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established automated tool.

MATERIALS & METHODS: A dataset consisting of 10 complete genomes of dengue virus type 2 from the NextSeq 550 (Illumina) sequencing platform system was processed through in-house and GDV pipelines. The in-house data analysis using Ubuntu, a Linux-based operating system, involved from pre-processing the raw data file to variant calling. Whilst the GDV, a web-based, fully automated platform designed specifically for viral NGS data analysis, involved uploading the raw data to the web. We then compared in-house data, including quality checks (FastQC), read alignment (BWA), variant calling (GATK), and manual review with GDV's results.

RESULTS: The comparison showed over 98% agreement for both methods, which accurately identify viral genomes. The discrepancies, which mainly consisted of indels in repetitive regions, were resolved by examining the alignment details and coverage map.

CONCLUSION: Ubuntu-based pipelines offer full control, transparency, and scalability, making them well-suited for complex or custom analysis; however, they require expertise in bioinformatics and the use of sophisticated computational tools. Genome Detective, on the other hand, provides rapid, standardized viral NGS analysis with minimal effort which is ideal for routine surveillance or validation of a much complex analysis platform, though it sacrifices flexibility, requires data upload to external servers and extra cost for purchasing the tool.

KEYWORDS: Validation, Next Generation Sequencing, Bioinformatics, Genome Detective Virus Tool, In-house analysis

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PERFORMING HLA TYPING FROM WHOLE-EXOME SEQUENCING DATA: CAN IT MATCH CONVENTIONAL METHODS?

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INTRODUCTION: Human leukocyte antigen (HLA) typing plays a crucial role in transplantation and disease association studies. With the growing availability of next-generation sequencing data, HLA typing from whole-exome sequencing (WES) is gaining attention. However, as WES is not specifically optimised for HLA regions, its accuracy compared to conventional methods requires validation.

OBJECTIVE(S): To assess the concordance of 2-digit HLA allele assignments obtained from WES using the Illumina DRAGEN pipeline with results from standard HLA typing methods.

MATERIALS & METHODS: WES was performed on 22 samples using the SureSelect Human All Exon V6 capture kit and sequenced on the Illumina HiSeq platform. HLA types were called using the DRAGEN Enrichment Pipeline. The 2-digit HLA results for loci HLA-A, -B, -C, -DRB1, and -DQB1 were compared with results previously obtained using PCR-based sequence-specific oligonucleotide (SSO) and sequence-specific primer (SSP) methods.

RESULTS: HLA typing from WES using the DRAGEN pipeline demonstrated 100% concordance at the 2-digit resolution across all five loci when compared to conventional SSO and SSP results. The mean number of reads supporting HLA calling was 2,056, 1,674, 1,560, 996, and 1,046 for the HLA-A, -B, -C, -DRB1, and -DQB1 loci, respectively.

CONCLUSION: DRAGEN-based HLA typing from WES shows excellent concordance with conventional typing methods at the 2-digit resolution, supporting its potential utility as a reliable approach for research applications. Future work should aim to assess concordance at the 4-digit resolution.

KEYWORDS: HLA Typing, Whole-Exome Sequencing, DRAGEN Pipeline, Concordance Study

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ORAL BACTERIA COMPOSITION BETWEEN HEALTHY AND MILD COGNITIVE IMPAIRMENT GERIATRIC PATIENTS USING NEXT-GENERATION SEQUENCING

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INTRODUCTION: Disruptions in the oral microbiome, particularly bacterial communities, have been linked to systemic inflammation and neurodegenerative diseases, including mild cognitive impairment (MCI). However, the oral bacterial profile

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of elderly individuals with MCI remains underexplored.

OBJECTIVES: This study aimed to compare the oral bacterial composition of healthy and MCI elderly individuals using next-generation sequencing.

MATERIALS & METHODS: A total of 17 geriatric participants were recruited, including healthy ($n = 8$), MCI ($n = 8$), and one with overt dementia. Dental plaque ($n = 11$) and saliva ($n = 6$) were collected. DNA extraction was followed by 16S rRNA sequencing targeting the V3–V4 region using the Illumina platform. Bioinformatic analysis assessed alpha and beta diversity and taxonomic composition of oral bacteria.

RESULTS: Alpha diversity (Shannon, Chao1, and ACE indices) was slightly higher in the MCI group, though not statistically significant. Beta diversity analysis showed overlapping bacterial communities, with no significant separation between groups based on PERMANOVA ($R^2 = 0.124$, $p = 0.515$). Most bacterial genera did not show large or consistent differences between groups. However, *Streptococcus*, *Treponema*, *Prevotella_7*, and *Neisseria* appeared more abundant in the healthy group, while *Veillonella*, *Fusobacterium*, *Leptotrichia*, and *Porphyromonas* were more abundant in the MCI group, although inter-individual variability was observed.

CONCLUSION: Preliminary findings suggest subtle differences in oral bacterial diversity and composition between MCI and healthy elderly individuals. Further analysis with a larger sample is underway to validate these trends.

KEYWORDS: Oral Bacteria, Mild Cognitive Impairment, Geriatric, 16S rRNA Sequencing, Microbial Diversity

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TRACKING THE ROLE OF MICROALGAE IN INFLAMMATION: A BIBLIOMETRIC ANALYSIS FROM 1998-2025

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INTRODUCTION: Microalgae serve as a promising resource spanning multiple applications across various fields including biochemistry, biotechnology, pharmaceuticals, environmental sustainability, and material engineering making them a valuable subject of multidisciplinary research. Among the various applications, studies on their role within the field of inflammation has been growing due to their ability to produce a wide range of essential substances including lipids, pigments, carotenoids, omega-3 fatty acids and vitamins. Despite the emerging literature in this area, a comprehensive overview of research trends and thematic evolution is still limited.

OBJECTIVE(S): This bibliometric study aimed to examine the current state of scientific research involving microalgae in inflammation-related contexts and identify publication trends, leading research themes, highly studied microalgal species, inter-country collaboration, and the emerging concepts within the field.

METHODS: A total of 529 publications from 1998 to 2025 were extracted from the Scopus database and the metadata were analysed using biblioMagika, OpenRefine, and VOSviewer. Co-authorship among countries and co-occurrence of author keywords were used to visualize collaboration networks, thematic clusters, and research hotspots.

RESULTS: Over 27 years, the annual publications demonstrated exponential increase, in contrast to citation counts which exhibited year to year variability. China is the most prolific country with 93 total publications, while Spain, United States, France, and Portugal were among the top collaborative countries based on total link strength. Prominent species identified include *Arthrospira plantensis*, *Chlorella vulgaris*, and *Phaeodactylum tricornutum* reflecting their relevance in inflammation research. Keywords co-occurrence analysis revealed key scientific research topics such as anti-inflammatory studies, cytokine modulation, and microalgae derived bioactive such as polyunsaturated fatty acids and fucoxanthin. The findings indicated growing interest in microalgae application on wound healing, neuroprotective effects, and gut microbiota.

CONCLUSION: To conclude, by highlighting the recent topics and research trends, this study contributes in bridging the existing knowledge gap within this field and supports future studies.

KEYWORDS: Microalgae, Inflammation, Bibliometrics, Scopus, Bioactive Compound

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TRANSCRIPTOMICS ANALYSIS OF AGEING IN *Drosophila melanogaster*

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INTRODUCTION: Ageing is a complex biological process characterized by the gradual decline of physiological integrity, leading to impaired function and increased vulnerability to diseases. As organisms age, they become increasingly prone to a range of age-associated disorders, including neurodegeneration, cardiovascular conditions, and cancer. These conditions are driven by molecular alterations, including

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