

August | Olympians' Performance & Heart Insights

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Distinct functional and molecular profiles between physiological and pathological atrial enlargement offer potential new therapeutic opportunities for atrial fibrillation

Yi Ching Chen, Seka Wijekoon, Aya Matsumoto, Jiating Luo, Helen Kiriazis, Emma Masterman, Gunes Yildiz, Jonathon Cross, Adam C. Parslow, Roger Chooi, Junichi Sadoshima, David W. Greening, Kate L. Weeks and Julie R. McMullen

Physiological model

- Cluster 220 – down in IGF1R vs Ntg
- Cluster 221 – up in IGF1R vs Ntg

Pathological model

- Cluster 1747 – up in DCM-dsMIX vs Ntg
- Cluster 1748 – down in DCM-dsMIX vs Ntg

Unlocking Peak Performance: Heart Health Insights

The first issue of the Implen NanoPhotometer® Journal Club is highlighting groundbreaking research by Chen et al. in the Journal of Clinical Science, poised to be a game-changer for athletes, particularly those aiming for gold at the 2024 Paris Olympics.

Elite athletes often experience their hearts growing stronger and more efficient with every stroke, lap, or lift. This phenomenon, known as physiological enlargement, typically boosts performance.

Consider the incredible performance of Team USA, who ended swimming at the Paris Olympics on Sunday with a standout relay, winning gold and breaking the world record in the women's 4x100-meter medley relay at Paris La Défense Arena. Their intense training and remarkable endurance likely led to healthy heart enlargement, enhancing their ability to perform at such high levels.

But there's a flip side. The same study also delves into a dangerous type of heart enlargement caused by genetic issues, which can lead to serious conditions like atrial fibrillation (AF). By understanding the differences between healthy and harmful heart changes, athletes and their medical teams can better safeguard their health while pushing the limits of their performance.

As the world's top athletes prepare for the Paris Olympics, this research highlights the importance of distinguishing between beneficial adaptations and potential risks. With this knowledge, doctors can provide tailored care to ensure athletes remain healthy and perform at their peak.

[Learn more](#)



A Pilot Study of miRNA Expression Profile as a Liquid Biopsy for Full-Marathon Participants

Tomoaki Kuji, Takehito Sugawara, Shin-ichiro Fujita, Seiko Ono, Yasushi Kawakami and Kazuhiro Takekoshi

Unlocking Marathon Potential: How Tiny Molecules in Blood and Urine Reveal the Secrets of Athletic Performance

Next issue is celebrating the close of the games by diving into a pilot study by Kuji et al., which explores how specific microRNAs (miRNAs) in urine and blood can indicate physical stress in marathon runners. This research involved 26 male participants, with samples taken at four key times: before the marathon, immediately after, two hours later, and the day after. The objective was to observe how miRNA levels shifted over time and identify potential biomarkers for monitoring stress during intense exercise.

This study revealed significant time-dependent changes in miRNA expression profiles in both urine and plasma. Certain miRNAs emerged as strong candidates for tracking physical stress. Their levels increased in both urine and blood after the marathon, suggesting they could be vital for monitoring the body's response to the rigors of long-distance running. Interestingly, while blood samples showed more consistent changes over time, urine samples uncovered unique miRNAs that could also serve as valuable biomarkers. This dual approach offers a more complete understanding of how the body responds to physical exertion.

These findings highlight the potential of miRNAs as non-invasive biomarkers for monitoring physical stress and enhancing athletic performance, paving the way for future research in sports physiology to develop new tools for optimizing athlete health and performance.

The NanoPhotometer® was used in this study to determine RNA purity.

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August | DNA & Dragonflies

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Analysis of Purity and Concentration of DNA Isolated in Dragonfly (*Onychogomphus forcipatus*)

Alfi Sophian, La Ode Nasir

Sample	Concentration (ng/ul)	Purity	
		A260/280	A260/230
1	65.05	1.851	0.822
2	65.05	1.864	0.821
3	65.45	1.892	0.819
4	66.00	1.880	0.821
5	66.65	1.859	0.818
6	67.60	1.875	0.816
7	68.20	1.899	0.812
8	67.95	1.844	0.776
9	68.00	1.866	0.778
10	68.15	1.906	0.814
11	68.10	1.929	0.814
12	68.40	1.831	0.760
13	68.95	1.834	0.760
14	68.16	1.861	0.763



Analyzing DNA Purity and Concentration in Dragonflies: Challenges and Insights During Dragonfly Season

As dragonfly season brings these fascinating insects into focus, this week's Implen NanoPhotometer Journal Club is highlighting the research by Sophian et. al. examining the purity and concentration of DNA isolated from the dragonfly species *Onychogomphus forcipatus*. This study is significant for molecular biology, especially in species identification, where high-quality DNA is crucial. Isolating DNA from dragonflies presents unique challenges due to their small, easily desiccated bodies, making it difficult to obtain sufficient and uncontaminated DNA samples.

The research utilized a combination of conventional DNA extraction techniques and robotic systems to enhance efficiency and accuracy. The DNA extraction involved critical steps such as cell lysis, DNA separation from other cellular components, and purification. The results showed that DNA concentration ranged within an acceptable range, with good overall quality. The DNA purity was assessed using two key ratios: A260/A280, indicating acceptable purity, and A260/A230, which fell below the optimal range.

The study concluded that while the DNA concentration and A260/A280 purity ratios were satisfactory, the A260/A230 ratio suggested possible contamination or incomplete extraction. The findings indicate that while the extraction technique was largely successful, further refinement is needed to improve purity, particularly regarding the A260/A230 ratio, providing valuable insights for future molecular biology research.

The NanoPhotometer® was used in this work to assess isolated DNA quantity and quality.

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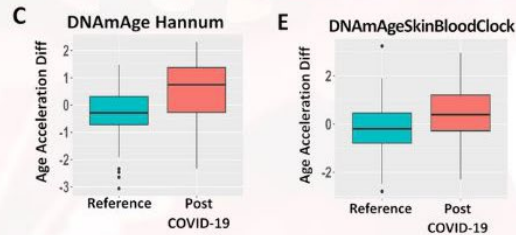
August | COVID 19 & Accelerated Aging

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Epigenetic patterns, accelerated biological aging, and enhanced epigenetic drift detected 6 months following COVID-19 infection: insights from a genome-wide DNA methylation study

Calzari Luciano, Dragani Davide Fernando, Gentilini Davide



COVID-19's Lasting Impact: New Study Reveals How the Virus Alters Our DNA

Our last August issue is spotlighting a groundbreaking study published this month by Luciano et. al. in the journal of Clinical Epigenetics that investigated the long-term epigenetic effects of COVID-19. This research explored how SARS-CoV-2 infection may accelerate biological aging and cause significant changes in DNA methylation patterns six months post-infection. These changes, detected through genome-wide DNA methylation analysis, were primarily observed in genes linked to glutamate metabolism, which may be associated with long-COVID symptoms such as fatigue and neurological issues.

This study involved analyzing blood samples from 96 individuals who had recovered from COVID-19, comparing their DNA methylation profiles to those of 191 healthy controls. 42 CpG sites were identified to have significant methylation differences, particularly in genes related to crucial biological pathways, including those governing insulin resistance, immune response, and vascular health. The findings suggest that COVID-19 may leave lasting epigenetic marks that could contribute to ongoing health issues in long-COVID patients.

The Implen NanoPhotometer® played a role in this research by ensuring the accuracy and quality of the DNA samples extracted from peripheral blood of the patients.

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