Department of Pharmacy

BRAC UNIVERSITY
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PHARMA HIGHLIGHTS

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The Drug That's Best for Both Kidney Failure and Arrhythmia Patients

Kidney failure, also referred to as end-stage renal disease (ESRD), is the last stage of chronic kidney disease. In other words, the kidneys have stopped working well enough for the person to survive without dialysis or a kidney transplant.

Arrhythmia is a cardiac condition characterized by irregular heartbeats. Patients with the most common type of arrhythmia, atrial fibrillation (AF) are susceptible to the risk of blood clots and stroke, and blood thinning agents can significantly reduce this risk. However, selecting the right blood thinning agent could be quite challenging. Blood thinning agents like warfarin may prove to be quite problematic when prescribed to patients with both AF and kidney failure, as they pose a risk of bleeding, even in patients without cardiac arrhythmia.

Patients with kidney failure are subjected to many treatment-related adverse effects and physicians need to be very careful while prescribing medicines. Thus, finding a safe blood thinning treatment is essential for the population of people with both AF and kidney failure. A study conducted at University of Michigan first demonstrated that a drug known as apixaban (a blood-thinning agent) was safer than warfarin for patients having both AF and kidney failure. Among kidney failure patients with AF on dialysis, use of apixaban may be associated with a lower risk of major bleeding compared with warfarin, and are also associated with reductions in thromboembolic and mortality risk. One of the researchers, Konstantinos Siontis, MD stated "We found patients on apixaban had a significantly lower risk of major bleeding [30 percent less than warfarin] with no difference in stroke, which is what we try to prevent by prescribing these anticoagulants." FDA approved Apixaban in 2013 to lessen the risk of systemic embolism and stroke in patients with AF.

Source: National Kidney Foundation, Bristol-Myers Squibb, Michigan

Genetic Mutation Provides Protection from Malaria

An uncommon genetic mutation that offers protection from malaria can be found in about a third of the people of African descent. Malaria is transmitted by Anopheles mosquitoes, containing the parasite, Plasmodium that infects liver cells and then moves on to invading and destroying blood cells. Common symptoms of malaria include illnesses resembling the flu, fever and chills. In 2016, over 400,000 deaths were caused by malaria from an estimated 200+ million cases of malaria infection.

A new genetic mutation currently under investigation, called PIEZO1, originally assumed to be a sporadic occurrence, has been found to be more common than previously thought to be, especially among populations living closely with the malaria-spreading Anopheles mosquitoes. In non-African populations, this mutation is rare.

Under normal function, PIEZO1 codes for a pressure-sensing protein, which is vital for the function and development of the heart; its deletion results in an increased blood pressure. This mutation triggers the dehydration of RBCs via a process known as hereditary xerocytosis. A consequence of this mutation, is the development of sickle cell anemia.

Having tested mutated PIEZO1 effects on a mouse model, researchers discovered that the dehydrated blood cells are harder for the malaria parasites to invade and infect; and leads to cerebral malaria, a problematic and severe neurological complication of malaria.

Further plans are to conduct a larger-scale genomic association study to confirm PIEZO1's role in resisting malaria, and seek associations in humans.

Source: Centers for Disease Control and Prevention, MedlinePlus.gov, Scripps Research Institute

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Hybrid Imaging of the Heart Predicts Heart Attack Risk

Coronary artery disease (CAD) is the worldwide leading cause of death for men and women worldwide. This condition arises when the arteries that supply blood to the heart become hardened and narrowed and as a result, blood supply becomes depleted. When the blood supply is completely cut off, a person has a heart attack. Studies from the University Hospital Zurich in Switzerland have shown that a hybrid diagnostic approach with two different types of imaging may be the most accurate way to predict which patients are at the highest risk for developing CADs. This diagnostic approach is less invasive than the current test that is used, invasive coronary angiography (ICA), and can also provide a measurement of how much blood perfusion is occurring when the coronary arteries are blocked. Hybrid diagnostic testing provides data on both stenosis and perfusion which could in turn predict the risk of heart attack in the long-term, helping doctors make treatment plans.

This new study was examined over a seven year time period and observed 428 patients. All patients were subjected to cardiac hybrid imaging. At the conclusion of the study, there were 160 adverse cardiac events (ACE), including 45 deaths. Patients whose diagnostic results presented signs of developing CAD in the context of both stenosis and perfusion were five times more likely to have an ACE than those who had normal results. The new study documented the relevance and importance of comprehensive cardiac assessment provided by hybrid imaging in accurate CAD prognosis.

Source: MedlinePlus, Radiological Society of North America

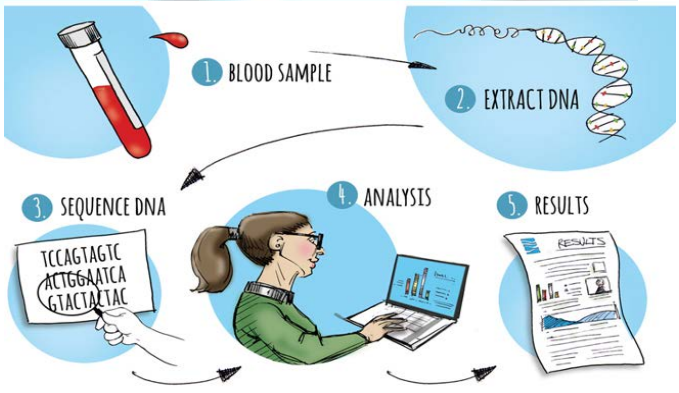
TRAF7 Mutation Responsible for Mysterious Disorder

Scientists from the Baylor College of Medicine, have identified that a mysterious multisystem developmental disorder that affected seven patients, may be related to mutations in a gene called TRAF7 (TNF receptor association factor 7). TRAF7 and other TRAF genes are involved in multiple biological processes, like embryonic development, tissue homeostasis, and immune regulation, which could explain the multisystem aspect of the disease. This developmental disorder is characterized by developmental delays and congenital heart defects with limb anomalies as a “key unifying feature.”

Scientists used whole exome sequencing to try to identify the possible genetic cause of the disease. They first studied the genomes of each of the seven patients. Their sequencing data exhibited that only the TRAF7 gene displayed mutations of four different kinds.

Further analysis revealed that TRAF7 mutations affected the activity of the ERK1/2 cellular pathway in a negative manner. This drove the scientists to further consider that there was a connection between the mutations and the corresponding developmental delays experienced by the patients.

"Finding gene mutations in a particular gene does not indicate that it is causing the disease,” explained corresponding author Dr. Xia Wang. “One way to show that the changes we found in gene TRAF7 could be causing the disease is to determine whether the mutations can affect the relevant signaling pathways associated with the gene.” Interestingly enough, the TRAF7 mutations associated with this study are also seen in cancer tissue, making it one of many genes associated with both cancer and human developmental disorders. Further studies are required to determine whether a link exits between the two groups of diseases.



Source: Baylor College of Medicine, Journal of Cellular Physiology.