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The first and only English student magazine for medcial laboratory sciences

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I am writing to express my interest in the publication of the first English student magazine for medical laboratory sciences in the country.
Every moment, the world faces a new challenge. A child is born with a disability, someone is diagnosed with cancer, a new virus infects humans, and many people pass away. Meanwhile, all scientists and healthcare providers are trying their best to save lives by identifying the causes of diseases and finding new approaches to treat or cure patients. We all need to stay updated in this infinite world of science to fulfill our responsibilities as effectively as possible. English, as the international language, is one of the most important tools someone needs to succeed on the way to their goal. Thus, learning it can help us communicate more easily with researchers in all countries, better understand their results, and successfully put forward our own ideas.
Our group made the decision to start a magazine, which might give motivation to all those who need to begin learning English and to those who like writing academically in this language. We would eagerly welcome all students in the fields of medicine, paramedicine, and biology to join us and take part in any part of this publication they would like.
Kind regards

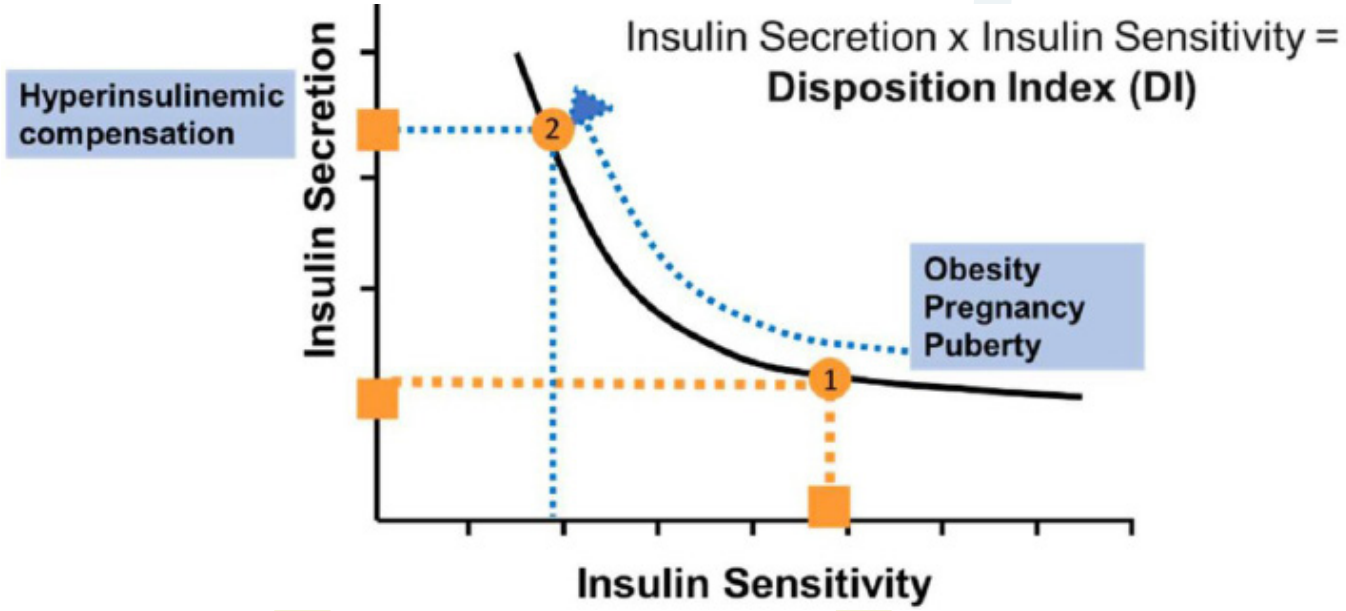
Arefeh Cheraghchi

Insulin Resistance in PCOS

Polycystic ovary syndrome (PCOS) is a complex endocrine disorder that is the most common cause of infertility in women of reproductive age.

PCOS affects 5–18% of women, can be reproductive or metabolic, and the incidence is also increasing worldwide. Three main features are physical or biochemical signs of androgen excess, ovulation disorders, poly-follicular ovarian morphology, and mental conditions that affect life expectancy.

Research that has been done in years showed that obese women with PCOS had significantly elevated basal and post-glucose-load insulin levels, so hepatic insulin resistance is found only in PCOS women who are obese.
Insulin is a hormone with different metabolic and mitogenic effects. Under normal circumstances, as insulin sensitivity decreases, insulin secretion increases to maintain glucose homeostasis. In women with PCOS, insulin secretion is inappropriately low for their degree of insulin resistance, which can be because of pancreatic beta cell dysfunction. This dysfunction can precede glucose intolerance in PCOS.
Insulin resistance plays a role in the pathogenesis of the reproductive characteristic of PCOS, and it contributes to anovulation. In obese women with PCOS who undergo weight loss, a reduction in basal and glucose-stimulated plasma insulin levels is associated with the resumption of ovulatory cycles.



There is no particular test to analyze polycystic ovary syndrome (PCOS). PCOS presents with a series of signs, symptoms, and nonspecific laboratory tests, which make it difficult to reach clear conclusions about it. The specialist may provide you with a conclusion about PCOS by analyzing the indications of increased androgens and irregular menstrual cycles in an individual and checking the sum of androgens within the blood sample and ultrasound of the ovaries. Moreover, in the conclusive determination of polycystic ovary syndrome, other causes of menstrual abnormality, such as thyroid dysfunction and prolactin hormone, ought to be examined.
Insulin resistance plays an essential role in triggering PCOS and/or perpetuating it. Once a woman has been diagnosed with this syndrome and reduced insulin sensitivity, even without clear alterations in glucose tolerance, she should immediately change her lifestyle (hypocaloric diet and physical activity) and start insulin-sensitizing treatment. The current therapeutic approach to women with PCOS is symptomatic and often based on the use of oestroprogestins, drugs that can enhance insulin resistance and alter the lipidic profile.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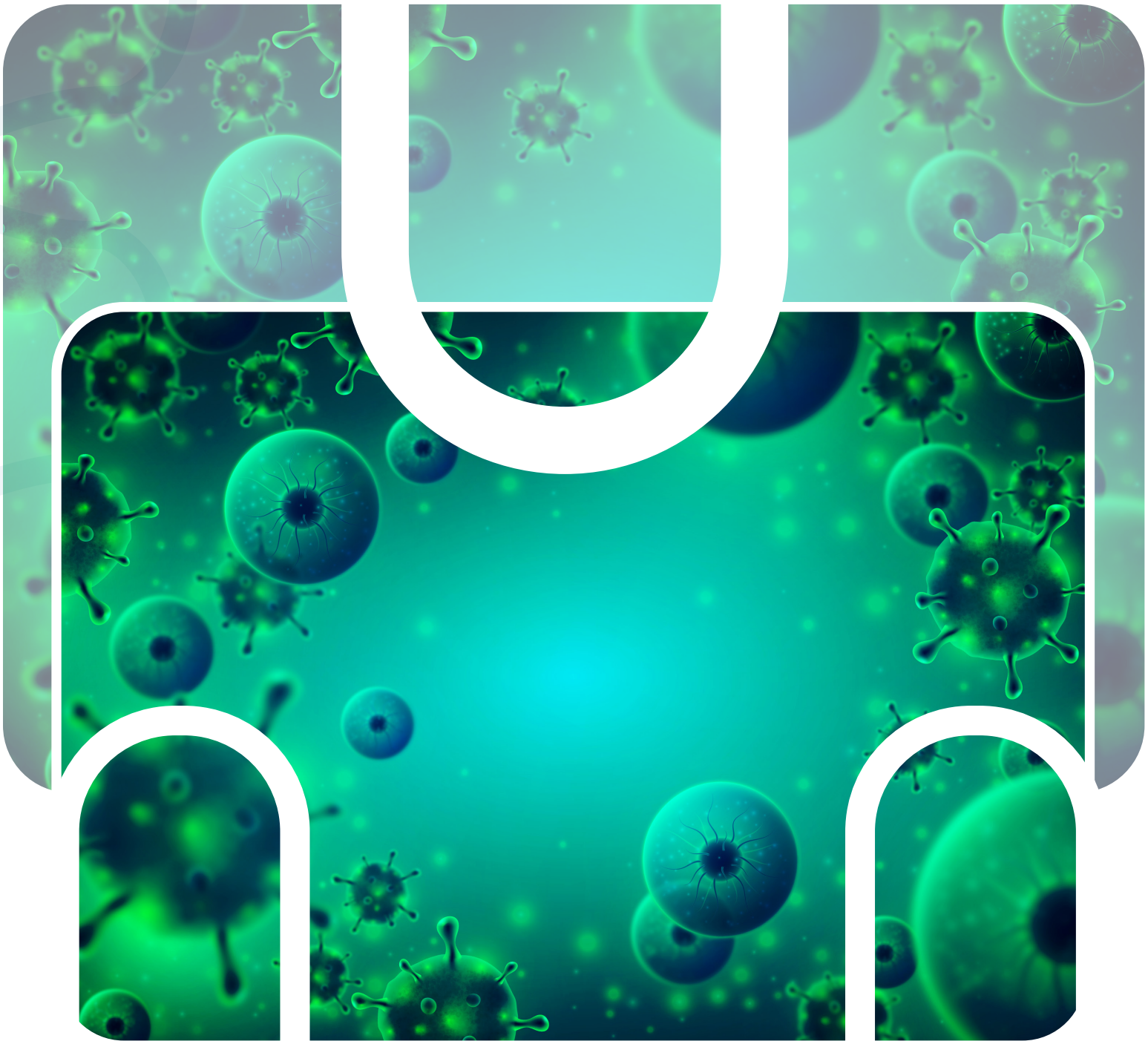

Biosensors Role in Cancer Diagnosis and Treatment

Cancer is one of the most feared diseases in the world. Annually, the American Cancer Society (ACS) reports the estimated numbers of new cancer cases and mortality in the United States. In 2023, 1,958,310 new cancer cases and 609,820 cancer deaths are projected to occur in the United States. The early diagnosis of diverse cancers is crucial for life expectancy, successful disease prognosis, and patient survival. Highly sensitive and accurate methods are urgently required for detecting the ultra-low levels of cancer biomarkers in the early stages of disease. Facilitating early-stage diagnosis and providing an adequate selection of cancer treatment are the properties of the suitable method that lead to the augmentation of patient survival rates.

Available cancer diagnostic tests like immunoassay techniques (e.g., ELISA) do not have enough sensitivity or even the ability to detect markers (proteins) at advanced stages of disease. On the other hand, time-consuming and expensive laboratory analyses in the crucial stage of a patient's disease lead to an increase in the replacement of simple, cheaper, faster, and one-step methods. Making results available to the patient in less than a few minutes will greatly improve the progress of disease monitoring and patient therapy.

Advances in molecular biology have led to a greater understanding of the potential cancer biomarkers that cancer cells secrete. Realizing the point-of-care (POC) diagnosis of cancer requires proper attention to the main challenge of multi-target detection. Arrays of biosensors or sensors, identifying protein signature patterns or multiple DNA mutations, can be used to help screen and guide therapy. Innovative and novel biosensing and sensing strategies will allow cancer detection to be performed faster, cheaper, and more reliably in a decentralized environment.

Over the past several decades, a lot of activities and research have been witnessed in the field of biosensors. Biosensors are small devices that use biochemical molecular detection properties as a basis for selective tests. The main processes involved in every biosensor system are: analyte detection, transduction of signals, and readout. Biosensors suggest helpful opportunities for many decentralized clinical applications, from "alternative site" analysis (e.g., doctor's office), bedside monitoring, emergency screening, or home self-testing.

The use of nanostructures/materials (e.g., semi-conductors and conducting polymer nanowires) incorporates great advancements in the biosensing device. Nanomaterial-based biosensors have excellent advantages, such as minimizing the device, signal enhancement, and increasing the sensitivity of biosensors through signal amplification. On the other hand, by using nanomaterials, multiplex sensing devices like high-density protein assays can be produced. The high surface-to-volume ratio of nanostructures is one of the reasons that led to high sensitivity, which is a desirable property in cancer biomarker diagnosis.

The diagnosis of cancer biomarkers in the early stages is crucial for the treatment, recovery, and survival of patients. Biosensors, as simple, selective, and sensitive diagnostic tools, can detect low-concentrated cancer biomarkers in various human body fluids. By using nanomaterials in the sensing device structure, the sensitivity of the device increases, which has an important role in the detection of cancer biomarkers in the early stages of disease.

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Are We Still Evolving?

Several unanswered questions in human genetic evolution would become tractable if we were able to directly measure evolutionary fitness. According to Charles Darwin's theory, the features of populations or species can change through time if heritable variation and differences in survival rates or reproductive success exist.

Therefore, in response to environmental pressures, the frequency of heritable characteristics will change from one generation to the next, and evolution will take place through natural selection.

Studies of the chimpanzee and human genome's diversions have focused on protein-coding genes. However, examples of amino acid changes among chimpanzees and humans have not been able to elucidate most of the phenotypic diversities between us and our fellow hominoids. King and Wilson (1975) proposed that the vast majority of all genomic changes that happened since the human-chimpanzee ancestor are in non-coding regions. In other words, regulatory changes drove the differences between our species. Non-coding DNA does not code proteins, but it has several other essential functions. There are many different types of non-coding DNA, such as centromeres and satellite DNAs, which are multi-copy tandemly repeated DNA sequences.

The challenge in the post-genomic era has been to distinguish the one human-specific non-coding sequence diversity out of millions that is responsible for the unique aspects of our biology. Jing Liu et al. express known mutations in human-specific loci linked to neurodevelopmental disorders, like autism spectrum disorder (ASD), neurodegenerative diseases, and schizophrenia.

Human accelerated regions (HARs) are short, evolutionarily conserved DNA sequences that have obtained significantly more DNA substitutions than expected since divergence from chimpanzees. Molecular evolutionary and population genetic modeling have indicated that most HARs have variant patterns consistent with positive selection, but some appear to have evolved through GC-biased gene conversion or loss of constraint. HARs can control genes involved in cortical development transcriptionally. HARs can also effectively regulate the amount of some gut microbes since the relative abundance of these microbes has changed rapidly through human evolution. Gut microbiota effects on numerous diseases are inevitable, so their populations may serve as an important mediator to link diseases to human genome evolution.

In addition to non-coding regions, DNA methylome differences discriminate between modern and ancestral humans.

Post-transcriptional mechanisms, including miRNAs, IncRNAs, and circRNAs, can also be involved in evolution. MicroRNAs (miRNAs) are short endogenous single-stranded RNAs (20–24 nts), which can influence species-specific brain modifications significantly by controlling gene expression. Corticospinal motor neuron (CSMN)-enriched miRNAs were recently discovered in the mammalian brain, and it was shown that misexpressing miR-409–3p increased CSMN neurons in vivo and in vitro at the expense of deep-layer neuron development. miRNAs have also been implicated in multiple aspects of primate divergence, including expansion of the germinal zones, neural differentiation, and increased neural progenitor complexity.

In contrast to short miRNAs, long-non-coding (lncRNA) transcripts are more than 200 nt, with an average length of ~3000 nt. The structure of IncRNAs is similar to that of mRNAs and is cytoplasmic. lncRNAs are involved in cortical development, such as neural stem cell maintenance, differentiation, and neural maturation.

Recent studies also indicate an impressive function of circular RNAs (circRNAs) in species evolution. circRNAs are single-stranded RNA molecules consisting of 1–5 exons that form a circle as a result of non-canonical back-splicing events. By comparing their expression systematically in humans, non-human primates, and mice, most of the circRNAs were detected to be human-specific. These observations state that the future study of circRNAs can give precious insights into cortical evolution.

About transcription factor binding sites (TFBSs), it has been found that more than 6,000 of them in the human genome have experienced accelerated evolution in Hominini, apes, and Old-World monkeys. Although each of these TFBSs shows relatively weak signals of accelerated evolution, they are more abundant than HARs. Accelerated evolution in Pol III binding sites may be driven by lineage-specific positive selection, whereas in other TFBSs might be the result of nonadaptive evolutionary forces.

Natural selection occurs in response to environment, and our environment is changing in the modern era, so survival can mean different things for our cells and genome. Also, with our advancing knowledge in science and technology, it cannot be ignored that, as well as natural selection, we may have artificial selection too

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CRISPR-Based Diagnostic Tool for Rapid Detection of COVID-19

Introduction

Coronaviruses are enveloped positive-sense RNA viruses that are commonly associated with acute respiratory infections. In the pandemic of SARS-CoV-2, accurate and rapid diagnosis was needed to provide timely medical support to the infected individual and lead the government agencies to manage the pandemic.

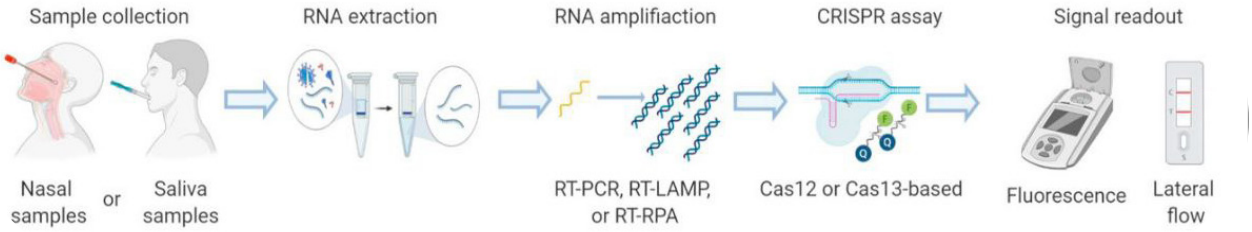
The current diagnostic technique for COVID-19 is based on genomic techniques using sequencing and reverse transcription-quantitative PCR (RT-qPCR)-based methods. In the past few years, the development of clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated (Cas) proteins has opened a new door of research towards molecular diagnostics. The revolutionary application of CRISPR-Cas9 technology in the field of gene editing led to the subsequent applications of other CRISPR-Cas systems for basic sciences and clinical medicine. For the first time in 2016, CRISPR-Cas9-based diagnostics were utilized for Zike virus detection and in 2017 for Staphylococcus aureus detection. In this article, we specifically focused on the recent progress of applying CRISPR-Cas12 and CRISPR-Cas13 for SARS-CoV-2 detection due to the growing interest in developing CRISPR-based diagnostic systems.

Assay

After nasal or saliva sample collection, RNA is needed to be extracted from the raw sample via several methods. After viral RNA isolation, an amplification step such as RT-PCR, RT-LAMP, or RT-RPA is adopted to boost the limit of detection and reduce the detection process time. RT-RPA is the most commonly used method because, compared to LAMP and RPA, it is more powerful, faster, and has a simpler primer design. After the CRISPR assay, we use fluorescence or colorimetric systems for the signal readout.

The Cas12 protein is one of the CRISPR family members that can be programmed with a CRISPR RNA (crRNA) to specifically bind to complementary single- and double-stranded DNA targets. But it doesn't need trans-activating crRNA. After activation by a target DNA, Cas12 can cleave the surrounding DNA or RNA in a process called trans-cleavage. CRISPR-Cas12a is often used for diagnostic purposes. In this process, regardless of whether they are DNA or RNA, they are targeted by CRISPR-Cas12a. It also cleaves reporters, which we added to the solution purposefully. The reporters are usually fluorophore quencher (FQ)-labeled single-stranded DNA or fluorophore biotin (FB)-labeled single-stranded DNA. After the trans-cleavage of the non-targeted ssDNA reporter, the signal readout can be performed as a fluorescence-based reaction or a single-plex colorimetric lateral flow reaction. Fluorescence readers are expensive, bulky, and not suitable for proof-of-concept (POC) applications. On the other hand, colorimetric sensors are suitable for POC applications since they are user-friendly, cost-effective, and accessible.

The Cas13 protein is another member of the CRISPR family, and unlike other CRISPR proteins, it targets



RNAs instead of DNA. Cas13 has four different subtypes and is implemented in most Cas13-based diagnostic programs. Like Cas12, Cas13 exhibits trans-cleavage activity when activated by an ssRNA sequence that is complementary to its crRNA spacer. However, activated Cas13 cleaves all surrounding ssRNAs instead of DNA. After amplification, additional transcription is required to convert DNA amplicons to RNA since RNA targets only activate Cas13a proteins.

Future

CRISPR technology presents an attractive opportunity to facilitate superior alternatives or improvements by providing a rapid, in-field, sensitive, and specific assay for the detection of SARS-CoV-2. So far, most CRISPR-Cas systems use Cas12 or Cas13 proteins as a CRISPR effector in their assays. The use of other types of CRISPR proteins can increase the targeting range and provide new signal readout methods. While CRISPR-based assays have shown great potential for cost-effective, sensitive, and specific nucleic acid detection over the past few years, the field is still in its infancy. For this purpose, the following challenges and issues should be addressed:

1. Integrated sample preparation according to WHO guidelines: Sample preparation is one of the most important parts of CRISPR-based diagnostic methods. This process increases the complexity of the CRISPR-based assay. It is beneficial to create a diagnostic test that combines all steps with only one action required by the user. Fortunately, several studies have previously investigated SARS-CoV-2 sample preparation to speed up and simplify the process.
2. Multiplexing: Many applications require the detection of more than one target in one reaction, which is called multiplexing. Multiplex detection of a single sample offers several advantages, such as fast turnaround time and low sample consumption. However, due to interactions between detection molecules and different analytes and possible cross-reactions, multiplex detection is challenging. One of the major issues with Cas12 and Cas13 systems for multiplex assays is the non-specific collateral cleavage of all ssDNA and ssRNA sequences, potentially destroying other targets.
3. Improving CRISPR assay performance: Nanomaterials and artificial intelligence were introduced to enhance CRISPR assay performance with respect to signal enhancement and classification. For example, Bao et al. developed a simple visual detection system with quantum dots as an ultrabright indicator and a CRISPR-Cas12a assay for isothermal viral DNA target detection via AI. They avoided large and complex measuring instruments and used a handheld flashlight to distinguish positive and negative samples.

Conclusions

Former detection methods have many limitations, such as signal-off detection format, low signal-to-noise ratio, requirements of high hybridization temperature, lack of probe universality, and low discrimination of color changes. These deficiencies increase our need for more efficient methods. Here, we presented a new colorimetric and fluorometric gene detection platform that is based on the CRISPR/Cas12a/13a system and has achieved several critical advances compared to the existing methods. There is hope that CRISPR-based methods will be used in laboratory diagnosis.

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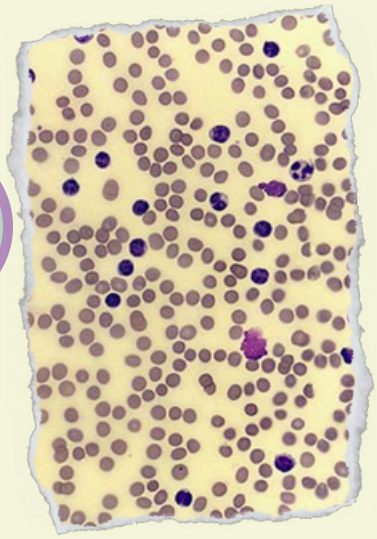
CLL
(Chronic Lymphocytic Leukeamia)

1 WHAT IS CHRONIC LYMPHOCYTIC LEUKAEMIA (CLL)?

A monoclonal disorder known as chronic lymphocytic leukemia (CLL) is characterized by an accumulation and progressive proliferation of mature lymphocytes that are functionally ineffective. The histologic sample in the image portrays the appearance of these lymphocytes. The most prevalent type of leukemia in adult Western nations is CLL. Some patients die within several years of diagnosis, usually due to complications from CLL, but most patients survive for at least five years.



2 CAUSES:

There is no known cause of CLL. There is no proof that exposure to chemotherapy, radiation, or chemicals raises one's risk of developing CLL. However, a person's chance of having CLL may be increased by the factors like family history, age, gender, race, Agent Orange, and monoclonal B-cell lymphocytosis.

3 SYMPTOMS:

- Fatigue
- Shortness of breath
- Bruising or bleeding more easily than usual
- Unintentional weight loss
- Night sweats
- Fever
- Swelling of the lymph nodes (glands) in your neck, armpit or groin

4 DIAGNOSIS:

Blood tests

Bone marrow aspiration and/or biopsy

Tests:

Flow cytometry and immunohistochemistry

Cytogenetics

Fluorescent in situ hybridization (FISH)

5 TREATMENT:

Chemotherapy

Targeted therapies, such as monoclonal antibodies, which help your immune system fight the cancer

A combination of these treatments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Gemtuzumab Ozogamicin in Acute Myeloid Leukemia

CD33 has different expression among blasts in nearly all patients diagnosed with acute myeloid leukemia (AML). The therapeutic targeting of CD33 has primarily centered around gemtuzumab ozogamicin (GO; Mylotarg), an antibody-drug conjugate that delivers a DNA-damaging calicheamicin derivative. While GO has shown optimal efficacy in cases of acute promyelocytic leukemia, it also induces remissions in other forms of AML and received approval in the United States back in 2000. However, due to a comprehensive follow-up study demonstrating no improvement in overall survival rates and increased instances of early deaths, the drug manufacturer voluntarily retracted their US New Drug Application for GO in 2010. More recently, a meta-analysis incorporating data from numerous trials indicated improved survival outcomes for adults with favorable- or intermediate-risk cytogenetics when treated with GO concurrently to intensive induction chemotherapy, though this benefit was not evident for those categorized under adverse-risk AML. Consequently, regulatory agencies have found it necessary to reassess GO. The reactions towards this particular substance are varied and in order to accurately predict its biological effects, reliable indicators of response are required. Alongside evaluating the risk of changes in chromosomes, it is believed that the activity of ATP-binding cassette transporters and potentially the presence of CD33 on AML blasts could offer insight into an individual's reaction to GO. However, there is a notable absence in established clinical trials and rigorous validation processes for these potential markers. Thus, further verification is necessary to establish this claim with certainty. Of significance are the markers that determine the sensitivity of AML cells towards calicheamicin. Sadly, there is a lack of accessible means to conduct useful assays for these markers. Although promising CD33-targeted medications have emerged as novel approaches to potentially overcome some of GO's limitations, whether these drugs will be more effective in individuals who benefit from GO treatment or if they can improve outcomes in patients who do not experience any advantages through GO therapy remains uncertain. Furthermore, determining what level of supportive care will be essential for their safe administration currently remains unknown. Conventional chemotherapy and hematopoietic cell transplants have provided some benefits to patients with acute myeloid leukemia (AML), although the progress has been modest.

Consequently, only cytogenetic risk should presently be employed as a criterion for selecting patients who will receive GO in combination with chemotherapy as their initial treatment. The administration of GO other than primary therapy combined with AML chemotherapy, such as its use in APL after the failure of ATRA and ATO treatments, lacks conclusive evidence and should therefore be viewed as experimental. Such utilization is best carried out within the framework of a clinical trial setting. Patients who suffer from other hematologic disorders that are characterized by the presence of CD33-positive cells, such as myelodysplastic syndrome, myeloproliferative neoplasms, subsets of lymphoblastic leukemias and macrophage activation syndrome, may also find potential benefits in GO therapy. However, it is important to note that these benefits have not been thoroughly studied or adequately proven. While there might be newer anti-CD33 therapies on the horizon that could potentially surpass GO in terms of efficacy and safety, none have been confirmed as superior to GO thus far. Scientists anticipate that upcoming clinical trials involving novel therapeutics targeting CD33 will shed light on whether these drugs can complement or replace GO. To be successful, it is crucial to acknowledge the significant variation in drug effectiveness among patients with acute myeloid leukemia (AML). Additionally, special attention should be given to any toxicity specific to normal tissues caused by these targeted drugs since this could limit their usage. The regulatory history and challenges associated with GO serve as a valuable reminder of the intricate nature of drug development.

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Diabetic Wounds: From Recognition To Treatment

With the advancement of civilization and the enhancement of living standards, diabetes affects over 500 million individuals worldwide. Over 10% of individuals with diabetes will experience diabetic wounds, and 80% of these wounds will recur, so development of novel treatments for diabetic wounds is crucial.

Furthermore, people with diabetes experience severe discomfort when wounds take a long time to heal. Nonetheless, one of the hardest problems facing the medical industry today is creating novel strategies to facilitate diabetic wound healing.

Diabetes-related skin ulcers appear as a painful sore in which the skin layers and subcutaneous tissue are disintegrated. These ulcerations are usually found on lower limbs, specially foot. Diabetic foot ulcer (DFU) typically results in significant damage to the ankle and foot`s soft tissues, bones, and joints. The majority of DFUs are caused by chronic wound healing impairment, which can result in bacterial infection. If left untreated, this infection can cause tissue loss and even lower limb amputation. Ulcerated skin is red and swollen like simple wounds, but it also generates pus or exudate and smells bad.

Thus, it is imperative to create new, efficient treatments to get over the difficulties associated with treating wounds in clinical settings. Thus far, there has been an increasing interest in living microbiological remedies using cell, bacteria, algae, etc. Specific-functioning bacteria and algae could be chosen based on the needs of treating a given illness.

Motivated by the inherent ability of algae to produce oxygen and the competitive advantage that beneficial bacteria possess over other microbes, scientists developed a living microecological hydrogel (LMH) featuring functionalized Bacillus subtilis and Chlorella encapsulation to achieve anti-infection and constant oxygen delivery, thereby fostering chronic wound healing. The hydrogel`s ability to swiftly and firmly adhere to the wound bed while maintaining a low temperature was made possible by the combination of thermosensitive Pluronic F-127 and wet-adhesive polydopamine in the LMH.

However, since the presence of pathogenic bacteria in the wound bed would prevent these algae from proliferating, it is typically difficult to employ them directly as oxygen supplies for wounds. On the other hand, the prevailing bacteria in nature have the ability to completely eliminate the colonization of harmful bacteria by multiplying quickly in order to take over the available space and by secreting a large number of antimicrobial compounds to increase their competitive advantage.

The Pluronic F-127 hydrogel was treated with the mussel-bioinspired polydopamine (PDA) to improve the anchoring strength between the hydrogel and the wound bed. While Chlorella and B. subtilis slightly prolonged the gelling time, PDA addition may have shortened Pluronic F-127`s this time.

The outcome showed that the thermosensitive, wet-ad hesive hydrogel containing encapsulated Chlorella and B. subtilis was useful for treating a variety of diseases and showed promise in treating difficult-to-heal wounds. Hydrogel`s structural integrity keeps getting better. Numerous cutting-edge hydrogels are made of unique polymers with distinct biologic functions as well as bioactive ingredients. There are now many different temperature-controlled, light-sensitive, and skin-friendly hydrogels available for treatment. In a clinical setting, a recently developed shape-programmable Hierarchical Porous Membrane Composite System has sped up the healing of diabetic wounds. Future developments in adaptive wound therapies can be expected.

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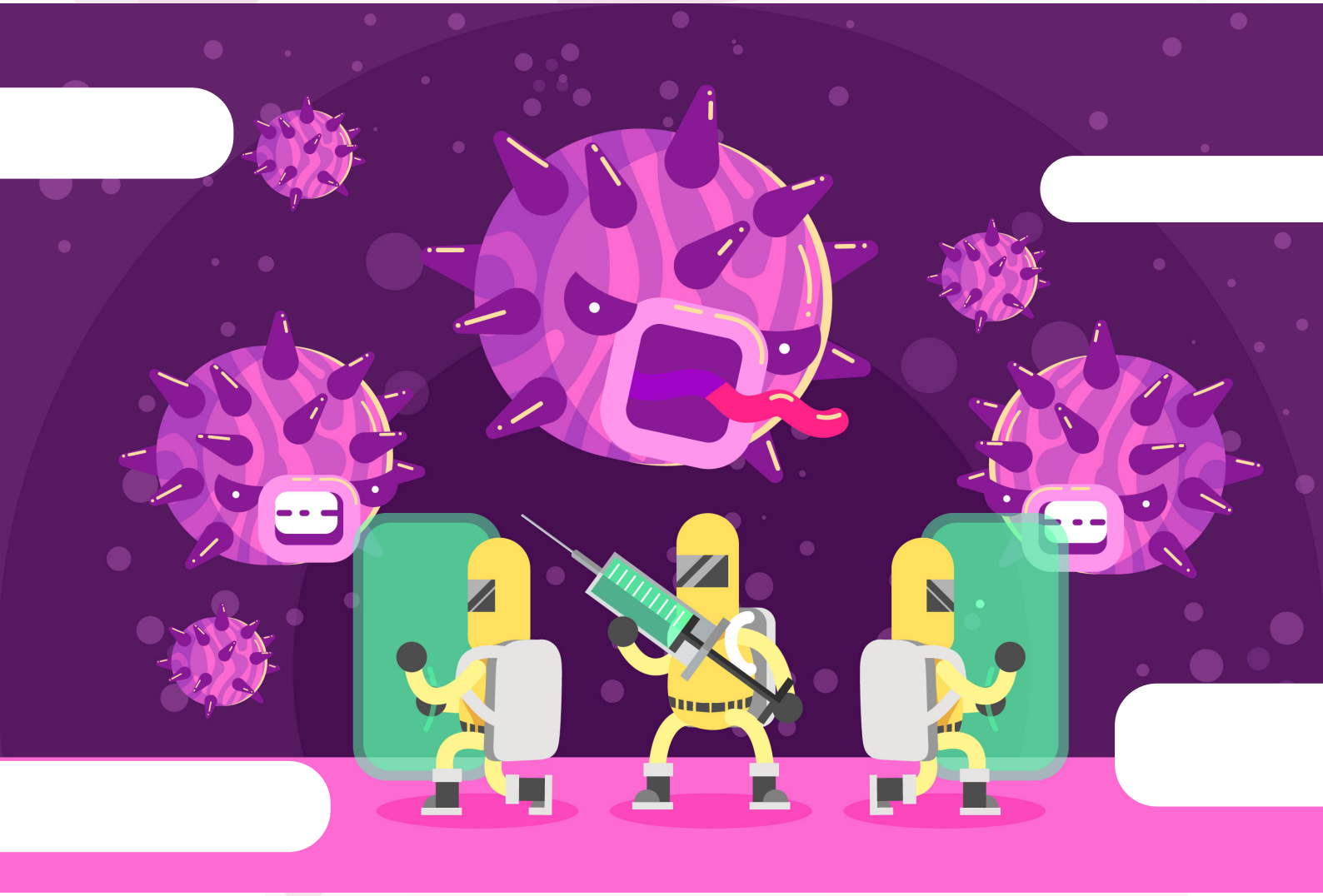
Which Virus Will Cause the Next Pandemic?



When we hear the word ‘pandemic’, we immediately think of COVID-19 and the loved ones we have lost. However, nowadays, the coronavirus is no longer a significant concern for us, and it is almost forgotten due to vaccination and implemented measures. But which virus could cause the next pandemic? Can we anticipate it? A pandemic is a disease that has spread across a large region, for instance, multiple continents. Examples of past pandemics include the H1N1 influenza pandemic in 2009 and the COVID-19 pandemic caused by the SARS-CoV-2 virus, which began in late 2019 and continued into the current time.

According to articles published in recent years and the World Health Organization, the biggest risk comes from pathogens that circulate in animals, making the jump into humans. As COVID-19 has shown, once someone is infected in one part of the world, trade and travel will rapidly carry the virus nearly everywhere else. Assessing which pathogens are most likely to make the jump enables us to get prepared with the help of vaccines and treatments.

The WHO has also identified several priority diseases with pandemic potential, including Crimean-Congo haemorrhagic fever, Ebola, Marburg, Lassa fever, MERS, SARS, Nipah virus infection, and Zika.

As a result, the next pandemic will likely result from a zoonotic event caused by a virus introduced into humans by mammals, including bats (which harbor the highest proportion of zoonotic viruses among mammals), and rodents, or avian species. It is also conceivable that the next pandemic will be caused by another zoonotic virus, such as yellow fever or the chikungunya virus. However, scientists think that a pandemic disease will be transmitted among humans via the air.

To prepare for future pandemics, the international research community needs to continue and further strengthen research efforts in various areas, such as cataloging the landscape and animal reservoirs of (human-infecting) viruses through surveillance and metagenomics, the development of animal models for viruses that may cause pandemics, basic research to better understand the molecular virology of such viruses, early-stage vaccine development and testing in animal models, and the development of broad antivirals as a first line of defense.

The US National Institute of Allergy and Infectious Diseases has suggested that prototype pathogens (selected from virus families that may cause pandemics) be selected for basic research and early-stage development of countermeasures. With reasonable resources and advanced technologies, the global community could be better prepared for future pandemics.

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A New Blood-Based Tool Rapidly Tests for TB in Children

A novel diagnostic tool for tuberculosis (TB) has been developed by an international research consortium, led by Ludwig-Maximilians-Universität München, to address the issue of misdiagnosis or late diagnosis, which is a major contributor to high mortality rates in children under five years old. The tool is based on measuring the activity of three specific genes in capillary blood and can provide a transcriptomic signature for TB diagnosis. The tool has the advantage of allowing blood samples to be conveniently taken from the fingertip, with results available in just over an hour. In a study involving 975 children suspected of having TB, the new tool identified almost 60 percent of children with TB and had a specificity of 90 percent compared to detection through bacterial cultures. Further adjustments to the signature calculation for children are expected to enhance the accuracy of the test.

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Further Test Administration Unchains Researchers from Their Lab Seat

All of your tube rack readers and scanners can be immediately connected to your LAN using DP5 Network, allowing you to operate them from a PC in your office or another location in the building. Because of its adaptability, you can simply place your reader or scanner next to freezers or compound storage and observe the results on your phone or desktop.

DP5 Network is quick and secure; it permits you to send out tube positions and barcodes in more formats than anybody else: JSON, XLS, CSV, Content, PDF, PNG, and Python, and send the information in an email to a colleague or your desktop PC.

While any camera-based reader can be upgraded to run DP5 Standard software, only Ziath Data Paq™ Express and DataPaq™ Mirage 2D-barcode rack readers can be currently supplied with LAN adaptors and RJ45 connectors to run the new DP5 Network software.

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