The Lord is like a strong tower, where the righteous can go and be safe.
Proverbs 18:10

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Be alert, stand firm in the faith, be brave, be strong.
1 Corinthians 16:13

RITM representatives inspect De La Salle Medical and Health Sciences Institute in Cavite

The Research Institute for Tropical Medicine (RITM) representatives inspected the De La Salle Medical and Health Sciences Institute in Dasmariñas, Cavite last May 7.

The Provincial Health Office has been anticipating the approval of the laboratory by the Department of Health (DOH) to begin operating and help stop the spread of the Corona Virus Disease 2019 (COVID-19) in Cavite.

According to the personnel of De La Salle Medical and Health Sciences Institute, they will run

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The LGU continues disenfection in the whole locality to prevent spreading the virus and distributing relief packs to 15,000 families, including the spaghetti fiesta packs as Barangays San Jose I and II were cerebrating their feast day May 1.

Noveleta opens first public hospital

NOVELETA, Cavite - The local government here formally opened its first public hospital amid the severe coronavirus epidemic last May 2.

Mayor Dino Reyes Chua together with Ms. April Rose Pascua, RN, MAN, Development Management Officer IV Department of Health (DoH) Center for Health Development, Municipal Health Officer Dr. Hilda Baca and other local officials lead the inauguration of P15 million worth Noveleta MedCare Hospital as a COVID 19 Care Facility.

The town has no recorded COVID 19 cases for the past three weeks according to Municipal Health Officer Dr. Hilda Baca.

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Cholesterol lowering drugs linked to improved gut bacteria composition in obese people

The human gut microbiota consists of trillions of bacteria, fungi and virus constituting an inner chemical factory producing a multitude of microbial compounds affecting immunity, neurobiology and metabolism of the human host.

It has for long been known that imbalances in the composition of gut microbes link with a variety of chronic human disorders spanning from obesity, diabetes, inflammatory bowel diseases to depression, schizophrenia, autism and Parkinson. In addition, it is known that unhealthy dieting and use of some medications, for instance stomach acid neutralizers, the so-called proton pump inhibitors, are associated with a further disruption of the microbial communities of the gut.

Now, in a new paper in the scientific journal Nature, The MetaCardis investigators explore gut bacteria in almost 900 individuals from Denmark, France and Germany.

The intestinal microbiota in obese individuals had previously been shown to differ from those in lean subjects with a poor bacterial diversity, a relative depletion of health promoting bacteria and the remaining bacteria dominated by an inflammatory tone.

In their Nature article, the researchers now define a cluster of bacteria called Bact2 enterotype, which is found in 4% of lean and overweight people but in 18% of obese individuals who did not use statin drugs, a group of cholesterol lowering medications.

However, in other obese study participants who were treated with statins, the prevalence of the unhealthy Bact2 enterotype was significantly lower (6%) than in their non-treated counterparts (18%) -- comparable to levels observed in non-obese participants (4%). The same trend was validated in a Flemish study sample of about 2000 participants.

(RITM... from page 1)

laboratory for 6 to 8 hours while the RITM representatives observe, submit the results to RITM, and wait for the institute's feedback.

Governor Jonvic Remulla stated that the inspection is the last step for the Health Sciences Institute to start the mass-targeted testing program in the province. There are 300, 000 test kits on the way.

The Provincial Health Office initially said that not only residents of Cavite will benefit from the laboratory but Region 4A residents as well.

(NOVELETA... from page 1)

The hospital can accommodate around 15 patients in the emergency area with 25 medical staffs from doctor, nurses, nursing aides, utilities, security guards and ambulance drivers and safety officer all in shifting operation.

The two-storey building was erected on 1,000 square meters property in Barangay San Jose I donated by Mayor Chua last April 3, 2017 across Municipal Hall and Public Market of historic Ilang Ilang river.

The escalation of the cases was prevented by the intense local government program here under the leadership of local chief executive Dino Chua and Local Disaster and Risk Reduction and Management Unit head Jeg Alix.

"There have been no reported COVID 19 positive cases in town for past three weeks," Dr. Hilda Buzu said.

The three positive cases - 58 years old male and 53 years old female both from San Jose I and 31 years old female from San Rafael 2 - all tested negative and all out of danger and now under 14 days monitoring.

The hospital was erected through funds from DoH (P5 Million) and Php 10 Million from LGU and will cater to mild, probable and severe cases.

"We will be operational on May 3, Monday and well equipped from Personal Protection Equipment (PPE) and other needs for Covid cases. Each room has TV, wifi, CR, and sanitation kits," Dr. Nilda Buzu said.

"We have 8 hour duty nurses, nursing aides, utilities, security guards and ambulance drivers in three shifts," Dr. Buzu added.

Mayor Chua also returned his January to December 2019 salary worth P1.2 million to buy relief goods to feed his 13,000 constituents in time of crisis. Chua also donated his whole year salary for year 2020 to buy food.

Senator Bong Revilla also distributed sacks of rice to the locality last April 29 together with Vice Governor Jolo Revilla.

AUCTION SALE

[illegible]

New computational method unravels single-cell data from multiple people

A new computational method for assigning the donor in single cell RNA sequencing experiments provides an accurate way to unravel data from a mixture of people. The Souporcell method, created by Wellcome Sanger Institute researchers and their collaborators could help study how genetic variants in different people affect which genes are expressed during infection or response to drugs.

Published last week in Nature Methods, the software could increase efficiency of single-cell experiments, assisting research into transplants, personalised medicine and malaria.

Single-cell RNA sequencing (RNA-seq) can reveal exactly which genes are switched on in each individual cell, revealing cell types and what they do. Pooling multiple people's cells into a single cell RNAseq experiment helps to identify how different genomes affect their gene expression. However it is essential to be able to separate the resulting data by individual, which can be very difficult.

The authors tested Souporcell* against three other computational methods using placental cells, pluripotent stem cell lines** and malaria parasites.

Haynes Heaton, the first author from the Wellcome Sanger Institute, said: "Our method, called Souporcell, is able to separate mixtures of individuals' cells in scRNAseq experiments without knowing each individual's full genome sequence beforehand, unlike previous methods. One of the key features of the method is that it estimates the amount of background RNA from dead cells, which is often referred to as the soup. This then allows the removal of that source of noise, and hence the name Souporcell."

Being able to combine the cells into a single experiment increases the accuracy, enabling more information to be found, and also reduces the cost of these experiments.

Dr Martin Hemberg, a senior author from the Wellcome Sanger Institute, said: "The exact genetic sequence of each person can affect their response to infections, or to drug treatments. The new method enables single cell expression data from multiple people to be analysed, to show links between genotype and phenotype, in diseases and in the presence of drugs. This will have implications for personalised medicine."

In addition, some samples inherently have a mix of cells with different genomes, including samples from transplant patients who have their original cells and cells from the donor, or populations of parasites, such as malaria, from an infected individual.

Dr Mara Lawniczak, a senior author from the Wellcome Sanger Institute, said: "This method is helping us understand malaria. People get infected with multiple strains of malaria at once, but we don't know how these strains are competing with each other to reproduce

Sewage poses potential COVID-19 transmission risk, experts warn

Environmental biologists at the University of Stirling have warned that the potential spread of COVID-19 via sewage "must not be neglected" in the battle to protect human health.

The response to the global pandemic has focused upon preventing person-to-person transmission, however, experts now believe the virus could also be spread in wastewater.

Earlier last week, it emerged that analysis of sewage in the UK could provide important data on the spread of COVID-19. However, Professor Richard Quilliam's new paper – published May 6 – now warns that the sewerage system itself could pose a transmission risk.

Writing in the journal Environment International, Professor Quilliam and colleagues from Stirling's Faculty of Natural Sciences are calling for "an investment of resources" to investigate their concerns.

Professor Quilliam – who is currently leading a £1.85 million study into the transport of bacteria and viruses in marine environments – said: "We know that COVID-19 is spread through droplets from coughs and sneezes, or via objects or materials that carry infection. However, it has recently been confirmed that the virus can also be found in human faeces – up to 33 days after the patient has tested negative for the respiratory symptoms of COVID-19.

"It is not yet known whether the virus can be transmitted via the faecal-oral route, however, we know that viral shedding from the digestive system can last longer than shedding from the respiratory tract. Therefore, this could be an important – but as yet unquantified – pathway for increased exposure."

The authors of the peer-reviewed paper presented the example of the severe acute respiratory syndrome (SARS) outbreak in 2002-2003, when SARS-CoV-1 – closely linked to the COVID-19 virus strain (SARS-CoV-2) — was detected in sewage discharged by two hospitals in China.

Professor Quilliam highlights that, as most COVID-19 patients are asymptomatic or experience just mild symptoms and remain at home – not in hospitals, there is significant risk of "widespread" distribution through sewers.

Professor Quilliam authored the paper alongside Professor Manfred Weidmann, Dr Vanessa Moresco, Heather Purshouse, Dr Zoe O'Hara, and Dr David Oliver.

The biologists said a lack of testing "makes it difficult" to predict the scale of the potential spread and the public health implications of the virus arriving at wastewater treatment works, whilst the implications of consequent discharge into the wider environment are only just beginning to be investigated.

They added that the structural makeup of COVID-19 – specifically its lipid envelope covering – suggests that it will behave differently in aqueous environments, compared to other viruses typically found in the intestine. There is currently limited information on the environmental persistence of COVID-19, but other coronaviruses can remain viable in sewage for up to 14 days, depending on the environmental conditions.

On the risk of human exposure, the authors said: "The transport of coronaviruses in water could increase the potential for the virus to become aerosolised, particularly during the pumping of wastewater through sewerage systems, at the wastewater treatment works, and during its discharge and the subsequent transport through the catchment drainage network.

"Atmospheric loading of coronaviruses in water droplets from wastewater is poorly understood but could provide a more direct respiratory route for human exposure, particularly at sewage pumping stations, wastewater treatment works and near waterways that are receiving wastewater."

Risk could be further increased in parts of the world with high levels of open defecation, or where safely managed sanitation systems are limited and waterways are used as both open sewers and sources of water for domestic purposes.

"Such settings are commonly accompanied by poorly resourced and fragile healthcare systems, thus amplifying both exposure risk and potential mortality," the authors said.

Currently, all published data on faecal shedding of SARS-CoV-2 derive from hospitalised patients – with limited information available on mild and asymptomatic cases.

Dual personalities visualized for shape-shifting molecule

Australian and US researchers have made a breakthrough in understanding the structure of a key genetic molecule, called RNA, and revealing for the first time how these changes impact RNA's function.

Publishing in the journal Nature, the research team developed a bioinformatics technique to resolve separate structures of RNA rather than viewing them as a 'blur' that averaged multiple structures. This underpinned their discovery that the structure of RNA can influence how cells function.

RNA is a DNA-like molecule that encodes genetic information. Certain viruses – including HIV and SARS-CoV2 – use RNA as their genetic material. The team were able to apply the techniques they developed to reveal how the structure of HIV's RNA genome influences which proteins the virus produces.

The international collaborative team was led by Walter and Eliza Hall Institute researcher Dr Vincent Corbin together with Mr Phil Tomezsko and Professor Sclvi Rouskin at the Whitehead Institute for Biomedical Research, Boston (US). The research team also included the Institute's Computational Biology Theme Leader Professor Tony Papenfuss and mathematician and PhD student Mr Lachlan McIntosh.

At a glance

- RNA is a molecule that carries genetic information, controlling how cells function.

- A collaborative research team has used advanced computational methods to detect different structures of RNA, which until now could not be distinguished.

- Using HIV as a model system, the team discovered that different structures of RNA influenced how the virus behaved. This is the first time changes in RNA structure have been shown to influence how this molecule controls cells' function.

RNA is a molecule found in all living things that carries genetic information. RNA is an important regulator of how cells function, directly controlling which proteins are produced in cells, and can also switch genes on and off.

RNA molecules have a two-dimensional structure which influences how the genetic information contained within them can be accessed, said Dr Corbin, who led the project's bioinformatics research.

'The big question in RNA biology has been whether RNA molecules have a single, constant structure, or whether they can shift between different structures – and what this means for the function of a particular RNA molecule," he said.

"Our collaborators, led by Professor Silvi Rouskin, developed a technique for deciphering the structure of RNA molecules. We wanted to understand whether what we were detecting was a single structure of RNA, or an 'average' structure that blurs multiple different structures together.

"It's a bit like seeing red and yellow stripes, or blurring them together and thinking you can see orange," he said.

By developing a computational algorithm, the team were able to detect and measure the amount of different RNA structures. "We could detect these both in a test tube and in living cells, so we next looked at whether these structures influenced how RNA functioned," Dr Corbin said.

When RNA is produced in cells, it starts in a longer form that is 'spliced' or trimmed to remove unwanted parts.

"RNA splicing can influence how it encodes proteins," Dr Corbin said. "There are many examples of how altered RNA splicing influences how a cell functions – and in some cases, changes in RNA splicing have been associated with cancer or neurodegenerative diseases."

Certain viruses use RNA for their genome, including HIV and SARS-CoV2 (the coronavirus that causes COVID-19). In the case of HIV, RNA splicing influences which protein the virus produces – which changes at different stages of the virus's lifecycle.

"Using the HIV genome as a model system, we looked at whether RNA structure influences how HIV's RNA is spliced. We discovered that RNA structure was a critical determinant of RNA splicing in HIV, and influenced which viral proteins were produced," Dr Corbin said.

Bat 'super immunity' may explain how bats carry coronaviruses, study finds

A University of Saskatchewan (USask) research team has uncovered how bats can carry the Middle East respiratory syndrome (MERS) coronavirus without getting sick – research that could shed light on how coronaviruses make the jump to humans and other animals.

Coronaviruses such as MERS, Severe Acute Respiratory Syndrome (SARS), and more recently the COVID19-causing SARS-CoV-2 virus, are thought to have originated in bats. While these viruses can cause serious and often fatal disease in people, for reasons not previously well understood, bats seem unharmed.

"The bats don't get rid of the virus and yet don't get sick. We wanted to understand why the MERS virus doesn't shut down the bat immune responses as it does in humans," said USask microbiologist Vikram Misra.

In research just published in Scientific Reports, the team has demonstrated for the first time that cells from an insect-eating brown bat can be persistently infected with MERS coronavirus for months, due to important adaptations from both the bat and the virus working together.

"Instead of killing bat cells as the virus does with human cells, the MERS coronavirus enters a long-term relationship with the host, maintained by the bat's unique super immune system," said Misra, corresponding author on the paper. "SARS-CoV-2 is thought to operate in the same way."

Misra says the team's work suggests that stresses on bats — such as wet markets, other diseases and possibly habitat loss — may have a role in coronavirus spilling over to other species.

"When a bat experiences stress to their immune system, it disrupts this immune system-virus balance and allows the virus to multiply," he said.

The research was carried out at USask's Vaccine and Infectious Disease Organization – International Vaccine Centre (VIDO-InterVac), one of the world's largest containment level 3 research facilities, by a team of researchers from USask's Western College of Veterinary Medicine and VIDO-InterVac.

"We see that the MERS coronavirus can very quickly adapt itself to a particular niche, and although we do not completely understand what is going on, this demonstrates how coronaviruses are able to jump from species to species so effortlessly," said VIDO-InterVac scientist Darryl Falzarano, who co-led the bat study, developed the first potential treatment for MERS-CoV, and is leading VIDO-InterVac's efforts to develop a vaccine against COVID-19.

So far, the SARS-CoV-2 virus has infected more than 3.5 million people worldwide and killed seven per cent of those infected. In contrast, the MERS virus infected nearly 2,500 people in 2012 but killed one in every three people infected. There is no vaccine for either SARS-CoV-2 or MERS. While camels are the known intermediate hosts of MERS-CoV, bats are suspected to be the ancestral host.

Coronaviruses rapidly adapt to the species they infect, Misra said, but little is known on the molecular interactions of these viruses with their natural bat hosts. A 2017 USask-led study showed that bat coronaviruses can persist in their natural bat host for at least four months of hibernation.

When exposed to the MERS virus, bat cells adapt — not by producing inflammation-causing proteins that are hallmarks of getting sick, but rather by maintaining a natural antiviral response, a function which shuts down in other species, including humans. Simultaneously, the MERS virus also adapts to the bat host cells by very rapidly mutating one specific gene, he said.

Operating together, these adaptations result in the virus remaining long-term in the bat but being rendered harmless until something — such as disease or other stressors — upsets this delicate equilibrium.

Obesity is linked to gut microbiota disturbance, but not among statin-treated individuals

In 2012, the European Union MetaCardis consortium, comprising 14 research groups from six European countries with multidisciplinary expertise set out to investigate a potential role of the gut microbiota in the development of cardio-metabolic diseases. This project, coordinated by Prof Karine Clément at INSERM (France) studies more than 2,000 deeply phenotyped European participants in health and at different stages of cardiometabolic disease (obesity, diabetes and cardiovascular diseases).

May 6, 2020, research teams led by Jeroen Raes (VIB-KU Leuven) and Prof. Clement (INSERM, Paris), together with the Metacardis consortium, publish their first findings in the authoritative journal Nature, identifying the common cholesterol-lowering drug statins as a potential microbiota-modulating therapeutic.

In their manuscript entitled 'Statin therapy associates with lower prevalence of gut microbiota dysbiosis', Jeroen Raes (VIB-KU Leuven) and colleagues explore gut bacteria in a Metacardis cohort subset comprising nearly 900 individuals from 3 different countries (France, Denmark and Germany) with BMI ranging between 18 and 73 kg.m-2. While the intestinal microbiota in obese individuals had previously been shown to differ from those in lean subjects, the unique experience of the Raes Lab in quantitative microbiome profiling allowed the researchers to shed a whole new light on microbiota alterations associated with obesity.

Prof. Jeroen Raes

'Recently, our lab identified a single gut microbiota configuration (enterotype) with increased prevalence among patients suffering from intestinal inflammation (Inflammatory Bowel Disease), multiple sclerosis, and depression. We observed this disturbed enterotype to be characterized by low bacterial abundances and biodiversity, notably deficient in some anti-inflammatory bacteria such as Faecalibacterium. In fact, even among healthy individuals, we detected slightly higher inflammation levels in carriers of what we refer to as the Bacteroides2 (Bact2) enterotype. As obesity is known to result in increased systemic inflammation levels, we hypothesized that Bact2 would also be more prevalent among obese study participants.'

Exploring gut microbiota configurations of lean and obese volunteers, the MetaCardis researchers observed that Bact2 prevalence increased with BMI. While only 4% of lean and overweight subjects were characterized as Bact2 carriers, percentages sharply rose to 19% among obese volunteers. The same trend was observed among 2,350 participants of the VIB-KU Leuven Flemish Gut Flora Project population cohort.

Sara Vieira-Silva (principal author, VIB-KU Leuven): We found systemic inflammation in participants carrying the Bact2 enterotype to be higher than expected based on their BMI. Even though this study design does not allow inferring causality, our analyses do suggest that gut bacteria play a role in the process of developing obesity-associated comorbidities by sustaining inflammation. While these key findings confirmed our study hypothesis, the results we obtained when comparing statin-treated and -untreated participants came as a total surprise.'

Statins are commonly prescribed to reduce risk of developing cardio-metabolic diseases. Besides their target cholesterol-lowering effects, statins also tend to appease patients' systemic inflammation levels. Now, Vieira-Silva and colleagues have identified an additional potential beneficial effect of statin therapy on the gut microbiota. In obese individuals, the prevalence of the dysbiotic Bact2 enterotype was significantly lower in those taking statins (6%) than in their non-treated counterparts (19%) —comparable to levels observed in non-obese participants (4%). These striking observations were validated not only in the independent Flemish Gut Flora Project dataset, but also in an additional MetaCardis subset consisting of 280 patients with cardiovascular diseases.

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Mutations in SARS-CoV-2 offer insights into virus evolution

By analysing virus genomes from over 7,500 people infected with Covid-19, a UCL-led research team has characterised patterns of diversity of SARS-CoV-2 virus genome, offering clues to direct drugs and vaccine targets.

The study, led by the UCL Genetics Institute, identified close to 200 recurrent genetic mutations in the virus, highlighting how it may be adapting and evolving to its human hosts.

Researchers found that a large proportion of the global genetic diversity of SARS-CoV-2 is found in all hardest-hit countries, suggesting extensive global transmission from early on in the epidemic and the absence of single 'Patient Zeroes' in most countries.

The findings, published May 5, 2020 in Infection, Genetics and Evolution, also further establish the virus only emerged recently in late 2019, before quickly spreading across the globe. Scientists analysed the emergence of genomic diversity in SARS-CoV-2, the new coronavirus causing Covid-19, by screening the genomes of over 7,500 viruses from infected patients around the globe. They identified 198 mutations that appear to have independently occurred more than once, which may hold clues to how the virus is adapting.

Co-lead author Professor Francois Balloux (UCL Genetics Institute) said: "All viruses naturally mutate. Mutations in themselves are not a bad thing and there is nothing to suggest SARS-CoV-2 is mutating faster or slower than expected. So far we cannot say whether SARS-CoV-2 is becoming more or less lethal and contagious."

The small genetic changes, or mutations, identified were not evenly distributed across the virus genome. As some parts of the genome had very few mutations, the researchers say those invariant parts of the virus could be better targets for drug and vaccine development.

Eyes send an unexpected signal to the brain

For decades, biology textbooks have stated that eyes communicate with the brain exclusively through one type of signaling pathway. But a new discovery shows that some retinal neurons take a road less traveled.

New research, led by Northwestern University, has found that a subset of retinal neurons sends inhibitory signals to the brain. Before, researchers believed the eye only sends excitatory signals. (Simply put: Excitatory signaling makes neurons to fire more; inhibitory signaling makes neurons to fire less.)

The Northwestern researchers also found that this subset of retinal neurons is involved in subconscious behaviors, such as synchronization of circadian rhythms to light/dark cycles and pupil constriction to intense bright lights. By better understanding how these neurons function, researchers can explore new pathways by which light influences our behavior.

"These inhibitory signals prevent our circadian clock from resetting to dim light and prevent pupil constriction in low light, both of which are adaptive for proper vision and daily function," said Northwestern's Tiffany Schmidt, who led the research.