



Review Article

Translational Molecular Microbiology in Infectious Diseases: Diagnostic Advances and Biotechnological Applications

Haider H. Khudair

Department of Basic Science/ College of Dentistry/ Al-Mustansiriyah University/ Baghdad

p-ISSN: 1608-9391

e-ISSN: 2664-2786

Article information

Received: 23/ 3/ 2026

Revised: 15/ 6/ 2025

Accepted: 28/ 6/ 2026

DOI: 10.33899/rsci.v35i3.61369

corresponding author:

Haider H. Khudair

haiderhamed@uomustansiriyah.edu.iq

ABSTRACT

Translational molecular microbiology has emerged as a key field at the interface between the basic research of microorganisms, clinical diagnosis, and biotechnology. Recent developments in nucleic acid-based methods have substantially enhanced the rapid and precise detection of infectious agents. Polymerase chain reaction, next-generation sequencing and CRISPR-based assays are common molecular tools that are widely used for the identification of pathogens, antimicrobial resistance, and epidemiological surveillance. Besides diagnostic uses, molecular microbiology plays a key role in biotechnological innovation, microbial genome engineering, optimization of metabolic pathways, and production of enzymes, vaccines, and therapeutic proteins through recombinant technologies. This review provides a comprehensive overview of the molecular diagnostic platforms and their translational relevance to public health and biotechnology is presented. Emphasis is placed on bidirectional interaction between the molecular diagnostics, bioinformatics analysis, and microbial engineering approaches.

Keywords: Translational molecular microbiology, Molecular diagnostics, Infectious diseases, biotechnology, CRISPR technology.

INTRODUCTION

Molecular microbiology has become a cornerstone of contemporary biomedical studies that offer powerful tools in the study of microorganisms at the genetic and molecular scale. The rapid development of novel methods in the molecular field has changed the conventional microbiology and enabled deeper insights to learn more about the pathogenesis of microorganisms, host-pathogen interaction, and the diversity of microorganisms (Seal, 2026; Deurenberg *et al.*, 2017).

Simultaneously, the role of translational research has grown, and it aims at applying basic molecular research to the applications directly influencing the clinical practice and biotechnology (Dabbagh *et al.*, 2025). Traditional microbiological techniques will not be replaced; but these have drawbacks of long turnaround times, relatively lower sensitivity and cannot identify non-culturable or emerging microorganisms.

Many of these shortcomings are surmounted in molecular methods, which target nucleic acids and select genetic markers and enable rapid and highly specific detection of the pathogen (Choudhary *et al.*; 2022). The use of PCR, sequencing-based assays and gene-targeted diagnostics has significantly improved diagnosis of infectious diseases, antimicrobial stewardship and the surveillance of outbreaks (Rodino and Simner, 2024; Jabłońska *et al.*, 2025). Outside diagnostics, molecular microbiology has had a significant impact on biotechnology with genetic engineering, recombinant DNA technology and synthetic biology. Such innovations have made it possible to create recombinant vaccines, therapeutic proteins, industrial enzymes and engineered microbial systems that can be used to serve a variety of medical and industrial purposes (Santos-Beneit, 2024). Molecular microbiology occupies the interface between the border of the discovery-based research and an application-focused innovation (Adli, 2018). Although there is a vast amount of literature written about the disciplines of molecular diagnostics and biotechnology, there has been limited integration between the two fields. Many existing reviews fail to look at the way that molecular data generated by diagnostics can inform downstream biotechnological design and clinical decision making (Alsharksi *et al.*, 2024; Manan *et al.*, 2025). To meet this gap, this review suggests the adoption of an integrated translational molecular microbiology framework, which links the molecular diagnostics with bioinformatics-based data interpretation and microbial engineering. This article is logically addressed in mentioning translational bottlenecks, and the two-way flow of data between diagnostics and biotechnology, which provides a holistic view of the application of molecular microbiology in improving the success of precision medicine, biotechnological innovation, and the overall management of infectious diseases worldwide.

Evolution of molecular microbiology techniques

The rise of molecular microbiology reflects a paradigm shift in terms of study on the basis of phenotype to a genome-based and systems-based approach. Culture, microscopy, and biochemical tests were used as the basis of initial microbiological studies. These methods failed to comprehend genetic mechanisms and could not adequately discover slow-growing organisms but were fundamental (Goyal *et al.*, 2023). Detection of the virulence factors and the pathways of regulation was conducted through such methods as the restriction enzyme digestion, plasmid cloning and hybridization tests. The other breakthrough was that PCR was invented which made detection of microbes much faster through amplification of the specific DNA or RNA sequence. The detection of pathogens, genetic typing and molecular epidemiology became the foundation of the PCR studies that were enhanced to enable quantitative and multiplex analyses (Zhang *et al.*, 2021). High-throughput sequencing technologies have brought a revolution to molecular microbiology because they have enabled comprehensive analysis of the genome, identification of the pathogen, and analysis of anti-microbial resistance AMR.

Such procedures offered resolution at a scale not previously observed before, yet posed problems in data analysis and interpretation (Quainoo *et al.*, 2017; Wheeler *et al.*, 2023). The translational flexibility of molecular microbiology has been extended by the more recent application of CRISPR-Cas systems and synthetic biology. CRISPR-related tools make it possible to precisely edit the genome and regulate genes and enable molecular diagnostics, bridge the gap between

fundamental research and commercial biotechnology (Sahel *et al.*, 2024). The additional advances in bioinformatics, automation as well as systems biology have allowed large-scale integration molecular data into predictive and translational models. All these developments have increased the translational usefulness of molecular microbiology in diagnostics, therapeutics, and biotechnology (Topol *et al.*, 2017; Pinu *et al.*, 2017).

Molecular Microbiology in Infectious Disease Diagnosis

Infectious diseases are increasingly difficult to diagnose without applying molecular microbiology tool enabling rapid, specific, and sensitive detection and characterization of pathogens. Unlike traditional diagnostics that rely on the culture of the microbes, molecular methods directly target nucleic acids thereby enabling the detection in clinical samples with minimal time (Ahsan and Damaševičius, 2025). This shift has substantially improved a great contribution to the accuracy of diagnosis and clinical decision-making. PCR-based assays represent the foundation of modern molecular diagnostics because of their reliability, standardization of operations and intermediate cost. RNA virus detection is widely employed by reverse transcription PCR and several pathogens or resistance genes can be detected by a multiplex PCR assay. Such methods facilitate therapeutic interventions on respiratory, gastrointestinal and bloodstream infections in a timely manner (Ahn *et al.*, 2025). Diagnostics have extended beyond targeted detection, by sequencing-based diagnostics. Targeted sequencing enables species-level identification, and NGS allows identifying pathogens unbiased and in-depth AMR profiles (Osei Sekyere, 2025). Metagenomic sequencing finds application in the identification of rare or emergent pathogens as well as outbreak studies. However, its routine clinical implementation is limited by its expense, turnaround time, and bioinformatic needs (Gu *et al.*, 2021). A comparative overview of major molecular diagnostic platforms is presented in (Table 1).

Table (1): Comparative Overview of Major Molecular Diagnostic Platforms (Deurenberg *et al.*, 2017; Hadfield *et al.*, 2018)

Platform	Principle	Key Applications	Major Advantages	Key Limitations	Translational Relevance
Conventional PCR	Targeted DNA amplification	Pathogen detection	High sensitivity, low cost	Target-dependent	Routine diagnostics
Real-time PCR	Quantitative amplification	Viral load, AMR genes	Rapid, quantitative	Specialized equipment	Clinical decision-making
Digital PCR	Absolute quantification	Low-abundance targets	High precision	High cost	Resistance monitoring
NGS	High-throughput sequencing	Pathogen discovery, AMR profiling	Comprehensive	Bioinformatics complexity	Surveillance
CRISPR-based diagnostics	Guide RNA detection	Point-of-care testing	Rapid, portable	Limited validation	Decentralized diagnostics

Beyond the comparative summary presented in Table 1, several translational challenges remain evident in real-world implementation. Although there has been significant advancement in molecular diagnostics, they have been translated into the clinical practice differently within different healthcare systems. Although many of the platforms provide high analytical sensitivity in a controlled laboratory setting however, their performance varies in real-world clinical settings because of sample variability, contamination risk, and infrastructure constraints (Parvin *et al.*, 2025). The rapid expansion of sequencing-based diagnostics also creates new, unaddressed issues such as how to interpret sequence-based data, what is the extent of the completeness of databases used to establish reference values, and what are the appropriate standards for clinical reporting (Lepuschitz *et al.*, 2020). These concerns illustrate that a uniform, standardized framework for validating these technologies will be needed. Moreover, future improvements will depend upon integrating the demonstration of the clinical usefulness and cost-effectiveness of diagnostic tests with their accuracy (Nie *et al.*, 2025).

Translational applications in biotechnology

Translational molecular microbiology plays a critical role in translating biotechnology into practice. The genetic engineering and recombinant technologies enable precise manipulation of the microbial genomes to produce vaccines, enzymes, hormones and therapeutic proteins. Microbial expression systems are scalable and cost-effective, and are used in pharmaceutical and industrial production (Sadanov *et al.*, 2025; Jin *et al.*, 2025). Developments in metabolic engineering and synthetic biology have extended the possibilities of biotechnology by enabling the systematic redesign of metabolic pathways. The use of engineered microbial cell factories is widely used to produce biofuels, bioplastics, antibiotics and fine chemicals, as alternatives to conventional chemical synthesis that are environmentally unsustainable. Strain optimization enabling enhanced stress tolerance, substrate utilization and product stability is also made possible by the use of molecular tools (Jiang *et al.*, 2025; Jeong, 2025). Molecular microbiology forms the basis of vaccine production and therapeutic design in the biomedical field of biotechnology. Reverse vaccinology, antigen discovery, and nucleic acid-based vaccine systems are based on genomic and proteomic analyses to facilitate rational design and fast adaptation to new pathogens. Together, these applications underscore the role of molecular microbiology in bridging discovery and implementation in a wide range of biotechnological applications (Pardi *et al.*, 2018). Despite significant advances in engineering technology, the ability of engineers to control microbial systems has not yet translated into scalable and stable industrial processes. Strains developed through genetic modification are often subject to metabolic burden, genetic instability, and decreased productivity when removed from the controlled environments of a laboratory (Abbate *et al.*, 2023). Regulatory approval of genetically modified organisms (GMOs) is also inconsistent among countries, further hindering the process of commercializing GMO-based products. systems biology modeling, adaptive laboratory evolution, and process optimization will need to work together to close the existing gap that exists between proof-of-concept innovations and deployable industrial biotechnological solutions (Rozas *et al.*, 2022; Turnbull *et al.*, 2021).

Integration of diagnostics and biotechnology

The combination of diagnostics and biotechnology is among the least developed but has the greatest potential for advancement in translational microbiology. Most literature currently treats these two areas separately and therefore fails to utilize diagnostic-derived molecular information for use in therapeutic or engineering design (Alsulimani *et al.*, 2023). A shift towards a closed-loop translational framework where genomic surveillance is utilized as input for therapeutics; and engineered interventions are used as input for further improvement in diagnostic technologies would likely increase response speed to new pathogen emergence and the increasing threat of antimicrobial resistance (Torres *et al.*, 2025). Beyond theoretical integration, practical applications in global health and antimicrobial stewardship are illustrative examples of how molecular microbiology can be used in a translational manner (Wu *et al.*, 2020). In the COVID-19 pandemic, RT-PCR diagnostic tests were rapidly designed as a result of the rapid sequencing of the SARS-CoV-2 genome, and the identification of critical antigenic targets in the genome was used to inform the design of vaccines, and the ongoing genomic monitoring of variants and informing vaccine updates (Hadfield *et al.*, 2018). Similarly, antimicrobial resistance is also a key area of translational use where molecular diagnostics directly contribute to biotechnological innovation. Conserved processes and novel therapeutic targets are identified using comparative genomic analyses and the identification of new therapeutic targets and the detection and monitoring of resistance determinants are achieved with high efficiency through gene-based assays and whole-genome sequencing (Papamentzelopoulou *et al.*, 2025). Collectively, molecular data derived from diagnostics facilitate the creation of next-generation antimicrobials, antivulence and CRISPR-based approaches, representing a bidirectional diagnostic-to-therapeutic pipeline and the hallmark of translational molecular microbiology (Strich and Chertow, 2019). The conceptual relationship between molecular diagnostics and biotechnological innovation is illustrated in Fig. (1).

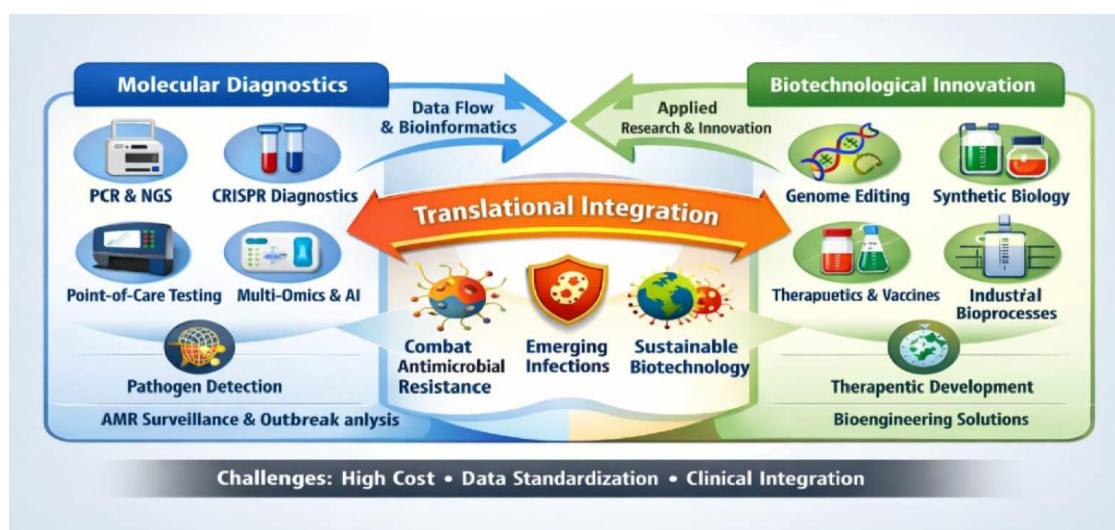


Fig. 1: Conceptual integration of molecular diagnostics and biotechnological innovation within a translational molecular microbiology framework.

Key diagnostic and biotechnological applications of molecular approaches are summarized in (Table 2).

Table (2): Translational Applications of Molecular Microbiology (Adli, 2018; Zhang *et al.*, 2021)

Molecular Approach	Diagnostic Application	Biotechnological Application	Translational Outcome
PCR-based assays	Rapid detection	Gene expression screening	Targeted therapy
Whole-genome sequencing	AMR profiling	Vaccine design	Precision medicine
Metagenomics	Unbiased identification	Strain discovery	Novel therapeutics
CRISPR-Cas systems	Rapid diagnostics	Genome editing	Personalized interventions
Multi-omics	Disease stratification	Metabolic engineering	Predictive biotechnology

Advantages, Limitations, and Technical Challenges

Molecular approaches offer high sensitivity, specificity, and flexibility in both diagnostic and biotechnological applications. Molecular methods enable identification of microorganisms in clinical or environmental samples quickly and precisely without the need long for culture periods (Cheng *et al.*, 2020).

Identifying species and strain-level targeting enable identification of microbes at a specific species-strain level to aid in clinical decision-making and antimicrobial stewardship. Molecular tools can be used in biotechnology enable controlled genetic manipulation, with reproducibility, and on a large scale, which are all crucial to industrial production and drug development (Xu *et al.*, 2020; Sharma *et al.*, 2020). Despite these assets, there are a number of limitations that limit widespread implementation of molecular microbiological methods. This costly nature of sophisticated instrumentation, reagents and maintenance limits accessibility particularly in resource limited environments (Majors *et al.*, 2017). It is also because specialized laboratory facilities and skilled workers are also required to implement external reference laboratories. Assay performance can be affected on genetic variability, contamination, or inhibitory substances and can lead to either false-positive or false-negative outcome in a diagnostic use (Kozel and Burnham-Marusich, 2017; Liu *et al.*, 2023). Technical malfunctions are particularly prone to such data-intensive approaches as

next-generation sequencing and multi-omics technologies. These systems generate large and complex datasets requiring efficient bioinformatics pipelines, mainstream reference databases and massive computational power (Shendure *et al.*, 2017). Substandard quality of data standards and absence of molecular results integration into clinical practices can limit translational impact. Genetic instability, off-target effects and metabolic burden are linked to engineered microbial systems in biotechnology especially when they are utilized in the large-scale production capacity (Schriml *et al.*, 2022; Cao *et al.*, 2025). A systems-level feedback model demonstrating the bidirectional relationship between diagnostics, biotechnology, and clinical outcomes is presented in Fig. (2).



Fig. 2: Systems model of feedback among diagnostics, biotechnology, and clinical outcomes.

Primarily, technological advancements alone will not overcome barriers to translation (i.e., socio-economic disparities; infrastructural disparities; workforce skills disparities) which significantly impact the success of implementation (Djatkiko *et al.*, 2025). The over-emphasis on high-tech solutions for technology development will only exacerbate existing global diagnostic and therapeutic disparities if there is no corresponding emphasis on developing accessible and interoperable technologies. Therefore, translational microbiology needs to be approached as both an engineering endeavor and as a systemic approach to improving public health (Harper and Schiff, 2024). There are also ethical, regulatory, and biosafety issues that are of serious concern to the application of molecular microbiology, particularly the use of genome editing instruments. In order to mitigate such shortcomings, there must be transparent regulatory standards and uniform validation standards and interdisciplinary cooperation (Rabuma *et al.*, 2024; Li *et al.*, 2025). The reduction of costs, automation and data reconciliation on a future scale will be necessary in enhancing the translational utility of molecular microbiology in diagnostics and biotechnology field (Wang *et al.*, 2022).

Emerging trends and future perspectives

Translational molecular microbiology is developing at a very fast rate, due to technological advancement and the need to acquire rapid, accurate, and scalable solutions (Banfield, 2024). Major emerging trends include the development of point-of-care molecular diagnostics. Portable platforms based on the application of isothermal amplification, microfluidics and CRISPR-based detection systems are also enabling decentralized testing, enabling early detection, outbreak control, and access to healthcare, particularly in resource-limited regions (Hassan *et al.*, 2025; Zhou *et al.*, 2025). Other direction of interest is the integration of multi-omics, genomics, transcriptomics, proteomics, and metabolomics to provide a global view of the microbial systems and host-pathogen interactions

(Zitnik *et al.*, 2019). When combined with sophisticated bioinformatics and systems biology, multi-omics data can be applied to support predictive modelling, rational therapeutic design and optimized microbial engineering (Argelaguet *et al.*, 2018; Subramanian *et al.*, 2020). Artificial intelligence and machine learning are reshaping molecular microbiology to enhance the interpretation of the data, detect pathogens and forecast antimicrobial resistance. Synthetic biological systems are also designed using computational algorithms, and processes (Rives *et al.*, 2021). Recent advancements in synthetic biology and genome engineering can also be used to design programmable microbial platforms to perform customized diagnostics, vaccines, and sustainable manufacturing (Voigt, 2020). The future influence of translational molecular microbiology will be determined by the interdisciplinary cooperation, data and responsible governance standardization. The ethical and biosafety issues and the regulation must be addressed to ensure that the new technologies are safely and efficiently translated into industrial and clinical practice (Kelson *et al.*, 2025; Ou and Guo, 2023).

CONCLUSION

Translational molecular microbiology represents a multidisciplinary interface between molecular research and practice. The integration of the more recent molecular technologies has not only revolutionized the diagnosis of infectious disease, but also facilitated substantial innovation in various areas of biotechnology. Despite the existing concerns on price, technical complexity, and regulatory oversight, translational impact should be enhanced by the further development of point-of-care diagnostics, multi-omics combination, artificial intelligence, and synthetic biology.

Further inter-disciplinary collaboration and responsible innovation will be required to realize the full potential of molecular microbiology in improving global health outcomes, advancing biotechnology, and contributing to sustainable development.

REFERENCES

- Abbate, E.; Andrion, J.; Apel, A.; Biggs, M.; Chaves, J.; Cheung, K.; Ciesla, A.; Clark-ElSayed, A.; Clay, M.; Contridas, R.; Fox, R.; Hein, G.; Held, D.; Horwitz, A.; Jenkins, S.; Kalbarczyk, K.; Krishnamurthy, N.; Mirsiaghi, M.; Noon, K.; Rowe, M.; Yerramsetty, K. (2023). Optimizing the strain engineering process for industrial-scale production of bio-based molecules. *J. Ind. Microbiol. Biotechnol.*, **50**(1), kuad025. DOI:10.1093/jimb/kuad025
- Adli, M. (2018). The CRISPR tool kit for genome editing and beyond. *Nat. Commun.*, **9**(1), 1911. DOI:10.1038/s41467-018-04252-2
- Ahn, Y. J.; Jung, C.; Rhee, J. E.; Kim, E. J. (2025). Overview of PCR-based diagnostic assays for emerging infectious disease pathogens. *Jugan Geon-gang Gwa Jilbyeong*, **18**(45), 1813–1832. DOI:10.56786/PHWR.2025.18.45.3
- Ahsan, M.; Damaševičius, R. (2025). Artificial intelligence-powered image analysis: A paradigm shift in infectious disease detection. *Artif. Intell. Med.*, **159**, 103025. DOI:10.1016/j.artmed.2024.103025
- Alsharksi, A. N.; Sirekbasan, S.; Gürkök-Tan, T.; Mustapha, A. (2024). From tradition to innovation: diverse molecular techniques in the fight against infectious diseases. *Diagnostics*, **14**(24), 2876. DOI:10.3390/diagnostics14242876
- Alsulimani, A.; Akhter, N.; Jameela, F.; Ashgar, R. I.; Jawed, A.; Hassani, M. A.; Dar, S. A. (2024). The Impact of Artificial Intelligence on Microbial Diagnosis. *Microorg.*, **12**(6), 1051. DOI:10.3390/microorganisms12061051
- Argelaguet, R.; Velten, B.; Arnol, D.; Dietrich, S.; Zenz, T.; Marioni, J. C.; Buettner, F.; Huber, W.; Stegle, O. (2018). Multi-Omics Factor Analysis framework. *Mol. Syst. Biol.*, **14**(6), e8124. DOI:10.15252/msb.20178124
- Bursle, E.; Robson, J. (2016). Non-culture methods for detecting infection. *Aust. Prescr.*, **39**(5), 171–175. DOI:10.18773/austprescr.2016.059
- Cao, Y.; Wu, Y.; Lv, X.; Li, J.; Liu, L.; Du, G.; Chen, J.; Liu, Y. (2025). Reduced Genetic Heterogeneity for Stable Bioproduction. *Microb. Biotechnol.*, **18**(6), e70162. DOI:10.1111/1751-7915.70162

- Cheng, M. P.; Papenburg, J.; Desjardins, M.; Kanjilal, S.; Quach, C.; Libman, M.; Ditttrich, S.; Yansouni, C. P. (2020). Diagnostic Testing for SARS-CoV-2: A Narrative Review. *Ann. Intern. Med.*, **172**(11), 726–734. DOI:10.7326/M20-1301
- Choudhary, M. I.; Römling, U.; Nadeem, F.; Bilal, H. M.; Zafar, M.; Jahan, H.; Ur-Rahman, A. (2022). Innovative strategies to overcome antimicrobial resistance and tolerance. *Microorg.*, **11**(1), 16. DOI:10.3390/microorganisms11010016
- Dabbagh, A.; Madadi, F.; Ebrahimi, M. (2025). Translational medicine: An effective approach to improve healthcare by research and innovation in developing countries. *Medicine.*, **104**(49), e46355. DOI:10.1097/MD.00000000000046355
- Deurenberg, R. H.; Bathoorn, E.; Chlebowicz, M. A.; Couto, N.; Ferdous, M.; García-Cobos, S.; Kooistra-Smid, A. M.; Raangs, E. C.; Rosema, S.; Veloo, A. C.; Zhou, K.; Friedrich, A. W.; Rossen, J. W. A. (2017). Application of next generation sequencing in clinical microbiology and infection prevention. *J. Biotechnol.*, **243**, 16–24. DOI:10.1016/j.jbiotec.2016.12.022
- Djatkiko, G. H.; Sinaga, O.; Pawirosumarto, S. (2025). Digital Transformation and Social Inclusion in Public Services. *Sustain.*, **17**(7), 2908. DOI:10.3390/su17072908
- Dudeja, C.; Mishra, A.; Ali, A.; Singh, P. P.; Jaiswal, A. K. (2025). Microbial genome editing with crispr-cas9: recent advances and emerging applications across sectors. *Ferment.*, **11**(7), 410. doi.org/10.3390/fermentation11070410
- Eren, A. M.; Banfield, J. F. (2024). Modern microbiology: Embracing complexity through integration across scales. *Cell*, **187**(19), 5151–5170. DOI:10.1016/j.cell.2024.08.028
- Gerrish, R. S.; Lee, J. E.; Reed, J.; Williams, J.; Farrell, L. D.; Spiegel, K. M.; Sheridan, P. P.; Shields, M. S. (2007). PCR versus hybridization for detecting virulence genes of enterohemorrhagic *Escherichia coli*. *Emerg. Infect. Dis.*, **13**(8), 1253–5. doi: 10.3201/eid1308.060428.
- Goyal, P. A.; Bankar, N. J.; Mishra, V. H.; Borkar, S. K.; Makade, J. G. (2023). Revolutionizing medical microbiology: How molecular and genomic approaches are changing diagnostic techniques. *Cureus*, **15**(10), e47106. DOI:10.7759/cureus.47106
- Gu, W.; Deng, X.; Lee, M.; Sucu, Y. D.; Arevalo, S.; Stryke, D.; Federman, S.; Gopez, A.; Reyes, K.; Zorn, K.; Sample, H.; Yu, G.; Ishpuniani, G.; Briggs, B.; Chow, E. D.; Berger, A.; Wilson, M. R.; Wang, C.; Hsu, E.; Miller, S.; Chiu, C. Y. (2021). Rapid pathogen detection by metagenomic next-generation sequencing of infected body fluids. *Nat. Med.*, **27**(1), 115–124. DOI:10.1038/s41591-020-1105-z
- Hadfield, J.; Megill, C.; Bell, S. M.; Huddleston, J.; Potter, B.; Callender, C.; Sagulenko, P.; Bedford, T.; Neher, R. A. (2018). Nextstrain: Real-time tracking of pathogen evolution. *Bioinform.*, **34**(23), 4121–4123. DOI:10.1093/bioinformatics/bty407
- Harper, J. R.; Schiff, S. J. (2024). Engineering principles and bioengineering in global health. *Neuros. Clin. N. Am.*, **35**(4), 481–488. DOI:10.1016/j.nec.2024.05.010
- Hassan, Y. M.; Mohamed, A. S.; El-Sayed, W. M. (2025). CRISPR-based rapid diagnosis: Recent developments. *Clin. Exp. Med.*, **25**(1), 33. DOI:10.1007/s10238-024-01540-8
- Jabłońska, A.; Sadkowski, A.; Richert-Przygońska, M.; Styczyński, J. (2025). Next-Generation sequencing for infectious disease diagnostics in pediatric patients with malignancies or after hematopoietic cell transplantation: A systematic review. *J. Clin. Med.*, **14**(18), 6444. DOI:10.3390/jcm14186444
- Jeong, K. J. (2025). Advancing microbial engineering through synthetic biology. *J. Microbiol.*, **63**(3), e2503100. DOI:10.71150/jm.2503100
- Jiang, X.; Ji, J.; Yang, Q.; Dou, Y.; Li, Y.; Yang, X.; Liu, C.; Dou, S.; Dong, L. (2025). Key Technologies of synthetic biology in industrial microbiology. *Microorg.*, **13**(10), 2343. DOI:10.3390/microorganisms13102343
- Jin, K.; Huang, Y.; Che, H.; Wu, Y. (2025). Engineered bacteria for disease diagnosis and treatment using synthetic biology. *Microb. Biotechnol.*, **18**(1), e70080. DOI:10.1111/1751-7915.70080
- Kelson, T. L.; Kaplan, H. B.; Dziejman, M.; Gadwal, S.; Hulede, I.; Bennett, J.; Greenwell, R.; Payne, S.; MacLea, K.; Miller, E.; Vullo, D. L.; Sparks-Thissen, R.; Bertolio, A.; Cervantes, J. (2025). Perspectives on the future of microbiology profession. *mSphere*, **10**(12), e00654-25. DOI:10.1128/msphere.00654-25
- Kozel, T. R.; Burnham-Marusch, A. R. (2017). Point-of-Care testing for infectious diseases: Past, present, and future. *J. Clin. Microbiol.*, **55**(8), 2313–2320. DOI:10.1128/JCM.00476-17

- Lepuschitz, S.; Weinmaier, T.; Mrazek, K.; Beisken, S.; Weinberger, J.; Posch, A. E. (2020). Analytical performance validation of next-generation sequencing based clinical microbiology assays using a k-mer analysis workflow. *Front. Microbiol.*, **11**, 1883. DOI:10.3389/fmicb.2020.01883
- Li, X.; Gao, Y.; Zhang, Z.; Deng, W.; Cao, W.; Wei, X.; Gao, Z.; Yao, L.; Wang, S.; Xie, Y.; Li, M. (2025). Biosafety considerations triggered by genome-editing technologies. *Biosaf. Health*, **7**(3), 141–151. DOI:10.1016/j.bsheal.2025.05.003
- Liu, Q.; Jin, X.; Cheng, J.; Zhou, H.; Zhang, Y.; Dai, Y. (2023). Advances in the application of molecular diagnostic techniques for pathogen detection. *Mol. Med. Rep.*, **27**(5), 104. DOI:10.3892/mmr.2023.12991
- Majors, C. E.; Smith, C. A.; Natoli, M. E.; Kundrod, K. A.; Richards-Kortum, R. (2017). Point-of-care diagnostics to improve maternal and neonatal health in low-resource settings. *Lab Chip*, **17**(20), 3351–3387. DOI:10.1039/c7lc00374a
- Manan, A.; Qayyum, N.; Ramachandran, R.; Qayyum, N.; Ilyas, S. (2025). Digital to Biological Translation: How the algorithmic data-driven design reshapes synthetic biology. *SynBio*, **3**(4), 17. DOI:10.3390/synbio3040017
- Nie, M.; Yao, Y.; Kim, J.; Liu, C. (2025). PRICE: a personalized recursive intelligent cost effectiveness analysis framework for rare disease diagnosis. *BMC Med. Inform. Decis. Mak.*, **25**(1), 452. DOI:10.1186/s12911-025-03277-0
- Osei Sekyere, J. (2025). Next-generation sequencing in infectious-disease diagnostics: Economic, regulatory, and clinical pathways to adoption. *Microbi. Open*, **14**(6), e70104. DOI:10.1002/mbo3.70104
- Ou, Y.; Guo, S. (2023). Safety risks and ethical governance of synthetic biology applications. *Front. Bioeng. Biotechnol.*, **11**, 1292029. DOI:10.3389/fbioe.2023.1292029
- Papamentzelopoulou, M.; Vrioni, G.; Pitiriga, V. (2025). Comparative evaluation of sequencing technologies for detecting antimicrobial resistance in bloodstream infections. *Antib.*, **14**(12), 1257. DOI:10.3390/antibiotics14121257
- Pardi, N.; Hogan, M. J.; Porter, F. W.; Weissman, D. (2018). mRNA vaccines — a new era in vaccinology. *Nat. Rev. Drug Discov.*, **17**(4), 261–279. DOI:10.1038/nrd.2017.243
- Parvin, N.; Joo, S. W.; Jung, J. H.; Mandal, T. K. (2025). Multimodal AI in biomedicine: Pioneering the future of biomaterials, diagnostics, and personalized healthcare. *Nanomater.*, **15**(12), 895. DOI:10.3390/nano15120895
- Petretto, D. R.; Carrogu, G. P.; Gaviano, L.; Berti, R.; Pinna, M.; Petretto, A. D.; Pili, R. (2024). Telemedicine, e-health, and digital health equity: A scoping review. *Clin. Pract. Epidem. Ment. Health.*, **6**(20), e17450179279732. doi: 10.2174/0117450179279732231211110248.
- Pinu, F. R.; Beale, D. J.; Paten, A. M.; Kouremenos, K.; Swarup, S.; Schirra, H. J.; Wishart, D. (2019). Systems biology and multi-omics integration: Viewpoints from the metabolomics research community. *Metabol.*, **9**(4), 76. DOI:10.3390/metabo9040076
- Pistone, D.; Bevivino, G.; Dipaola, M. G.; Bandi, C.; Lombardo, F. (2026). Current and emerging molecular diagnostic approaches in the detection of human parasites. *Parasitol. Res. Mar.*, **125**(1), 50. doi: 10.1007/s00436-026-08660-y.
- Quainoo, S.; Coolen, J. P. M.; van Hijum, S. A. F. T.; Huynen, M. A.; Melchers, W. J. G.; van Schaik, W.; Wertheim, H. F. L. (2017). Whole-genome sequencing of bacterial pathogens: The future of nosocomial outbreak analysis. *Clin. Microbiol. Rev.*, **30**(4), 1015–1063. DOI:10.1128/CMR.00016-17
- Rabuma, T.; Moronta-Barrios, F.; Craig, W. (2024). Navigating biosafety regulatory frameworks for genetic engineering in Africa. *Front. Bioeng. Biotechnol.*, **12**, 1483279. DOI:10.3389/fbioe.2024.1483279
- Rives, A.; Meier, J.; Sercu, T.; Goyal, S.; Lin, Z.; Liu, J.; Guo, D.; Ott, M.; Zitnick, C. L.; Ma, J.; Fergus, R. (2021). Biological structure and function from large-scale protein learning. *Proc. Natl. Acad. Sci. U.S.A.*, **118**(15), e2016239118. DOI:10.1073/pnas.2016239118
- Rodino, K. G.; Simner, P. J. (2024). Status check: next-generation sequencing for infectious-disease diagnostics. *J. Clin. Invest.*, **134**(4), e178003. DOI:10.1172/JCI178003
- Rozas, P.; Kessi-Pérez, E. I.; Martínez, C. (2022). Genetically modified organisms: adapting regulatory frameworks for evolving genome editing technologies. *Biol. Res.*, **55**(1), 31. DOI:10.1186/s40659-022-00399-x

- Sadanov, A. K.; Baimakhanova, B. B.; Orasymbet, S. E.; Ratnikova, I. A.; Turlybaeva, Z. Z.; Baimakhanova, G. B.; Amitova, A. A.; Omirbekova, A. A.; Aitkaliyeva, G. S.; Kossalbayev, B. D.; Belkozhaev, A. M. (2025). Engineering useful microbial species for pharmaceutical applications. *Microorgan.*, **13**(3), 599. DOI:10.3390/microorganisms13030599
- Sahel, D. K.; Giriprasad, G.; Jatyana, R.; Guha, S.; Korde, A.; Mittal, A.; Bhand, S.; Chitkara, D. (2024). Next-generation CRISPR/Cas-based ultrasensitive diagnostic tools: current progress and prospects. *RSC Adv.*, **14**(44), 32411–32435. DOI:10.1039/d4ra04838e
- Santos-Beneit, F. (2024). What is the role of microbial biotechnology and genetic engineering in medicine? *Microb. Open*, **13**(2), e1406. DOI:10.1002/mbo3.1406
- Schriml, L. M.; Munro, J. B.; Schor, M.; Olley, D.; McCracken, C.; Felix, V.; Baron, J. A.; Jackson, R.; Bello, S. M.; Bearer, C.; Lichenstein, R.; Bisordi, K.; Dialo, N. C.; Giglio, M.; Greene, C. (2022). The human disease ontology update. *Nucleic Acids Res.*, **50**(D1), D1255–D1261. DOI:10.1093/nar/gkab1063
- Seal, B. S. (2026). Advances in molecular microbiology—from recent advances to the future. *Curr. Issues Mol. Biol.*, **48**(1), 51. DOI:10.3390/cimb48010051
- Sharma, S.; Chauhan, A.; Ranjan, A.; Mathkor, D. M.; Haque, S.; Ramniwas, S.; Tuli, H. S.; Jindal, T.; Yadav, V. (2024). Emerging challenges in antimicrobial resistance. *Front. Microbiol.*, **15**, 1403168. DOI:10.3389/fmicb.2024.1403168
- Shendure, J.; Balasubramanian, S.; Church, G. M.; Gilbert, W.; Rogers, J.; Schloss, J. A.; Waterston, R. H. (2017). DNA sequencing at 40: Past, present and future. *Nature*, **550**(7676), 345–353. DOI:10.1038/nature24286
- Strich, J. R.; Chertow, D. S. (2019). CRISPR-cas biology and its application to infectious diseases. *J. Clin. Microbiol.*, **57**(4), e01307-18. DOI:10.1128/JCM.01307-18
- Subramanian, I.; Verma, S.; Kumar, S.; Jere, A.; Anamika, K. (2020). Multi-omics data integration and interpretation. *Bioinform. Biol. Insights*, **14**, 1177932219899051. DOI:10.1177/1177932219899051
- Topol, E. J. (2019). High-performance medicine: The convergence of human and artificial intelligence. *Nat. Med.*, **25**(1), 44–56. DOI:10.1038/s41591-018-0300-7
- Torres, L. M.; Johnson, J.; Valentine, A.; Brezak, A.; Schneider, E. C.; D'Angeli, M.; Morgan, J.; Brostrom-Smith, C.; Hua, C. N.; Tran, M.; Lucas, D.; De Leon, J. G.; MacKellar, D.; Dykema, P.; Kauber, K. J.; Black, A. (2025). Integrating genomic data into public health surveillance for multidrug-resistant organisms. *Emerg. Infect. Dis.*, **31**(13), 25–34. DOI:10.3201/eid3113.241227
- Turnbull, C.; Lillemo, M.; Hvoslef-Eide, T. A. K. (2021). Global regulation of genetically modified crops amid the gene edited crop boom—a review. *Front. Plant Sci.*, **12**, 630396. DOI:10.3389/fpls.2021.630396
- Uddin, T. M.; Chakraborty, A. J.; Khusro, A.; Zidan, B. R. M.; Mitra, S.; Emran, T. B.; Dhama, K.; Ripon, M. K. H.; Gajdacs, M.; Sahibzada, M. U. K.; Hossain, M. J.; Koirala, N. (2021). Antibiotic resistance in microbes: History, mechanisms, therapeutic strategies and future prospects. *J. Infect. Public Health*. **14**(12), 1750–1766. doi: 10.1016/j.jiph.2021.10.020.
- Voigt, C. A. (2020). Synthetic biology products changing our world. *Nat. Commun.*, **11**(1), 6379. DOI:10.1038/s41467-020-20122-2
- Wang, H.; Zhang, W.; Tang, Y. W. (2022). Clinical microbiology in detection of emerging pathogens. *Emerg. Microbes Infect.*, **11**(1), 2579–2589. DOI:10.1080/22221751.2022.2125345
- Wheeler, N. E.; Price, V.; Cunningham-Oakes, E.; Tsang, K. K.; Nunn, J. G.; Midega, J. T.; Anjum, M. F.; Wade, M. J.; Feasey, N. A.; Peacock, S. J.; Jauneikaite, E.; Baker, K. S.; SEDRIC Genomics Surveillance Working Group. (2023). Innovations in genomic antimicrobial resistance surveillance. *Lancet Microbe.*, **4**(12), e1063–e1070. DOI:10.1016/S2666-5247(23)00285-9
- Wu, F.; Zhao, S.; Yu, B.; Chen, Y. M.; Wang, W.; Song, Z. G.; Hu, Y.; Tao, Z. W.; Tian, J. H.; Pei, Y. Y.; Yuan, M. L.; Zhang, Y. L.; Dai, F. H.; Liu, Y.; Wang, Q. M.; Zheng, J. J.; Xu, L.; Holmes, E. C.; Zhang, Y. Z. (2020). A new coronavirus associated with human respiratory disease in China. *Nature*, **579**(7798), 265–269. DOI:10.1038/s41586-020-2008-3
- Xu, Y.; Li, Z. (2020). CRISPR-Cas systems: Overview, innovations and applications in human disease research and gene therapy. *Comput. Struct. Biotechnol. J.*, **18**, 2401–2415. DOI:10.1016/j.csbj.2020.08.031

- Yan, X.; He, Q.; Geng, B.; Yang, S. (2024). Microbial cell factories in the bioeconomy era: From discovery to creation. *Biodes. Res.* **21**(6), 0052. doi: 10.34133/bdr.0052. PMID: 39434802
- Zhang, S.; Li, X.; Wu, J.; Coin, L.; O'Brien, J.; Hai, F.; Jiang, G. (2021). Molecular methods for pathogenic bacteria detection and recent advances in wastewater analysis. *Water*, **13**(24), 3551. DOI:10.3390/w13243551
- Zhou, Z.; Cho, I.-H.; Kadam, U. S. (2025). CRISPR-cas-based diagnostics in biomedicine. *Biosensors*, **15**(10), 660. DOI:10.3390/bios15100660
- Zitnik, M.; Nguyen, F.; Wang, B.; Leskovec, J.; Goldenberg, A.; Hoffman, M. M. (2019). Machine learning for integrating data in biology and medicine. *Inf. Fusion*, **50**, 71–91. DOI:10.1016/j.inffus.2018.09.012
-

علم الأحياء المجهرية الجزيئية الانتقالي: الربط بين تشخيص الأمراض المعدية والابتكار في التكنولوجيا الحيوية

حيدر حامد خضير

فرع العلوم الأساسية/ كلية طب الأسنان/ الجامعة المستنصرية/ بغداد

الملخص

برز علم الأحياء المجهرية الجزيئية الانتقالي كمجال محوري يربط بين البحث الأساسي في الكائنات الدقيقة والتشخيص السريري والتكنولوجيا الحيوية. وقد أسهمت التقنيات المعتمدة على الأحماض النووية في تحسين سرعة ودقة الكشف عن العوامل الممرضة، ومن أبرزها تفاعل البلمرة المتسلسل، والتسلسل الجيني من الجيل التالي، والاختبارات المعتمدة على كريسبر، والتي تُستخدم لتحديد الممرضات ورصد مقاومة المضادات الحيوية والمراقبة الوبائية. ولا يقتصر دور هذا المجال على التشخيص، بل يمتد إلى دعم الابتكار التقني الحيوي عبر هندسة الجينوم الميكروبي وتحسين المسارات الأيضية وإنتاج الإنزيمات واللقاحات والبروتينات العلاجية باستخدام التقنيات المؤتلفة. ويستعرض هذا البحث منصات التشخيص الجزيئي وأهميتها التطبيقية للصحة العامة والتكنولوجيا الحيوية، مع التركيز على التفاعل المتبادل بين التشخيص الجزيئي وتحليل المعلوماتية الحيوية وهندسة الميكروبات.

الكلمات الدالة: علم الأحياء المجهرية الجزيئية الانتقالي؛ التشخيص الجزيئي؛ الأمراض المعدية؛ التكنولوجيا الحيوية؛ تقنية كريسبر