project that will continue within the Biology Olympiads the coming years as it is valuable both academically and socially. Thank you for organizing it this year.

I am beyond grateful that I got to be a part of this project. It was a really interesting task and a fantastic opportunity to make friends with like-minded individuals in different countries in the world. Thank you, IBO Challenge 2020 for making that happen!

I would like to thank very much for the opportunity to participate in the project as it was really great to make connection with participants from all over the world. It was for the first time in my life when I worked together with people from different countries on the same project and it was an amazing experience. If the next-year IBO will be held virtually, I'd like to suggest organizing of similar activity as was the International Group Project 2020.

I'd rather have the group project being worked intensively one or two week after the IBO-C Test than having it span over 3 months after the test. For me it gives extra anxiety. Nevertheless, i love the idea and i want to communicate more with other competitors in other opportunities.

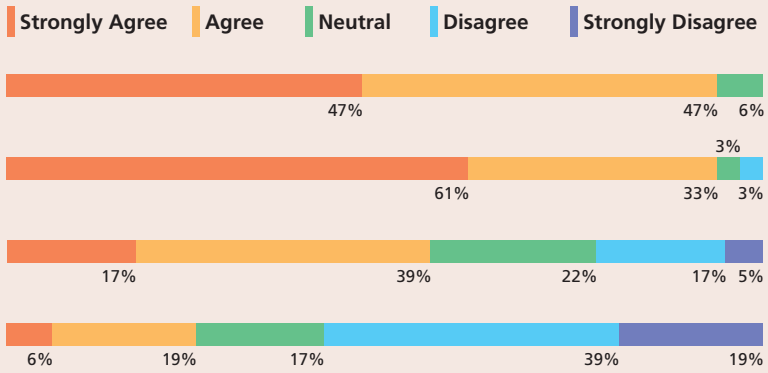
I would like to sincerely thank the people responsible for the IBO2020 international group project. For as this project has helped me to develop and learn crucial skills. And this project has also let me meet wonderful people from different countries which lead to exchange of knowledge, tradition and much more. This project has been a great experience and I hope the best for all.

It was a wonderful experience to learn from other team members while staying safe during this pandemic.

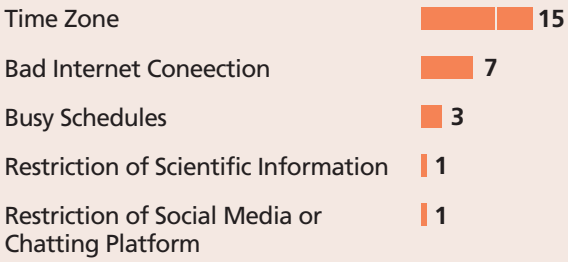
Questionnaire Summary

Facilitators

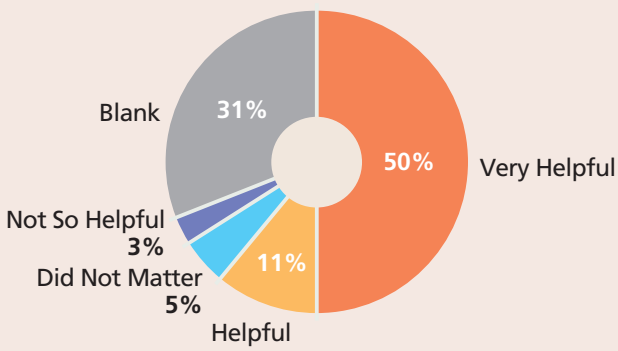
- The number of group members per group (FOUR) was appropriate.
- The number of facilitator per group (ONE) was sufficient.
- My group(s) experienced some logistical difficulties
- Gaps in English proficiency negatively affected the group activities.



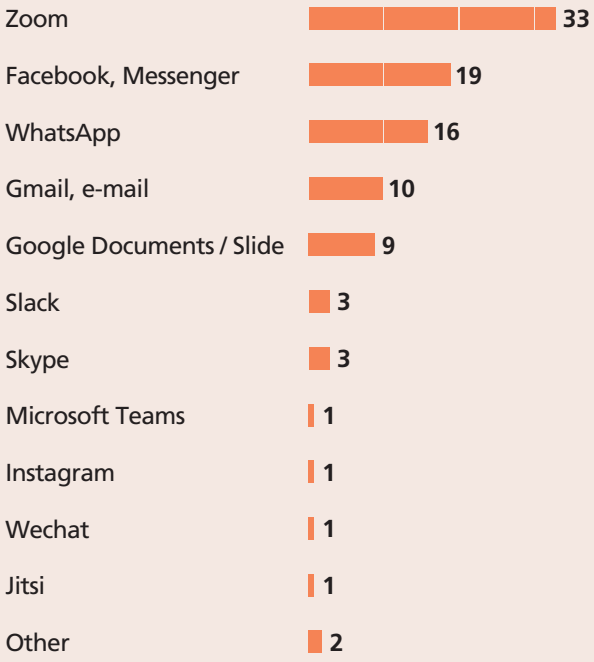
What kind of logistical difficulties did you experience?



If you acquired a Zoom account from us: how helpful was it?



Please list all the communication tools your group(s) used.

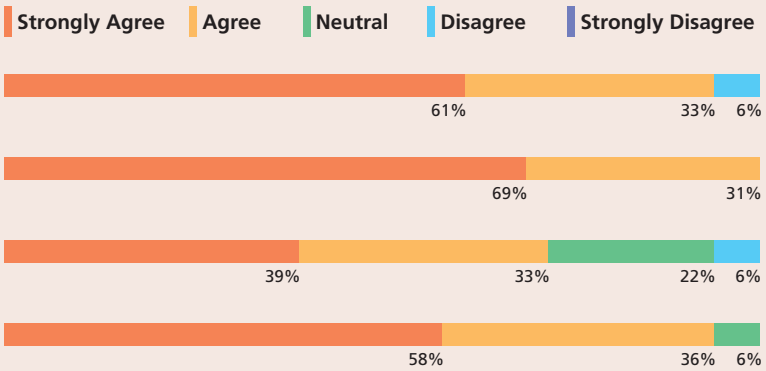


This experience as a facilitator was meaningful to myself.

Support from the organizers (via Slack, email, etc.) was helpful.

I would work as a facilitator even without the payment.

I'd like to sign up to be a facilitator again in the future.



Comments

This IBOC group project is definitely worth doing for participants. Working internationally on scientific theme (for such a long term) with strongly passionate peers is very rare and valuable opportunity for high school or university students.

The previous physical IBOs didn't have group projects, but this online version did. As such, I'm really impressed by the creativity and initiative some people took, which is far more interesting to see than the ability to just answer question papers.

Students actually got to experience SCIENCE and its ambiguity, facing the complexity they have to deal with. It is different from following written protocols and reading textbooks, because you actually have to start from scratch and dive into the scientific enterprise. This could be a nice complementary activity to IBO.

In this event, students of different nationalities and cultures have to put their differences aside and work together as a team. Although, I believe it would have been better to be there physically, I think this element is something fresh, exciting and also quite challenging.

I like how this project brings together a small group of people from different countries and allows them to bond together over a sustained project.

I would like to thank from the bottom of my heart all including IBO 2020 committee for their tremendous efforts to deal with today's situation and to provide such a wonderful opportunity for participants this year!

Overall, I am grateful to have been part of this project and I hope to participate in many more international events.

Project Facilitators

Consisting mostly of IBO alumni, project facilitators played a highly crucial, supportive role throughout the International Group Project. Assigned to one or two groups, each facilitator was tasked to handle various responsibilities for more than two months. Sometimes they acted as a "tour guide" for their group by asking insightful questions. Other times, they were mentors who introduced useful articles or shared their own research experiences. Most importantly, they were great supporters who made sure that the group activities proceeded as smoothly as possible.

During the project, group progress and documents were shared via cloud services, which all members from different time zones could access whenever most convenient. Meetings were held through online video conference tools.

The effort and contributions of facilitators were essential to the success of this completely online project. When a group member couldn't make it to an online meeting, most facilitators recorded and shared the meeting or created meeting notes for them. If a member struggled with communication in English, a lot of facilitators supported them by setting up a private meeting before or after a main meeting or sending separate emails in easier English to help them participate in the discussions more actively. Many operations and supportive methods were, in fact, taking advantage of the online nature of the event.

Here, we would like to thank all facilitators who generously offered their time and energy despite their multiple academic and non-academic responsibilities.

1A01

Jiwoo Nam
(South Korea)

I'm able to deliver my opinion in English fluently, but I can lose some of biological terms, so I'm studying them.

1A02 & 1B07

Lilian Demolin
(Belgium)

Med student and IBO competitor in UK 2017 and guide in Hungary. IBO community is the best in the world!!!

1A03

Valentino Sudaryo
(Indonesia)

Greetings from a fellow IBO 2014 competitor and IBO 2017 volunteer! Looking forward to a great time with all of you.

1A04 + 1B02

Akhila Imantha Nilaweera
(Sri Lanka)

As a past participant in IBO 2015,It's with great pleasure I'm joining this year's programme.

1A05 & 1B03

Birnur Sinem Karaoglan
(Turkey)

I'm quite excited about the dawning of new ideas and friendships which will be resulted from this IBO CHALLENGE!!!

1A06

Pavel Loginovic
(Lithuania)

1A07 & 1B01

Parmida Sadat Pezeshki
(Iran)

with fresh ideas, motivated minds, and big dreams, once we get started, we get ahead!

1B04

Nahida Harim
(Belgium)

IBO 2019 was the best moment of my life so I can't wait to join this new project and meet new people !

1B05

Jenna Tynninen
(Finland)

I'm a sporty golfer and future med student from Finland. As a former IBO competitor, I love the unique IBO community.

1B06

Ayaka Eguchi
(Japan)

I was a competitor of IBO2017. I'm sure this online project will be a very good experience for you. Have fun! :)

1B08

Anitra Zīle
(Latvia)

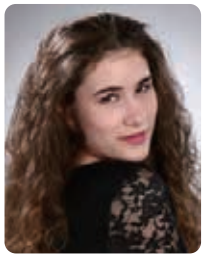
to be or to bio? - both

2A01

Diego Eduardo Kleiman
(Mexico)

My name is Diego Kleiman, from Argentina. I participated in IBO '14 and I am excited to volunteer for this online event!

2A02 & 2B04



Alexandra Nóra Piti
(Hungary)

Thank you to the IBO community for organizing this online event! I hope everyone will enjoy creating their proposals!

2A03

Rawand Fatah Abdalla Aziz
(Iraq)

2A04

Edwin Alejandro Chávez Esquivel
(Mexico)

Hi I'm Ed, from Mexico. I'm here because I want to support you in this edition of IBO, thank you for the opportunity c:

Project Facilitators

2B01

Anastasiya Valakhanovich
(Belarus)

Hi, I'm Anastasiya and I want to share my love for Biology with participants, volunteers, and the organization team!

2B02

Egemen Erbayat
(Turkey)

2B03

Mithun Diumantha Samaranayake
(Sri Lanka)

2B05

Maria Janine Juachon
(Philippines)

Hello everyone! Let's try to make the best out of our current situation! :)

3A01 & 3B09

Christopher Wang
(USA)

Hi! I'm Chris from the United States. I competed in the 2019 Hungary IBO and am a current neuroscience major in college.

3A02 & 3B04

Auddithio Nag
(Bangladesh)

Hi everyone! Auddithio here, although most friends just call me Audi. Looking forward to e-meeting all of you soon!

3A03 & 3B06

Diego Maldonado de la Torre
(Argentina)

Hi! My name is Diego, I am from Tijuana, Mexico. It is an honor to be a facilitator at IBO Challenge. Let's have fun!

3A04

Atahan Durbas
(Turkey)

I have been to IBO in 2016. It was an unfinished story for myself, that's why I am here to complete your story together!

3A05 & 3B01

Martyna Petrulyte
(UK)

3A06

Stuti Khandwala
(India)

Extremely excited to be a part of the first ever virtual IBO; looking forward to different but life-long relationships!

3A07 & 3B05

Anh Thi Minh Tran
(Vietnam)

Thank you to the IBO community for organizing this online event! I hope everyone will enjoy creating their proposals!

3A08 & 3B08

João Victor Silva Ribeiro
(Brazil)

Hi, guys.My name's Victor, 19 yo and I'm a medical student. I love doing cultural exchange and learning new languages :)

3A09 + 3B02

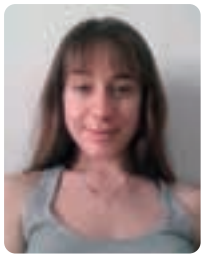
György Laszlo András
(Hungary)

Hey All! I'm Andris, and without IBO I doubt that I would have found my passion in biology. And I wasn't a competitor ;)

3A10

Shino Suda
(Japan)

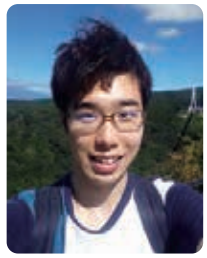
3B03



Danai Theou
(Greece)

I hope the students have as much of a great experience as I did when I was a competitor!

3B07



Eiichiro Kanatsu
(Japan)

4A01

Tomoyuki Wakashima
(Japan)

4A02

Vaidehi Devendra Rakholia
(India)

4A03

Uzuki Horo
(Japan)

4B02

Dominik Kopčak
(Slovakia)

4B03

Tymofii Sokolskyi
(Ukraine)

Hi! My name is Tym and I am a Ukrainian rising fourth-year student at Duke university.

4B04

Yasna Yeganeh
(Iran)

Hi this is Yasna!I am more than happy to help you and be at your service. let's make IBO2020 unique (^_^) がんばって！

Facilitator

Jiwoo Nam (South Korea)

Competitors

Ahmed Kashif (Pakistan)

Barbara Anna Buchalska (Poland)

Dinmukhammed Urazbayev (Kazakhstan)

Gencay Kaan Polat (Turkey)

Nicholas Man Dac Vo Bui (Australia)

Cross Immunity of C

Introduction

December 2019 marked the emergence of the Covid-19 pandemic, the deadliest and most infectious disease since the Spanish Flu. The deadliness of the Covid-19 comes from its protean complications and high infectivity through droplet spread and even possibly airborne. Scientists throughout the world have spent significant effort for nearly a year now, trying to understand the virus' pathogenicity and find a treatment for the condition. Recognising the urgency of the situation, many countries have simultaneously and parallelly taken up the challenge to produce a vaccine. Unfortunately, we still do not have a definitive front runner vaccine and a date of vaccine availability.

The key to developing a safe and effective vaccine is an excellent understanding of the virus' antigenicity and the subsequent body immunity against it. In the same light, there are questions regarding the possible cross-immunity between the Covid-19 and other viruses, and possible conferred protection against it.

Each virus contains a large array of macromolecules including proteins, polysaccharides and lipid molecules, some of which can form epitopes and potentially activate an immune response. Our body can also mount an immune response, not just against the epitopes, but also against the tertiary structure of the macromolecules. Contact with a complex entity such as a virus will elicit multiple immune responses from our body against the various epitopes and macromolecules presented on the virus' surface, but only a small number of these immune responses are effective or lethal against the pathogen. Because of these multiple, less-specific immunological reactions, some of the reactions will be cross-shared between different pathogens which have similar macromolecules or similar tertiary structures of the macromolecules. Individually, these cross immunological reactions may not be lethal to the pathogens, but they will weaken the pathogen to a various degree, reduce their infectivity and lethality. It is possible even that a combination of these cross immunological reactions may render the virus harmless. This approach presents as a possible weapon in our armamentarium in the treatment, containment, and vaccine development against the Coronavirus. Our paper aims to determine the feasibility of the cross-immunity approach against the Covid-19.

Purpose

There are two components to
identify the viruses with the l
Covid-19. The second part ai
viral species can be used in p

Methods

In our experiment we used s
compare SARS CoV-2 Spike
antigens.
At first in Immune Epitope I
found epitopes that are simil
used *Blast – 70%* function to
similar in 70% to SARS CoV
CoV-2 epitopes were obtaine
multi-epitope vaccine against
Then we compared in BLAS
sequence (NCBI Reference S
Epstein-Barr virus nuclear ar
Protein Data Bank by 1VHI
has epitopes similar to SARS
in RCSB PDB Protein Comp
strain envelope protein E seq
Bank by 6IW4 code) with Sp
from Protein Data Bank by 6
algorithm.
Furthermore, we used Structu
to search for allergens that ar
glycoprotein (NCBI Referenc

References

[1] Tamalika Kar, Utkarsh Narsa
Filippo Castiglione, David M. M
candidate multi-epitope vaccine

: Coronavirus

Nicholas Bui, Ahmed Kashif, Barbara Buchalska, Dinmukhammed Urazbayev, Gencay Polat

onents to our proposal. The first is to with the highest antigenic similarity to the id part aims to identify whether different used in producing a vaccine for Covid-19.

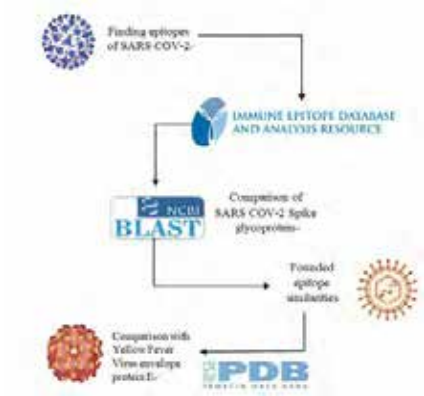
ve used some bioinformatic programs to -2 Spike glycoprotein sequence with other

Epitope Database and Analysis Resource we are similar to those from SARS CoV-2. We action to locate linear epitopes which are RS CoV-2 epitopes. Sequences of SARS e obtained by us from an article *A candidate e against SARS-CoV-2* [1].
in BLAST program Spike glycoprotein ference Sequence: YP_009724390.1) with uclear antigen 1 sequence (obtained from y 1VHI code), because Epstein-Barr virus to SARS CoV-2 epitopes. We also compared in Comparison Tool Yellow Fever Virus 17D ein E sequence (obtained from Protein Data) with Spike glycoprotein sequence (obtained ank by 6VXX code) using Smith-Waterman

ed Structural Database of Allergenic Proteins ns that are similar to SARS CoV-2 Spike Reference Sequence: YP_009724390.1).

arsh Narsaria, Srijita Basak, Debashrito Deb, avid M. Mueller & Anurag P. Srivastava A e vaccine against SARS-CoV-2

Methods



Results

Some studies have shown that there are some similarities between various antigens and Sars-CoV-2 epitopes. These similar epitopes are: Mycobacterium tuberculosis(MTB) epitopes , Penicillium chrysogenum epitopes, Leishmania infantia epitopes, Epstein-Barr virus epitopes and some epitopes of species causing severe diseases. There is some similarity between HBV nuclear protein and spike protein too.
Actually some previous studies have shown that BCG vaccine ,which is used for Mycobacterium tuberculosis, may decrease mortalitiy.
This highly similar epitope sequences give us an idea that we can use this vaccines to provide a cross-immunity. MTB can shown as an example to contribute this idea and there is strong evidences that HPV (Human Papilloma Virus) vaccines may have some possitive effects on decreasing the mortality. These strong evidences are contributing our idea that we can provide cross-immunity which is mediated by different vaccines that based on similar epitope sequences. HBV nuclear protein is strong candidate for being vaccine which can decrease the mortality rate of Sars-CoV-2.

Conclusion

As shown above, cross-reactivity between SARS CoV 2 and other viruses is a significant factor when dealing with immune responses to the virus as seen in many studies. Viral transmission can be reduced when pockets of susceptible communities show resistance to infection due to cross-immunity. This factor also needs to be considered in integrated efforts against viral spread. Populations which do not exhibit any cross-immunity are more vulnerable to SARS CoV 2. These populations can be vaccinated first and so mortality rates can be decreased.
Studies can be conducted to determine whether existing cross-immunity can contribute to herd immunity. This might reduce demands of vaccines in such populations. Dual immune responses to SARS CoV 2 which consist of cross-reactive immune cells and immune cell lines established by vaccines specific to SARS CoV 2 can counter the virus better than solely vaccine established immune responses. A more generalized immune response can be made because the cross reactive immune cell can target a different part of the virus than the vaccine established immune cell line. This can make it more difficult for the virus to mutate around the immune response. Thus complete viral annihilation can be achieved.
An indispensable part of preparing a sort of integrated management of the pandemic using existing vaccines with cross reactivity to SARS CoV 2 is to conduct detailed studies on the possibilities of immunopathology. Respiratory diseases have caused antibody dependent enhancement of disease (ADE) as observed in studies. Trial plans for the cross reactive vaccine and SARS CoV 2 vaccines could be performed concurrently to observe any damage to the respiratory epithelium/lung tissue. ADE in Covid19 could be ameliorated by using these cross reactive vaccines which are known not to cause ADE. Less trials might be needed to pass the cross reactive vaccine for use as trials have already been carried out and side effects of vaccines have already been explored.
Vaccines for yellow fever might be used as these vaccines require only one dose and provide lifelong protection. A cocktail of vaccines might also be used (BCG and yellow fever vaccine).
Inoculation should be done through normal routes used for yellow fever and other vaccines. However, the animals which most closely mirror human responses to SARS CoV 2 (syrian hamsters) can be used.
Successful destruction of the virus will support the practical utility of a cross reactive mechanism to counter SARS CoV 2.

1A02 Quantification of structural response to prion disease of recombinant G127V-mutated and silenced PRPc in primary hippocampal mice cells using CRISPR-Cas9 and siRNAs

Facilitator

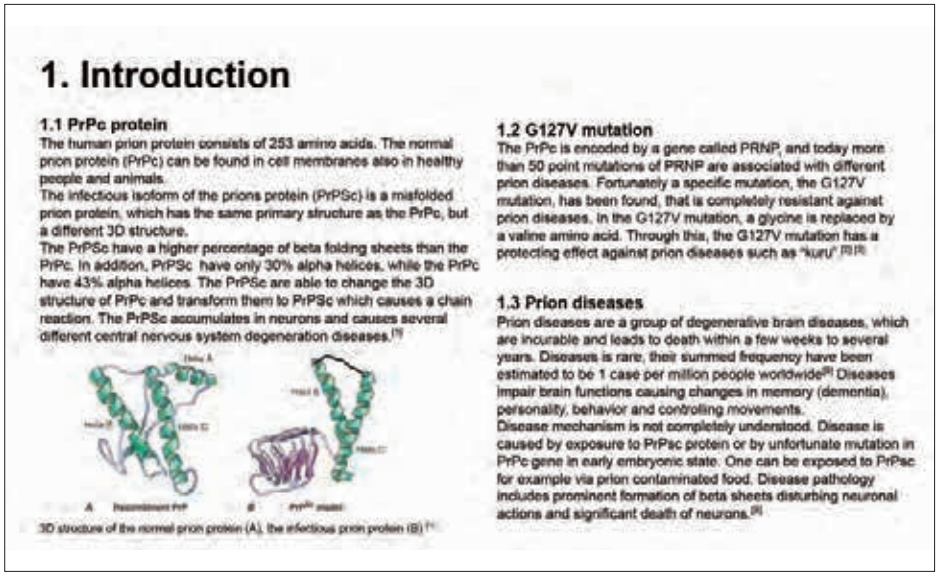
Lilian Demolin (Belgium)

Competitors

Anna Salud (Switzerland)

Sean Red Cruz Mendoza (Philippines)

Suvi Linnea Laitinen (Finland)



1. Introduction

1.1 PrPc protein

The human prion protein consists of 253 amino acids. The normal prion protein (PrPc) can be found in cell membranes also in healthy people and animals.
The infectious isoform of the prions protein (PrPSc) is a misfolded prion protein, which has the same primary structure as the PrPc, but a different 3D structure.
The PrPSc have a higher percentage of beta folding sheets than the PrPc. In addition, PrPSc have only 30% alpha helices, while the PrPc have 43% alpha helices. The PrPSc are able to change the 3D structure of PrPc and transform them to PrPSc which causes a chain reaction. The PrPSc accumulates in neurons and causes several different central nervous system degeneration diseases.[1]

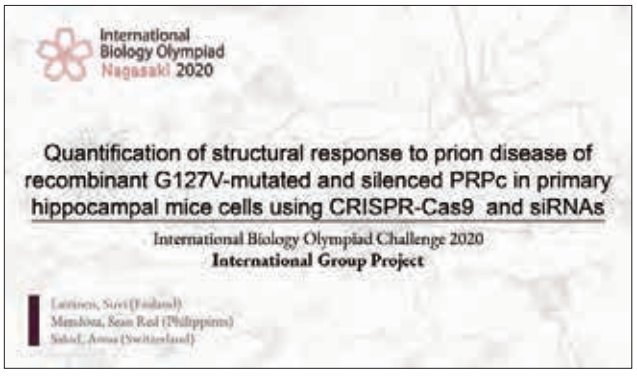
3D structure of the normal prion protein (A), the infectious prion protein (B) [1]

1.2 G127V mutation

The PrPc is encoded by a gene called PRNP, and today more than 50 point mutations of PRNP are associated with different prion diseases. Fortunately a specific mutation, the G127V mutation, has been found, that is completely resistant against prion diseases. In the G127V mutation, a glycine is replaced by a valine amino acid. Through this, the G127V mutation has a protecting effect against prion diseases such as "kuru" [2] [3].

1.3 Prion diseases

Prion diseases are a group of degenerative brain diseases, which are incurable and leads to death within a few weeks to several years. Diseases is rare, their summed frequency have been estimated to be 1 case per million people worldwide[3] Diseases impair brain functions causing changes in memory (dementia), personality, behavior and controlling movements.
Disease mechanism is not completely understood. Disease is caused by exposure to PrPsc protein or by unfortunate mutation in PrPc gene in early embryonic state. One can be exposed to PrPsc for example via prion contaminated food. Disease pathology includes prominent formation of beta sheets disturbing neuronal actions and significant death of neurons.[5]

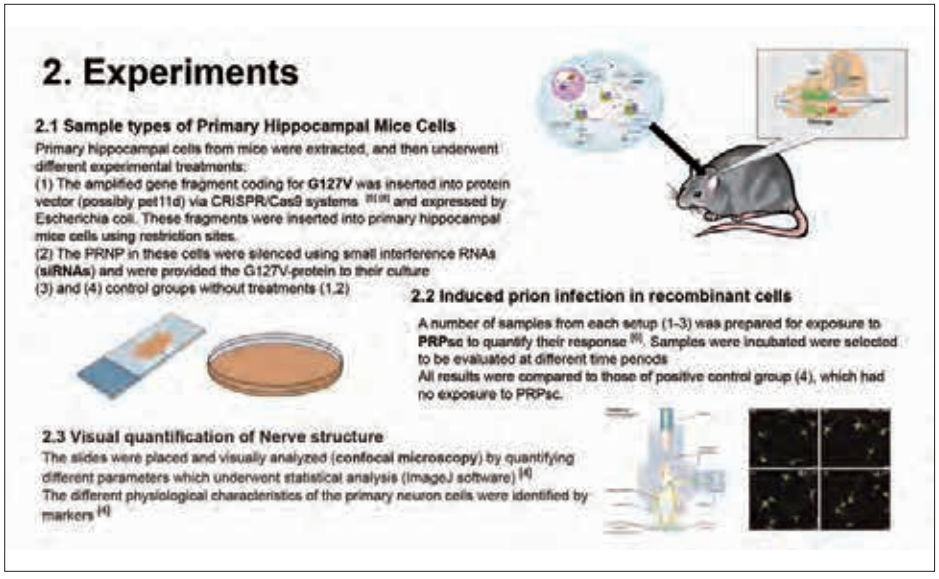


International Biology Olympiad Nagasaki 2020

Quantification of structural response to prion disease of recombinant G127V-mutated and silenced PRPc in primary hippocampal mice cells using CRISPR-Cas9 and siRNAs

International Biology Olympiad Challenge 2020
International Group Project

Laitinen, Suvi (Finland)
Mendoza, Sean Red (Philippines)
Salud, Anna (Switzerland)



2. Experiments

2.1 Sample types of Primary Hippocampal Mice Cells

Primary hippocampal cells from mice were extracted, and then underwent different experimental treatments:
(1) The amplified gene fragment coding for **G127V** was inserted into protein vector (possibly pet11d) via **CRISPR/Cas9 systems** [6] [7] and expressed by Escherichia coli. These fragments were inserted into primary hippocampal mice cells using restriction sites.
(2) The PRNP in these cells were silenced using small interference RNAs (**siRNAs**) and were provided the G127V-protein to their culture
(3) and (4) control groups without treatments (1,2)

2.2 Induced prion infection in recombinant cells

A number of samples from each setup (1-3) was prepared for exposure to **PRPsc** to quantify their response [8]. Samples were incubated were selected to be evaluated at different time periods
All results were compared to those of positive control group (4), which had no exposure to PRPsc.

2.3 Visual quantification of Nerve structure

The slides were placed and visually analyzed (confocal microscopy) by quantifying different parameters which underwent statistical analysis (ImageJ software) [4]
The different physiological characteristics of the primary neuron cells were identified by markers [4]

3. Methods and variables

3.1 Variables
The performance of each experimental treatment in preventing or limiting the propagation of PRPsc infection is compared using the below parameters

According to protein simulations, the presence of the G127V mutation in human PRP seems to prevent the formation of stable beta sheets and dimers in the host. This, in conjunction with other parameters indicating neurogenesis such as: development of synaptic-like contacts; neuronal polarity and axonal elongation; and life span of each cell, was used as a strategy in determining the efficacy of treatment 1 and 2

3.2 Hypothèses

Both gene editing with Crispr-Cas9, and silencing with siRNA/miRNA when compensatory protein is provided, would extend the lifespan of an individual neuron due to the significantly reduced formation of beta sheets. We hypothesize that in group 1 formation of beta sheets would not exist and it would be remarkably decreased in group 2. In addition, both groups (1,2) would have almost as high axonal elongation, formation rate of synaptic-like-connections and neuronal polarity than the positive control group (4)

3.3 Comparison of methods

Gene editing with Crispr-Cas9
- more modern technology with a lot of focus and investment
- wide array of mechanisms and methods to tackle prion infection: protein PcPr is important in neuron cell functions
- may not prevent neurodegenerative diseases as mechanisms of prion infection are not yet fully understood
- potential side effects to other structures and functions

Gene silencing
- siRNA / miRNA
- may not completely eliminate the presence of PrPc proteins that can still be infected

4. Discussion

4.1 Discussion about experiments

In this study, only statistical information should be analyzed for several reasons. Firstly, the Crispr-Cas9 is a method which might cause other mutations in the genome of neurons and therefore resulting inaccuracy in single cells behavior. Secondly, cells would be extracted from a scatter of mice in maximum and therefore they may have even a major divergence between them.

4.2 Limitations of results

As our experiments would be performed *in vitro*, interactions between extracellular components and other cell types in brain would not have been taken into account. In addition, our inquiry is based on disease model in mice and therefore deductions cannot be straight generalized into humans. Hence, all results from these experiments would be rather suggestive than determinative.

4.3 Consideration about additional experiments

Extensive additional experiments would have to be performed to confirm the results. To inquire the effect of actual cellular environment to these methods, some experiments should be carried out *in vivo*. Moreover, with other variables more suitable to mature neurons, should these experiments be implemented to human cell samples from real patients.

4.4 Proposed methods to reduce PRPsc as possible therapies

Comprehensive further studies (considered briefly in 4.4) could lead to novel therapies for prion disease.

4.4.1 RNA-silencing
If RNA-silencing decreased significantly the progress of prion disease in extensive further examination, this method could possibly be developed to a therapy. It would be more affordable and it is rather treatment than prevention, which enables to be applied only to the patients. Nevertheless, RNA-silencing therapy would have significant disadvantages as well. Identifying patients as early as possible is crucial to this approach since there aren't any mechanism to cure damage already happen, rather to inhibit further losses. The therapy would lean to a lifelong medication and the delivery method would need to be deeply invasive such as brain pumps since both the silencing RNA and compensatory protein (G127V) has to be provided for the patient on a daily basis. However, patients are likely to accept troublesome treatment forasmuch as the disease is lethal.

4.4.2 Crispr-Cas9
Even though, we hypothesize that the Crispr-Cas9-treatment would have more significance in cellular experiments and perhaps in in vitro as well, the method scarcely could be applied as a future therapeutics. Indeed, the therapy would be exceedingly expensive: it would have to be applied in embryonic state and to everyone since there are very little or no possibility to identify future patients in forehand. In addition, gene-editing for embryos includes grave ethical concerns especially when the Crispr-Cas9 has induced unwanted changes in genome. [10] Even if those mutations are rare, in this application they would certainly cause problems due the massive number of patients.

5. Bibliography

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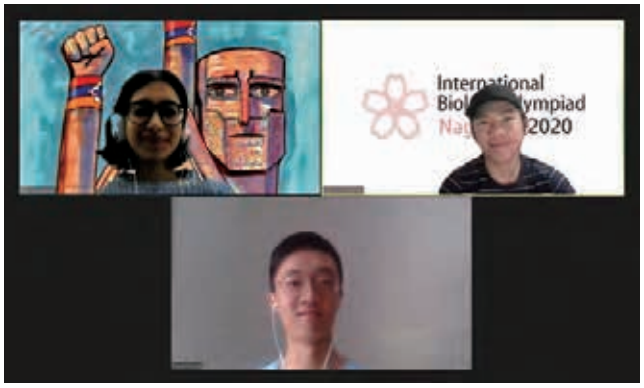
1A03 New Antibody-drug Conjugate strategy to Treat Novel SARS-CoV-2 virus



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1

IBO Project:

New Antibody-drug Conjugate strategy to Treat Novel SARS-CoV-2 virus

Naeri Sohrabian and Lok San Wong

2

1. Intorduction

Coronavirus disease (COVID-19) is an infectious disease caused by the newly discovered severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1], a member of the subfamily Coronaviridae, and is involved in human and vertebrate diseases [3]. SARS-CoV-2 is similar to SARS-CoV in its pathogenicity, clinical spectrum, and epidemiology [2]. The virus is likely transmitted mainly through respiratory droplets produced by an infected person [3], and because of that, the disease was easily spread among individuals, and became a pandemic.

From the onset of infection, some drugs have shown to slow down Covid-19 spread or to relieve the symptoms. Those include antiviral drugs such as Remdesivir, Lopinavir/Ritonavir protease inhibitors, antimalarial – chloroquine, hydroxychloroquine and anti-inflammatory drugs such as Tocilizumab. These drugs target some specific pathways that the virus uses for invading the cell and its RNA replication. One of the commonly used drugs is Remdesivir which was originally evaluated in clinical trials against Ebola outbreak[4]. Remdesivir acts as a prodrug of adenosine analogue and inhibits viral genome replication by targeting RNA-dependent RNA polymerase. Chloroquine/hydroxychloroquine inhibits endosome maturation by suppressing lysosomal function. Proteases such as Lopinavir/Ritonavir interact and inhibit viral polypeptide maturation. Other drugs have been also used to block the interaction between certain proteins on the surface of the virus and certain cell surface receptors.

Apart from binding to the surface proteins on SARS-CoV-2 to disrupt viral function, a variety of different modifications can be applied to enhance the nanobodies' functions.

For example, bispecific nanobodies can be engineered to increase the affinity to the target antigen.[5] Also, by attaching a drug molecule on the antibody to form a antibody-drug conjugate (ADC), a higher therapeutic effect can be achieved. [6]

In the case of SARS-CoV-2, as introduced, there are many developing drugs to treat the virus and its symptoms. Attaching drug molecules to the nanobody proposed could enhance the effect of the therapy. A antibody-drug conjugate consists of a linker molecule that attaches the target drug to the antibody.[7] A peptide-based linker could guarantee the antibody to reach the targeted cells intact and release the drug such as Cathepsin B.[8] Such linker could be utilized to attach drugs or other anti-cytokines agent to the antibody. [9] As nanobodies provide an easier penetration to tissues[10], the drug molecules would

3

detach and are thought to have better therapeutic results. Such modification on antibody and nanobody treatment is proposed to enhance the efficacy to reduce infection by SARS-CoV-2.

2. Methods and Results

To produce an effective antibody-drug conjugate against SARS-CoV-2, an existing nanobody being developed to target the RBD on the virus could be used. A specific immunomodulatory drug that inhibits cytokine level in patients could be used to alleviate the symptoms brought by cytokine storms in COVID patients. Therefore, in this research proposal, anti-IL6 drug Tocilizumab, is used.[11,12] Nanobodies named H11-D4 targeting RBD domain on virus spike protein are used specifically.[13]

1. Attachment of drug to antibody

To effectively bind the drug to the antibody, dithiothreitol(DTT) in PBS is incubated with the designated antibody in order to reduce the disulfide bond in the antibody. A drug linker molecule is used after reduction to create a drug-linker-ligand conjugate on the nanobody. A peptide linker called Cathepsin B is to be used. The drug can thus be released via hydrolysis of the peptide linker on the ADC.[14] The peptide linker is incubated with the nanobodies in ice and purified over a desalting column. It is purified through a size exclusion chromatography on G25 column containing DTPA. The larger size linked antibody could therefore be purified from other reacting agents. [15]

2. Confirmation Of the antibody-drug linkage

Proper linkage of the drug to the nanobody could be tested through an non-reducing SDS-PAGE analysis. SDS-PAGE measures the shift rate of proteins through the SDS gel, the larger ADC would move more slowly and therefore has a shorter shift rate than unreacted ones. By loading the modified nanobodies and control nanobodies into the gel separately, appropriately bonded ADC are expected to have a higher molecular weight than that of the control nanobodies. The expected result are shown below:

4

In order to measure the effectiveness of a potential drug, next generation *in vivo* tests have been conducted [16,17]. These tests are usually done on isolated tissues, organs, cells or on animals like rabbits, rats and canines.

Receptor-binding domain of the viral spike protein is a highly specific target of antibodies in SARS-CoV-2 patients. Thus many antibody tests are based on the receptor-binding domain (RBD) of the spike protein [20].

A new drug has to be tested in multiple steps, before making it into the market. Three important things have to be measured. Those include the efficacy of the drug (in our case: how well our antibody binds and neutralizes spike proteins), toxicity (harmfulness and side effects) and the dosage [21].

3. *In vivo* testing in animal model

A number of studies have investigated non-human primates as models for human infection. Rhesus macaques, Grivets, and common marmosets can become infected SARS-CoV-2 and become sick in laboratory settings [20, 22, 24]. Using animals such as those listed above in vivo tests are preferable (e.g. Rhesus macaques).

For this procedure we could divide Rhesus macaques into three groups.

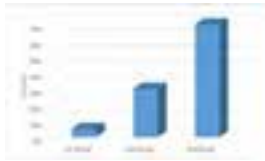
1st group: Test Subjects will be given only the pseudo virus, which have SARS-CoV-2 Spike Proteins expressed on the surface.

2nd Group: Test Subjects will be given both the pseudo virus and the unmodified, control antibody.

3rd Group: Test Subjects will be given the pseudo virus and the antibody with the selected ADC.

5

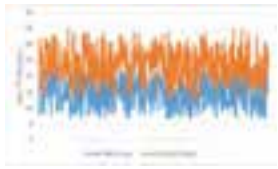
During 6 weeks survival percentage should be calculated from each group [23]. If the results are shown as below, then we predict that these conjugated drugs decrease mortality and are recommended as treatments. Additionally, the immune repertoire (immune cells and cytokine levels) of each primates could be characterized through flow cytometry and ELISA.



4. Clinical trials

If the conjugated drugs showed promising results on non-human primates, then final tests have to be done on humans. For example, patients could be randomly assigned into two Groups (Control Group and Test Group). Patients belonging to the Control Group should be given Placebo drugs, in contrast to patients of the Test Group, which will be given the active form of drug.

If the statistical results of the trail are shown as in Figure 2, then the drug has passed the tests and could be added on the market.



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3.Conclusion and final remarks

At present, COVID-19 is spreading very rapidly and there is yet no specific treatment. Some drugs have shown to slow down Covid-19 spread and to relieve the symptoms. Patients are given conjugate drugs to increase both the effectiveness of the treatment and to decrease recovery time. Finding and selecting the right drugs is a multistep complicated task. First compatible antibodies have to be selected from different animals or be made artificially. Then *in vitro* and *in vivo* experiments should be done to test which conjugated drugs are easing the symptoms, decreasing the recovery and the mortality rate.

7

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Modelling the Spread of Covid-19

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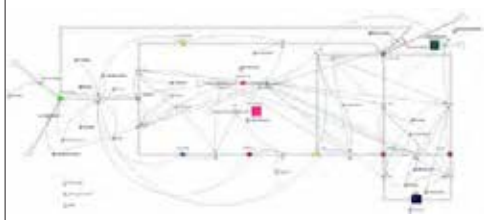
Aadim Nepal , Nepal

Hypothesis and Methodology

Previous research has investigated how COVID-19 spreads and how human intervention affects this spread. However, very little research extends this to predict how SARS-CoV-2 will consequently evolve to maximise its infectivity and minimise its mortality. We hypothesise that by modelling the spread of COVID-19, we can use the results to predict the future spread e.g. second waves, hence we can better prepare for them. Also, the model will demonstrate how our precautions against the spread of COVID-19 may affect the evolution of SARS-CoV-2.



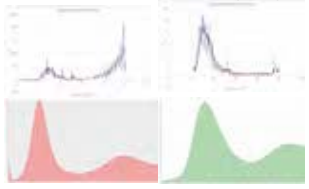
We created detailed flux charts in Anylogic to model the COVID-19 outbreak in Moscow, Paris and Tokyo. These models allowed for different parameters to be adjusted to study their effect on the spread of COVID-19. The parameters we chose to investigate were:

- if people with COVID-19 symptoms are isolated
- if quarantine orders were disregarded

Preliminary results

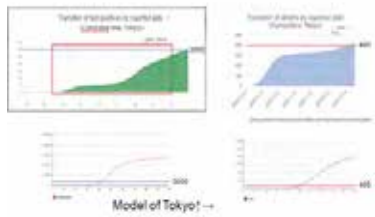
The results for Paris did predict the resurgence of infections after approximately 175 days. However, the scale is different. **Death counts support the hypothesis of underreporting of case numbers early on in the pandemic.**

Official cases/death counts (Paris):



Our Model for Paris

We could not make the model of Tokyo close to the actual numbers in time.
Although its curves look a little similar with real ones, the model shows about ten times the actual numbers. Some of Tokyo's parameters seem to be far more different from others than we expected.

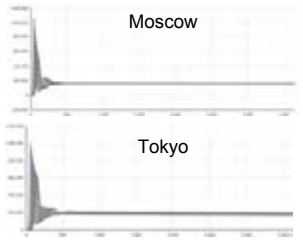


Model of Tokyo↑ →

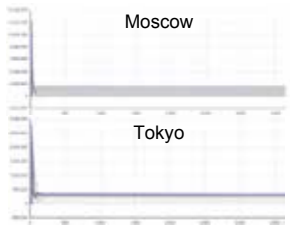
Preliminary Results - Moscow, Tokyo

How isolating people with COVID-19 symptoms affects its spread:

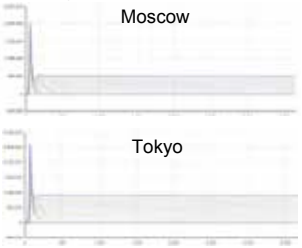
People with medium/severe infections are isolated in hospitals

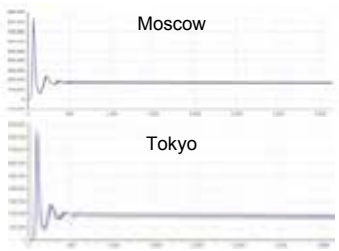


above: if people with light symptoms are isolated, increasing the duration of light infections does not affect COVID-19 infections significantly at equilibrium.



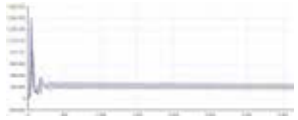
above: SARS-CoV-2 may evolve to increase the duration of asymptomatic infections. This significantly increases infections because asymptomatic people are not isolated.





left: increased asymptomatic spread vs right: increased symptomatic spread (e.g. coughing). Thus COVID-19 may evolve to infect more effectively in an asymptomatic way e.g. persisting on surfaces.

How ignoring quarantine affects the spread (Moscow):



above: increased symptomatic infection (as people are not isolated) increases cases at equilibrium.

above: SARS-CoV-2 may evolve to persist for a longer time in the body. This increases the number of infections at equilibrium significantly. This may lead to more severe infections.

above: SARS-CoV-2 may evolve to minimise the immunity loss period as this increases case numbers.

Conclusion

Our model, while not perfectly refined, was able to predict some characteristics of an outbreak.

Furthermore, executing this experiment with a greater database and more detailed parameters would further increase the accuracy of the model and make it possible to reveal additional properties of SARS-Cov-2, such as giving better estimates about unreported case numbers.

Finally, it enables predictions about outbreaks in case the virus should mutate and its epidemic characteristics were changed. From our model, we found that SARS-CoV-2 will have three major directions of evolution if we isolate people who display symptoms:

1) Being asymptomatic rather than symptomatic
2) Evolving to spread effectively in an asymptomatic manner e.g. surviving longer on surfaces
3) Evolving to have less notable antigens, so that our immune system is more likely to lose memory about it, and immune loss will happen at a faster pace

If we disregard quarantines, symptomatic carriers will have more contact with susceptible people. Thus, SARS-CoV-2 will evolve to become more symptomatic and evolve to spread better through coughing and sneezing (i.e. symptomatic transmission).

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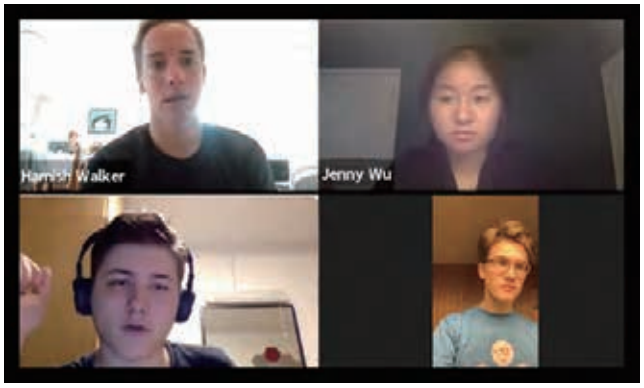
1A06 Dependence of prion uptake and colocalization on SDC3



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Introduction

Background

Prion diseases are fatal neurodegenerative diseases, also termed 'transmissible spongiform encephalopathies' They are characterized by neuronal loss, vacuolation and activation of microglia and astrocytes. Prion diseases can undergo long incubation periods, ranging from years to decades, but the course of the disease is usually rapid and drastic after onset of clinical symptoms. They are caused by an infectious proteinaceous agent, the prion. Prions consist primarily of aggregates of PrP^{Sc}, a misfolded form of the cellular PrP^{C} protein, and are thought to multiply through a nucleation and fragmentation process. It is currently unclear how prions enter cells.

Other neurodegenerative disorders, including Alzheimer's disease and Parkinson Disease have now also been linked to protein misfolding and aggregation. There is evidence that the proteins tau and α-synuclein are prion like, with high beta sheet content, and a similar ability of spreading and seeding of their misfolded protein aggregates. This acts as a central mechanism for neurodegeneration. A very recent study (Hudak et al, 2019) reported that a major cellular uptake route of tau and α-syn was through syndecan-mediated, lipid raft dependent, caveolae dependent endocytosis. The neuron predominant SDC3 exhibits the highest affinity for both proteins.The aim of the proposed experiment is to investigate whether a similar relationship exists between SDC3 and PrP^{Sc}.

Hypothesis

Amini and White found that SDC3 overexpression positively correlates with α-synuclein and tau protein pathology through internalisation and fibrillation in various human immortalized cell lines (2013). We hypothesize that a similar correlation might exist between SDC3 and prion internalization.

Both tau fibrils (Dregni et al., 2019) and prions (Torrent et al., 2019) also contain a cross-β-structure. Our hypothesis is backed by the aforementioned proteins' shared ability to form fibrils on cell surfaces as the result of protein misfolding, which is due to their cross-β-structure.

Methodology

Ethics Statement

We will adhere to the Canadian Council on Animal Care's Guide to the Care and Use of Experimental Animals (2020) when handling animals.

Safety Disclaimer

This lab will be performed in a biosafety level 2 laboratory environment. We will keep in mind the safety guidelines as outlined in Michigan State University's Recommended Biosafety Procedures for Handling Prions and Prion-Infected Tissues.

Materials

1.PC12 rat pheochromocytoma cells (ATCC, Manassas VA)
2.Retinoic acid, RA (Fisher Scientific)
3.DMEM/F12 medium (Thermo Fisher, Mississauga ON) for PC12 cells containing 10% fetal bovine serum (FBS) (Thermo Fish, Mississauga ON) and 5% horse serum (HS) (Thermo Fisher, Mississauga ON)
4.NGF solution (100 ng/ml) (Thermo Fisher, Mississauga ON)
5.Serum-free F-12 medium (Thermo Fisher, Mississauga ON)
6.SDC3 plasmid (Sino Biological Inc., Wayne PA)
7.Empty pCMV3-untagged negative control vector (Sino Biological Inc., Wayne PA)
8.Calcium phosphate transfection kit (Takara Bio, Mountain View CA)
9.6-8 week old wild type mouse
10.Phosphate buffer solution (Millipore Sigma, Oakville, ON)
11.Liquid nitrogen
12.Terminally ill, prion infected mouse.
13.Glass beads (Millipore Sigma)
14.CD230 (PrP) Recombinant Rabbit Monoclonal Antibody (Thermo Fisher, Mississauga, ON)
15.Alexa Fluor 532 antibody labeling kit.
16.0.4% Trypan blue (Thermo Fisher, Mississauga ON)
17.Citrate buffer solution(Millipore Sigma, Oakville, ON)
18.4% Paraformaldehyde solution (Boster Bio)
19.4',6-diamidino-2-phenylindole (DAPI), (Thermo Fisher, Mississauga ON)
20.Triton X-100 (Millipore Sigma, Oakville, ON)
21. Propidium Iodide solution (Thermo Fisher, Mississauga ON)
22.APC-labeled SDC antibodies (Novus Bio)
23.Goat Serum (Thermo Fisher, Mississauga ON)
24.Sodium Pentobarbitone (Fisher Scientific)
25.BD FACscan flow cytometer.
26. Olympus FV1000 confocal laser scanning microscope equipped with three lasers: An argon laser diode (Excitation, 405 nm) and a band pass filter (420-480 nm); a Nd:YAG laser line (Excitation, 532 nm) and standard Rhodamine 6G filters (550-575 nm); a helium/neon laser (Excitation, 543 nm) and a band-pass filter (650-675 nm).

Protocol

1. Transfection of PC12 cells with gene for SDC3 with following steps adapted from established protocol from research by Amini and White (2013)
-Culture PC12 rat pheochromocytoma cells on 60 mm poly-D-lysine coated dishes at a density of 1 x 10^5 cells per 60 mm dishes in DMEM/F12 medium containing 10% fetal bovine serum (FBS). Maintain PC12 cells at 37 degrees Celsius in a humidified atmosphere containing 7% CO_2 in Heracell VIOS 250i CO_2 Incubator
-Induce differentiation for 5 days upon plating on collagen IV-coated dishes and treating with 20 ng/ml nerve growth factor (NGF) in serum-free medium
-Stimulate the cells with C3 transferase at 1 µg/ml for 1 hour
-Divide cells into 4 groups, following schematic outlined in Figure 1
-With 3 of the groups, create knockout cells using CRISPR Cas9 using established protocol from research by Giuliano et al. (2019). The forward gRNA sequence will be 5' CACCG-CGAGUAGAGGUCGUCUAGUU 3' and the backward one will be 3'-C–GCUCAUCUCCAGCAGAUCAA–CAAA-5'. Exons were selected from e!Ensembl data on the ENSMUSE00001290926 exons and then sequences were made using IDT gRNA design checker. gRNAs are cloned into expression vectors using BsmBI digestion.
-With 1 of the groups from the previous step, create overexpression cells by transfecting with SDC3 plasmid (2 µg each) using calcium phosphate transfection kit
-With another one of the groups, transfect it using calcium phosphate transfection kit with the empty pCMV3-untagged negative control vector.

Depend

Methodology

-Transfected PC12 cells will be selected measuring expression with flow cytom using APC-labeled anti-SDC3 antibody
2. Protocol for PrP^{Sc} generation adapted fr established protocol from Morales et al, (20 protocol for uptake and colocalization study imaging adapted from established protocol f Hudak et al, (2019).

Generation of PrP^{Sc}

-By intraperitoneal injection of buffered diluted sodium pentobarbitone with l anesthetic, euthanize 6-8-week-old wild mouse.
-Perfuse the animal with phosphate bu solution via cardiac puncture
-Remove the brain and rinse in phosphate bu
-Homogenize the brain in CB at 10 % (wt/ using a homogenizer on ice.
-After homogenization, remove tissue debris centrifuging the brain homogenate at 805 4 degrees C for 45s.
-Remove the supernatant and discard the pe Place the supernatant on ice and mix it we vortexing. Aliquot the supernatant into 1.5 RNAse-free microcentrifuge tubes.
-Freeze with liquid nitrogen and store at degrees Celsius. This is the normal b homogenate, NBH.
-Euthanize a terminally ill, prion infected mo with IP injection of buffered and diluted sod pentobarbitone with local anesthetic.
-Remove the brain and homogenize it at Centrifuge the brain as before.
-Add four glass beads into 0.2 ml PCR tube (inocula) with 108 µl NBH substrate in the P
-Place tubes in a rack and then into clean w 37 degrees. Incubate for 29 min 40 s, then s

-Label CD230 Recombinant rabbit antibody kit according to the manufacturer's instructi

Analysis of Protein uptake: Flow Cytometry

-Take a 6 × 10^5 cells/ml sample from each Wash each twice in ice cold PBS and resusp
-Introduce PrP^{Sc} to a concentration of 5 µM overexpression cell groups. Incubate for 18
-Introduce labelled anti PrP antibody into the
-Mix equal volumes of this solution and stoc ice-cold 0.1 M citrate buffer at pH 4). This effect of trypan blue on surface bound fluor
-Cellular uptake of PrP^{Sc} can then be mea minimum of 10,000 events per sample s determined using PI in the cell suspension scatter against side scatter plot to exclude sample with no PrP^{Sc} added is the control t in order to circumvent the issue of backgrou

Analysis of Uptake and colocalization: Micros

-Take a 6 × 10^5 cells/ml sample from each Introduce PrP^{Sc} to a concentration of 5 µ and overexpression cell groups. Incubate fo
-Rinse the cells twice with ice cold PBS, ther DAPI for 5 minutes.
-For colocalization study, cell membranes sh then 1 h treatment with APC-labeled SDC 1:1000).
-Rinse all samples three times with PBS co then stain with DAPI for 5 minutes and wash
-Embed samples on Fluoromount G. Analy FV1000 confocal laser scanning microsc (Excitation, 405 nm) and a band pass filt signal recorded as blue; a Nd:YAG laser lin 6G filters (550-575 nm) to capture the sign laser (Excitation, 543 nm) and a band-pass as red.
-Sections presented should be taken fro Acquisition and analysis of images can b Colocalization can be quantified by calculat

pendence of prion uptake and colocalization on SDC3

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flow cytometry
ntibody
n adapted from
ies et al, (2012);
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f buffered and
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t 10 % (wt/vol)

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iscard the pellet.
nd mix it well by
tant into 1.5 ml
es.
nd store at -80
e normal brain

infected mouse
diluted sodium
thetic.

genize it at 10% in PBS containing Propidium iodide (PI).

ml PCR tubes. Mix 12 µl brain homogenate containing PrP^{Sc}
trate in the PCR tubes. Mix well by pipetting.
into clean water filled sonication horn, inside dry incubator at
n 40 s, then sonicate for 20s. Repeat cycle for 72 hours.

bit antibody (anti PrP) with Alexa Fluor 532 antibody labelling
er's instructions.

Cytometry
e from each cell group, and an additional wild type sample.
S and resuspend in 0.5 ml physiological saline.
ion of 5 µM into the SDC3 knockout, one of the wild type and
ubate for 18 h at 37°C.
body into the cell culture. Incubate for 1 hr.
ion and stock solution of trypan blue (500 µg/ml dissolved in
pH 4). This lowers sample pH to 4.0, optimizing quenching
bound fluorescent proteins.
hen be measured via flow cytometry using a FACScan. A
er sample should be analysed. Viability of cells should be
suspension (10 µg/ml) and appropriate gating in a forwards
t to exclude dead cells, debris and aggregates. The wild type
the control to which other cell groups should be compared to,
of background noise from antibody binding to native PrP^{C}.
ation: Microscopic visualization
e from each cell group, and an additional wild type sample.
ation of 5 µM into the SDC3 knockout, one of the wild type
. Incubate for 18 h at 37°C.
old PBS, then fix in 4% paraformaldehyde and stain nuclei with

embranes should be permeabilized with 1% Triton X-100, and
abeled SDC antibodies and labeled anti-PrP antibodies (both

with PBS containing 1% goat serum and 0.1% Triton X-100,
tes and wash three times with PBS.
unt G. Analyze distribution of fluorescence on an Olympus
ing microscope equipped with three lasers. A laser diode
nd pass filter (420-480 nm) should be used to capture the
'AG laser line (Excitation, 532 nm) and standard Rhodamine
ture the signal recorded as yellow; and finally, a helium/neon
band-pass filter (650-675 nm) to capture the signal recorded

e taken from approximately the mid-height of the cells.
nages can be done using the Olympus Fluoview software.
d by calculation of Manders' colocalization coefficient.

Figure 1. Generation of 4 experimental groups: After inducing differentiation, cells are separated into 4 groups. After following the steps described in the protocol above, there will be 1 wild-type group (orange), 2 groups with no SDC expression (light and dark green)—1 of which undergoes calcium phosphate transfection without a plasmid—and 1 group overexpressing SDC3 (yellow).

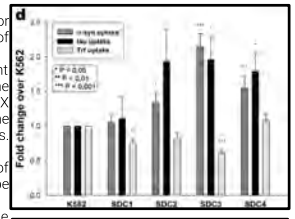
Methodology

-The wild type sample with no PrP^{Sc} added is the control to which other cell groups should be compared to, in order to circumvent the issue of background noise from antibody binding to native PrP^{C}.

3. Qualitative and quantitative analyses with following steps adapted from research by Hudak et al. (2019).

Qualitative analysis
-Colours, shapes, textures, and patterns, will be noted for each of the 4 experimental groups. Nuclei will show up as blue, prions as yellow-green, and SDC3 as red.
-Use flow cytometry to measure fluorescence in the range of 550-625 nm to evaluate the expression of SDC3 for each experimental group separately.
-Combine this data in one graph with a line representing each experimental group's fluorescence levels

Quantitative analysis
-Using the Olympus Fluoview software, determine the fluorescence intensities of all experimental groups at the emission spectra for each dye.
-Generate all computer images and compare
-Normalize each experimental group's fluorescence intensity as percent deviation from the value of fluorescence intensity determined for the wild-type group. Calculate this as [(X-Y)/X]*100% where X is the fluorescence intensity calculated for the wild-type group without prion infection and Y is the fluorescence intensity calculated for the other experimental groups.
-Perform a one-way ANOVA test between the fluorescence intensity of each experimental group and the fluorescence intensity of the wild-type group with for prion protein. Determine a p_1 value
-Graph this data as a bar graph. Indicate error bars representing 1S.D.
-Digitally overlap images containing green-yellow (prions) and red (SDC) layers.
-Calculate Manders Colocalization Coefficient (MCC) for each experimental group. This reflects the extent of colocalization of prion protein and SDC3.
-Normalize each experimental group's MCCs as percent deviation from the value of MCCs determined for the wild-type group. Calculate this as [(X-Y)/X]*100% where X is the MCC calculated for the wild-type group and Y is the MCC calculated for any of the other experimental groups. Determine a p_2 value
-Perform a one-way ANOVA test between the MCCs of each experimental group and the MCCs of the wild-type group.
-Graph this average MCC data as a bar graph. Include error bars representing 1 S.D. Place an asterisk by bars that have p<0.05 from the one-way ANOVA test.



Example of bar graph where data is shown as compared to the values in the control group (in this case, K562 values) (Hudak *et al.* 2019)

Results & Discussion

This experiment could yield 3 cases with regards to the relationship between SDC3 expression and prion uptake. Within each case, there would be 3 subcases with regards to the relationship between SDC3 expression and colocalization with PrP^{Sc}.

Case 1: There is no correlation ($p_1 > 0.05$) between SDC3 expression and prion uptake by neuronal cells. There may not be a direct relationship between SDC3 and prion uptake. Results will be similar in all cell categories; that is, the results from amalgamated flow cytometry data should be very similar, but all have predominantly low intensity emissions.

a)No correlation ($p_2 > 0.05$) between SDC3 expression and colocalization. Correspondingly, the MCC results would need to demonstrate that there is little colocalization between SDC3 and PrP^{Sc} in all of the cell groups, and that all would have similar values for the MCC, in order to conclude this.

b)There is a positive correlation ($p_2 < 0.05$) between SDC3 expression and colocalization. SDC3 is likely a good binding site on the membrane compared to other potential binding sites. SDC3 is likely not directly involved in prion uptake. We could conclude this if the MCC value for the overexpression cell group was significantly higher than the wild type (prion infected) group, and the MCC value for the wild type (prion infected) group was significantly higher than the knockout group.

c)There is a negative correlation ($p_2 > 0.05$) between SDC3 expression and colocalization. SDC3 is most likely a poor binding site compared to other potential sites on the membrane. Proportionally,in cells with greater quantities of SDC3, less area of the membrane has greater binding affinity. We could conclude this if the MCC value for the overexpression cell group was significantly lower than the wild type (prion infected) group, and the MCC value for the wild type (prion infected) group was significantly lower than the knockout group.

Case 2: positive correlation ($p_1 < 0.05$) between SDC3 and prion uptake by neuronal cells. Prion uptake is likely promoted by SDC3. For this scenario, flow cytometry histograms of the emission spectra of the prion fluorescent antibodies may indicate that the greatest signal was seen for the overexpressed SDC3 group, next greatest for wild-type, and the lowest for the SDC3 knockout group.

a)Negative correlation ($p_2 < 0.05$) between SDC3 expression and colocalization: SDC3 is likely to promote PrP^{Sc} uptake, however, the mechanism for PrP^{Sc} uptake doesn't involve direct PrP^{Sc} to SDC3 binding. We would conclude this if the bar for the overexpressing experimental group has much lower MCC than the wild-type group with prion infection, and if the wild-type group with prion infection had a significantly lower MCC than the knockout cells.

Results & Discussion

b)No correlation ($p_2 > 0.05$) between SDC3 expression and colocalization: SDC3 is likely to promote PrP^{Sc} uptake, however, the role of SDC3 can not be determined. We would conclude this if the bars for any pair of wild-type, knockout, or overexpressing groups were not significantly different.

c)Positive correlation ($p_2 < 0.05$) between SDC3 expression and colocalization: SDC3 is likely to directly promote PrP^{Sc} uptake by binding to it. We would conclude this if the bar for the SDC3 overexpressing experimental group had a significantly higher MCC than the wild-type group with prion infection, and if the wild-type group with prion infection had a significantly higher MCC than the knockout cells.

Case 3: negative correlation ($p_1 < 0.05$) between SDC3 expression and prion uptake by neuron-like cells. Prion uptake is likely inhibited by SDC3. For this scenario, flow cytometry histograms of the emission spectra of the prion fluorescent antibodies may indicate that the greatest signal was seen for the knockout groups, next greatest for the wild-type group, and the lowest for the SDC3 overexpressing group.

a)Negative correlation ($p_2 < 0.05$) between SDC3 expression and colocalization: SDC3 is likely a poor binding spot compared to other potential binding sites on the cell membrane. Because on cell membranes with high SDC3, it covers a higher proportion of the membrane, then there are fewer areas where prions actually have a greater binding affinity. We would conclude this if the bar for the overexpressing experimental group has much lower MCC than the wild-type group with prion infection, and if the wild-type group with prion infection had a significantly lower MCC than the knockout cells.

b)No correlation ($p_2 > 0.05$) between SDC3 expression and colocalization: SDC3 is likely not a significantly better or worse binding spot compared to other potential binding sites on the cell membrane. Thus, if there is a cell-surface protein that contributes to the intake of prion protein, it is likely not SDC3, and further research is required. We would conclude this if the bars for any pair of wild-type, knockout, or overexpressing groups were not significantly different.

c)Positive correlation ($p_2 < 0.05$) between SDC3 expression and colocalization: SDC3 is likely a good binding spot compared to other potential binding sites on the cell membrane. However, the prion pathogenic activity would be limited to the membrane level and SDC3 effectively anchors the prions there. We would conclude this if the bar for the overexpressing experimental group has much higher MCC than the wild-type group with prion infection, and if the wild-type group with prion infection had a significantly higher MCC than the knockout cells.

Conclusion

Case 1: SDC3 is likely not involved directly in the process of prion internalization into neuronal cell culture. It is possible that an alternative endocytic pathway may be involved in the process. New hypotheses must be posed to investigate these alternate mechanisms.

Case 2: PrP^{Sc} like α-syn and tau, is very effectively internalized into neuronal cell culture as a result of SDC3 expression. Depending on the level of colocalization, the mechanism for internalization could involve PrP^{Sc} binding to SDC3 or another mechanism which does not involve direct PrP^{Sc} to SDC3 binding. Further research must be conducted to determine the exact mechanism of PrP^{Sc} internalization.

Case 3: PrP^{Sc}, unlike α-syn and tau, is not very effectively internalized into neuronal cell culture as a result of SDC3 expression. This may be due to a number of structural and chemical reasons. Efforts should be made to identify alternative proteins or other cell membrane components that could contribute to the internalization of PrP^{Sc}.

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Acknowledgements

We would like to thank our group project facilitator, Pavel Loginovich, for his tremendous support during the entire duration of this project. We also greatly appreciate the organizers of the International Biology Olympiad 2020 for providing us this opportunity.

All group members contributed equally and have approved the final proposal.

1A07 How Climate Change affects Infectious Diseases

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The Antarctic and Subantarctic

Due to the anthropogenic climate change, different environments are changing. One of them is the Arctic with its permafrost [1]. It is prognosed that 20-25 years from now, the permafrost will be reduced by 10-12% [2]. Its depth can be up to one kilometer and it makes up about 25% of the hard surface on our planet. As the permafrost constantly has subzero temperatures, it holds a sample of stored microorganisms. Therefore, the thawing of the permafrost poses a threat towards animals and humans, as diseases may (re-)emerge from the permafrost [3]. In the year of 2020, the world knows the threat of a new pathogen and therefore awareness of the thawing of the permafrost should be a priority.

Already, the thawing permafrost has claimed victims, such as the 12-year-old Russian boy, who in 2016 died due to an Anthrax exposure [4]. A concern is that grazing livestock consumes the endospores from Anthrax and thus exposes humans to Anthrax [2].

Furthermore, Revich, Boris et al. have uttered their concern for a prolonged activity of insect vectors, such as ticks, due to a prolonged amount of summer days. The warmer temperatures could increase the insect vector's chance of survival. In fact, there has been an increase in cases of borreliosas and encephalitis in the northern European Arctic [2].

Covid-19

Beginning at the end of 2019, the world has faced a new threat: Covid-19. Easily spreading across the globe due to modern transportation such as airplanes, the virus has struck different countries with different severity. Climate change helps lay the groundworks for pandemics, such as Covid-19.

When a catastrophe hits, as seen in India and in the USA (Michigan) in May, a big amount of people needs to be relocated in a short amount of time. Upholding precautions in regard of Covid-19 is difficult during an emergency, thus leading to a greater spread of the disease [23], which is illustrated by the flow chart (figure 6). Furthermore, air pollution is an often-seen consequence due to our industrialization. Research from Harvard sheds light on the link between a greater mortality of Covid-19 cases and air pollution [24].

So far, no one has found a direct link between climate change and Covid-19. However, there are many factors resulting from climate change that affect human health and/or potential pathogens. With increasing temperatures or deforestation migration of animal species comes, thus resulting in new contact possibilities between humans, animals, and pathogens. Another factor is large livestock farms where spillover of infections can happen [25].

Figure 6: Flow-chart of factors contributing to epidemics

The Tropics

nd sleeping sickness have always been owever, due to climate change, there has different regions, as some habitats have r accommodating pathogens and their

causes African trypanosomiasis. It is transmitted tis, and their development and mortality rates are produced in the Zanabezi valley shows that the he reason for lower tsetse abundance and links wer trypanosomiasis risk [20].

sm at elevated temperatures and must feed more frequently. As temperatures lower, and smaller pupae are produced. Rates of pupal fat consumption also d fat levels in young adults decrease the chances to find its first meal before fat uffers excess mortality as a consequence of taking additional risks in attempting

East African highlands, a consistent rise in mperature over several decades relates to a gher prevalence of malaria [21]. Although the dy concluded that changes in climate caused global warming are the key reasons, shifts in nd-use, human movement, and population owth were also at play. However, these factors e, in part, connected to climate change [22].

Figure 5: Mean monthly temperature (°C) anomalies in relation to a specific 1960–1990 period. [20]

The Subtropics

The subtropics are known for its diversity in climate types. In northern Africa it is very arid, whereas southern Asia has its seasonal rainfalls, the monsoons. For example, Pakistan, experiences severe and frequent floods – one of the climate conditions worsened by climate change. Consequently, the country faces epidemics of diseases that are vector and water borne, such as diarrhea, leptospirosis, and malaria. Significant, however, is the morbidity and mortality of cases with respiratory infections after floods [17].

In a study by Chen, Mu-Jean et al. a link between extreme precipitation and outbreaks of water- and vector borne diseases, such as cholera and malaria, is investigated. An issue is the occurrence of stagnant water, which is an ideal environment for disease-carrying vectors. A figure from their study (figure 2) illustrates the occurrence of bacillary dysentery and the precipitation in different areas after the typhoon Nari in Taiwan in 2001 [18].

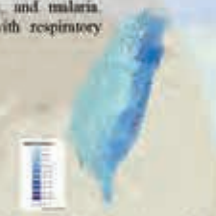

Figure 2: Mean precipitation is shown in shades of blue (se legend) and is normalized in mm. The red dots represent cases of bacillary dysentery [18].

A review article by Metcalf C. et al from 2017 shows that the R_0 of an infectious disease plays a role in the incidence rate and the impact of precipitation on the occurrence of the disease. Figure 3 shows that an infectious disease with a low R_0 shows a greater correlation with the precipitation than an infectious disease with a high R_0 [19].

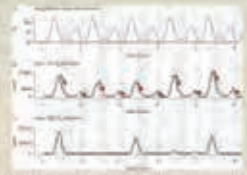

Figure 3: Low precipitation is shown periodically in a shade of grey. a) 6 years of simulated precipitation. b) Simulated cases of an infection with a low R_0. c) Identical infection as in b) but with a higher R_0 [19]

Conclusion

Possible Solutions and Scientific Experiments

Researches outline three key factors that are needed to conclude that climate change causes variance in vector-borne infectious disease prevalence: 1. Evidence of biological sensitivity of the vector or parasite to climate; 2. Meteorological proof of climate change; 3. Possible evidence of any entomological and epidemiological changes that are connected with climate change [26]. If the correlation is proven, scientists try to forecast future climatic influences on infectious diseases by creating various models.

Statistical models look at the current geographic distribution of the disease and the specific climatic conditions in the location. With human intervention taken into account, the influence of climate change is assessed. Statistical equations that describe possible climate scenarios allow estimating the distribution in the future [27]. Landscape-based models join the climate-based models and spatial analytical methods to study the effects of climatic and other environmental factors. For instance, the influence of different vegetation types is investigated. Among other, it was used in several studies to estimate how future climate-induced changes at the ground level and the surface of water bodies in Africa would affect mosquitoes and tsetse flies and, in turn, malaria and sleeping sickness abundance [27]. Process-based or mathematical models use equations that reflect the relationship between climatic variables and biological parameters, for example, survival, biting rates, vector breeding, and incubation length. It allows assessing how climate change affects vector and parasite biology and, thus, disease transmission. This model has shown that small temperature increases raise the potential of malaria. If the global temperature rose by 2-3°C, the number of people at risk of malaria would increase by around 3-5% (about several hundred million new cases), and the seasonal duration of malaria surges would increase in endemic areas [28].

Considering recent and old events and the facts presented, this project suggests among others a greater international cooperation to assess the climate change's effect on infectious diseases. More research is needed, using the above-mentioned key factors, to unravel the potential links between climate and infectious diseases, such as malaria, TBE, anthrax, and Covid-19. In regards of anthrax, one should take samples of soil in northern regions to ensure that no anthrax is found (e.g. by searching for eDNA). Also, one could make the TBE-vaccine more available to the population and continue developing a vaccine against borreliosis.

Furthermore, this project concretely proposes to also focus on 1) a better weather surveillance worldwide, 2) less deforestation, thus securing animal's natural habitats, 3) less use of fossil fuels and better filter systems on factories and vehicles to raise air quality, 4) smaller livestock farms to minimize spillover of infections and 5) more international focus on the overall health care system and its capacity and response in regard of natural disasters as well as epidemics/pandemics in each country, as infectious diseases in our modern world know no national borders.