ARTICLE



Precision medicine in Asia enhanced by next-generation sequencing: Implications for Thailand through a scoping review and interview study

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Funding information

National Science, Research, and

Abstract

Next-generation sequencing (NGS) significantly enhances precision medicine (PM) by offering personalized approaches to diagnosis, treatment, and prevention of unmet medical needs. Little is known about the current situation of PM in Asia. Thus, we aimed to conduct an overview of the progress and gaps in PM in Asia and enrich it with in-depth insight into the possibilities of future PM in Thailand. This scoping review focused on Asian countries starting with non-cancer studies, including rare and undiagnosed diseases (RUDs), non-communicable diseases (NCDs), infectious diseases (IDs), and pharmacogenomics, with a focus on NGS. Subsequent in-depth interviews with experts in Thailand were performed, and a thematic analysis served as the main qualitative methodology. Out of 2898 searched articles, 387 studies were included after the review. Although most of the studies focused on cancer, 89 (23.0%) studies were related to RUDs (17.1%), NCDs (2.8%), IDs (1.8%), and pharmacogenomics (1.3%). Apart from medicine and related sciences, the studies were mostly composed of PM (61.8%), followed by genetics medicine and bioinformatics. Interestingly, 28% of articles were conducted exclusively within the fields of medicine and related sciences, emphasizing interdisciplinary integration. The experts emphasized the need for sustainabilitydriven political will, nurturing collaboration, reinforcing computational infrastructure, and expanding the bioinformatic workforce. In Asia, developments of NGS have made remarkable progress in PM. Thailand has extended PM beyond cancer and focused on clinical implementation. We summarized the PM challenges, including equity and efficiency targeting, guided research funding, sufficient sample size, integrated collaboration, computational infrastructure, and sufficient trained human resources.

Sutatip Pongcharoen and Jiraluck Nontarak contributed equally.

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Innovation Fund, Grant/Award Number: R2566B001

Study highlights

WHAT IS THE CURRENT KNOWLEDGE ON THE TOPIC?

Precision medicine, propelled by advancements in Next-generation sequencing (NGS), has profoundly transformed healthcare. It has paved the way for disease prevention, early detection, enhanced diagnosis, the classification of disease subgroups, and personalized treatment strategies.

WHAT QUESTION DID THIS STUDY ADDRESS?

This study aimed to identify gaps in precision medicine in Asia and underscore the challenges related to bioinformatic technology and the bioinformatic workforce in the context of implementing precision medicine at a national level.

WHAT DOES THIS STUDY ADD TO OUR KNOWLEDGE?

Precision medicine in Asia primarily focused on cancer and expanded into infectious diseases, rare and undiagnosed diseases, non-communicable diseases (NCDs), and pharmacogenomics. However, there is ample room for greater interdisciplinary collaboration across the fields of medicine, genetics, precision medicine, and bioinformatics. Experts emphasize the importance of sustainable political support, fostering collaboration, strengthening computational infrastructure, and expanding the bioinformatics workforce.

HOW MIGHT THIS CHANGE CLINICAL PHARMACOLOGY OR TRANSLATIONAL SCIENCE?

The future of precision medicine in Thailand entails expanding population-based research, conducting cost-effectiveness analyses, and ensuring that the translation to clinical practices of universal health coverage is equitable and sustainable.

INTRODUCTION

In light of recent advances in genomic medicine, precision medicine has transformed healthcare through the prevention and early detection of disease, refining diagnosis, classifying subpopulations of disease, and tailoring treatments. Moreover, precision medicine offers promise for innovations in identifying disease mechanisms, drug discovery, and drug repurposing, reducing healthcare costs, and improving healthcare outcomes, especially in unmet medical needs.²⁻⁵ Next-generation sequencing (NGS) technology, also known as massively parallel sequencing, has revolutionized the field of precision medicine with its higher sequencing capacity, speed, and accuracy, along with its increasing affordability. 6-8 Additionally, vast amounts of data generated by NGS require sophisticated computational frameworks that can handle large datasets, perform complex data analysis, and generate reliable sequencing results.8 With various sequencing platforms and methods, bioinformatic analysis could become complicated and require constant refining and improvement to handle larger datasets and more complex analyses. 9 Computational infrastructure and a bioinformatic workforce have also been proposed as crucial challenging steps in the national adaptation of precision medicine. 10,11

Globally, there are several nationwide program initiatives to facilitate precision medicine implementation. 12-14 However, most of the genomic datasets are predominantly based on the population of European ancestors; for instance, only 14% of the non-European genomic data were presented in the Genome-wide association studies (GWAS) catalog in 2021. 15-17 Given the concern for the disparity of racial representation, there were efforts to increase the genomic diversity in Asia; for example, China, ¹⁸ Japan, ¹⁹ South Korea, ²⁰ Singapore, ²¹ Malaysia, ²² Indonesia, ²³ and Thailand. 10,24 To close the gap, sustainable and strategic funding, improving the institutional capacity and collaboration, and developing a skilled workforce were highlighted as the contributing factors, especially in low- or middle-income countries. 10,11 The collaboration of multidiscipline is also a key component of the achievement of precision medicine by generating genetic profiles and family histories, continuously monitoring health data, and recommending personalized interventions using integral information of biological, environmental, behavioral, epidemiological, and clinical data.²⁵

Since pioneering projects of precision medicine have focused on pathological genomic variants, the fields of cancer and rare diseases have been impactful and have shown great potential for clinical implementation.²⁵ In addition, worldwide, over two-thirds of research findings have been

distributed in cancer and rare diseases.^{26,27} However, medical attention has moved on to other themes; for instance, malaria and infectious diseases in African countries,¹³ newborn sequencing,²⁸ screening of inherited diseases, non-communicable diseases (NCDs),²⁹ and environmental exposure.^{30,31} As such, the progression of precision medicine research is still needed in non-cancer areas.³²

Approximately 75% of Thailand's population is under the universal health coverage (UHC) scheme. Precision medicine is one of the health benefit packages that should be provided, despite the downside of imposing a highcost care burden on Thailand's Gross Domestic Product (GDP). Thus, Thailand has strategically funded the Human Genome Project Initiative for Precision Medicine, "Genomics Thailand", which has commissioned not only cancer but also four other scopes of precision medicine from rare and undiagnosed diseases, NCDs, infectious diseases, and pharmacogenomics. Ultimately, the initiative has envisioned that precision medicine ought to be implemented in routine clinical use with a collaborative medical network and established healthcare system. The aims of this study include identifying the gaps in bioinformatics technology focusing on the next-generation sequencing in Asian countries and investigating the current situation and potential future directions of precision medicine through a scoping review and expert insights.

This study aims to identify gaps in precision medicnine implementation in Asia and underscores the challenges related to bioinformatic technology and the bioinformatic workforce in the context of implementing precision medicine enhanced by next-generation sequencing at the national level.

METHODS

Study design

A sequential scoping review of the literature conducted in Asia, followed by in-depth interviews with Thai experts, was undertaken to relate the current situations to the potential future directions of precision medicine in Thailand.

Data sources and search strategies

This scoping review followed the Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) checklist³³ as shown in Table S1. Searches were undertaken in three electronic bibliographic databases comprising Medline, EMBASE, and Scopus, between 2000 and 2022, up to October 31, 2022. A combination of three different blocks containing three MeSH

terms or free text words was applied as follows: (1) precision medicine, (2) genetic testing, and (3) Asian countries.

Eligibility criteria

Only original research on humans was included, thus limiting the scope to the five pillars of precision medicine (cancer, infectious diseases, NCDs, rare diseases, and pharmacogenomics). The articles were required to state genetic testing (whole-exome/-genome sequencing, nextgeneration sequencing, or genome-wide association) in the title and/or abstract, introduction, methods, and/or results. In this study, we focus on NGS because it significantly enhances precision medicine by offering personalized approaches to the diagnosis, treatment, and prevention of unmet medical needs with increasing usage, especially in Thailand. Given the large number of precision medicinerelated publications, we included three East Asian countries, that is, China, Japan, and South Korea, to represent the big picture of precision medicine in Asian countries. To represent the diversity of genomic and financial resources, we included four middle- to upper-income economies, that is, Indonesia, Malaysia, Singapore, and Thailand. Editorial articles, conference abstracts or posters, dissertations, and irrelevant topics, e.g., genomic platform development, optimization of genetic testing techniques, non-genetic testing, using a genomic library or sequencing data as a main study cohort, or outside of the scope (such as prenatal diagnosis, forensic, and no-clinical correlation) were excluded, along with articles not published in English.

Study selection and data extraction

Two authors (C.P. and J.N.) independently performed the abstract screening using an open-source machine learning systemic review tool, ASReview^{34,35} (V 0.17, University of Utrecht, The Netherlands). Briefly, the authors actively screened the records of the abstracts by labeling them as relevant or irrelevant. After the records were ordered by relevance, we evaluated the remaining records until reaching 100 irrelevant records, which were predefined as a stopping criterion. Next, the screened abstracts were reviewed for their eligibility. Any disagreement was resolved by discussion within the review committee (C.P., P.P., J.R., and J.N.).

The data were independently extracted by three authors (C.P., J.R., and J.N.), including the demographic data (title, first author, years of publication, and number of participants), patient characteristics, study objective, genetic testing methods, international collaboration, and interdisciplinary collaboration. Again, any discrepancies were



reviewed and discussed by the review committee. The data were analyzed and summarized narratively in the text, and presented in tables and graphs. The full search strategy and search terms are listed in Tables S2 and S3.

Methods for the in-depth interview

We conducted in-depth, semi-structured interviews with leading Thai researchers to provide insights into the current situation and potential future directions of precision medicine. The researchers were contacted through expert connections and nominated potential participants (snowball sampling technique) until the point of data saturation (eight experts were interviewed). Ethics and research approval were obtained from the Committee for Human Research, Faculty of Public Health, Mahidol University (No. MUPH 2022-075).

The in-depth interviews were conducted via Zoom (Zoom Video Communications Inc., USA) between May 2022 and June 2023. All interviews were conducted in the Thai language and were audio recorded. The guided questions were sent to the experts prior to the interview. Prior informed consent was also obtained from all the experts. J.N., P.P., and J.R. conducted the interview.

Once the recorded interviews were transcribed, two authors (J.N. and J.R.) read the complete data and independently identified the codes using open and axial coding. Both authors reviewed and agreed on the final codes. The review committee (C.P., P.P., J.N., and J.R.) thematically analyzed the data using the framework analysis outlined by Braun and Clarke. The themes and sub-themes were reviewed and finalized with the agreement of the review committee. The quotes listed in the supplement were translated from the Thai language to English.

Ethics approval

The study was approved by the Committee for Human Research, Faculty of Public Health, Mahidol University (No. MUPH 2022-075).

RESULTS

Article screening

The literature search yielded 4461 articles across the three electronic databases. After the removal of any duplicates and irrelevant items, 2898 records of abstracts were screened. A total of 998 articles were selected for full-text screening. Finally, there were 387 original articles. The selection of the studies is presented in Figure 1.

Characteristics of the included studies

Most of the included studies were from East Asia (93.8%) led by China (63.6%), followed by South Korea (15.8%), and Japan (14.5%). Among the Southeast Asian countries, Singapore predominately led (3.1%), followed by Thailand (2.1%) and Malaysia (1.0%). Most studies were about cancer (77.0%), followed by rare diseases (17.1%), NCDs (2.8%), infectious diseases (1.8%), and pharmacogenomics (1.3%). There has been a significant surge in publications since 2018, whereas only 38 articles (10.0%) were published before 2018. A summary of the study's characteristics is presented in Table 1. Cancer was the main theme for each country except Thailand (Figure S1A). There was also an increasing proportion of non-cancer studies over the period, that is, non-cancer studies comprised 15.8% of the total number before 2018, then increased to 27.5% in 2022 (Figure S1B).

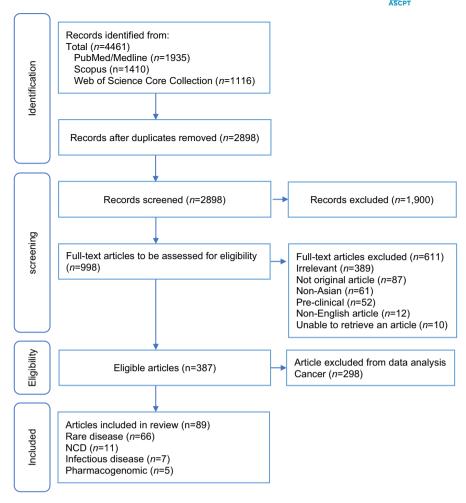
Given that the number of non-cancer articles was quite low, in this study, we focused on those studies to determine the trend and gap in these themes in precision medicine in Asia. For non-cancer studies, 62 studies were performed in China (69.7%), with the majority on the theme of rare diseases (75.8%). The overview of the non-cancer study is summarized in Table 2, and a detailed description is provided in Table S5. The median number of participants was 44 (range of 1-11,495). International collaboration was conducted in 22 studies (24.7%), where the United States and the United Kingdom were the majority with 12 (54.5%) and seven (31.8%) studies, respectively. Techniques were mostly done by whole exome sequencing (WES) (51.7%), followed by targeted sequencing (29.2%). Furthermore, the sources of funding were not documented in the four studies. Of the studies with listed sources of funding (95.5%), a substantial portion (91.0%) received financial support from governmental entities, including federal, provincial, or non-profit organizations. The remaining studies indicated no funding (4.5%), and most studies were funded by multiple sources (75.3%). The studies' source of funding is detailed in Table S4.

Interdisciplinary studies in precision medicine

We reviewed the disciplines of the included studies by sorting the affiliation into four categories: namely, (1) medicine and related sciences, (2) precision medicine, (3) genetics, and (4) bioinformatics. Full-sorted affiliations are listed in Table S4. Medicine and related sciences were involved in all articles, followed by precision medicine (61.8%), genetics (44.9%), and bioinformatics (10.1%). The integrated disciplines are illustrated in Figure 2.

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FIGURE 1 Flow diagram of the study selection process. PRISMA diagram illustrating the undertaken process for this scoping review. Abbreviations: *n*, number; NCD, non-communicable diseases; PRISMA, Preferred Reporting Items for Systematic Reviews and Meta-Analyses.



Interestingly, there were 25 (28.1%) articles, which were performed only under medicine and related sciences without any involvement of either precision medicine, genetics, or bioinformatics.

accordance with the different dimensions of precision medicine. Table S7 provides the selected quotes utilized in this discourse.

Interview results

Having updated the current landscape from the scoping review, we explored the prospects of precision medicine in Thailand through in-depth interviews with eight pivotal experts (three clinicians, two researchers, and three bioinformaticians). The sociodemographic information of the experts is presented in Table S6. Two overarching themes emerged from the interviews: delineating the existing adoption of precision medicine and the challenges encountered. The latter encompassed four distinct subthemes: political will, collaboration and data sharing, computational infrastructure, and the availability of a proficient bioinformatic workforce. The following results encapsulated the findings derived from the interviews, which were organized in accordance with distinct dimensions of precision medicine. The ensuing paragraphs encapsulate the findings from the interviews and were categorized in

Current precision medicine adoption in Thailand

Precision medicine commenced in Thailand around 2017 when the prices of high-throughput sequencing technology decreased. Due to advancements in sequencing technology, the sequencing of the whole genome has evolved from the realm of fundamental laboratory research to the practical application of medicine. Genomics laboratories belong to university hospitals, mostly located in Bangkok, where research and clinical services are conducted. For clinical services, precision medicine for cancer, rare diseases, and pharmacogenomics have already been adopted in routine clinical practice. However, precision medicine for NCDs or infectious diseases is currently in the research and data collection phase. To accelerate more clinical implementation, more population-based research and costeffectiveness analysis would be needed. This would also be crucial for increasing the laboratory capacity, including



TABLE 1 Characteristics of included studies^a.

TABLE 1 Characteristics of included studies.				
Characteristics	n	%		
Country ^b				
China	246	63.6		
Japan	56	14.5		
South Korea	61	15.8		
Malaysia	4	1.0		
Singapore	12	3.1		
Thailand	8	2.1		
Theme				
Cancer	298	77.0		
Infectious disease	7	1.8		
NCD ^c	11	2.8		
Pharmacogenomic	5	1.3		
Rare disease	66	17.1		
Year ^d				
Before 2018	38	10.0		
2018	40	10.3		
2019	67	17.3		
2020	76	19.6		
2021	97	25.1		
2022	69	17.8		

Abbreviation: NCD, non-communicable diseases.

shortening the turnaround time, increasing the diagnostic yield, and expanding the clinical indications for genetic testing. The competency of clinical implementation would significantly depend on the indication of genetic testing covered by a reimbursement plan. For example, government decisions regarding the coverage or reimbursement for human leukocyte antigen (HLA) typing for drug allergies have a lengthy process of 78 years. Nonetheless, with the successful establishment of BRCA1-2 mutation detection in Genomics Thailand, the coverage decision for BRCA testing could be expedited within 1 year. This underscores the significance of supporting scientific evidence through collaboration among researchers, which is instrumental in driving the integration of precision medicine into national health policies.

Genomics Thailand, a national initiative of genomics research, emerged through a collaborative effort of the Health Systems Research Institute (HSRI), Ministry of Higher Education, Science, Research, and Innovation (MHESI), Ministry of Public Health (MOPH), and

 TABLE 2
 Overview of included studies.

		Median n	International collaboration	Sequencing techniques ^a (%)	es _a (%)			
Theme	Included article	(Min-Max)	(%)	Targeted sequencing	WES	WGS	GWAS	Othersb
All	68	44 (1–11,495)	22 (24.7%)	26 (29.2%)	46 (51.7%)	9 (10.1%)	3 (3.4%)	5 (5.7%)
Infectious diseases	7	60 (24–5053)	5 (71.4%)	2 (28.6%)	2 (28.6%)	3 (42.8%)	(%0)0	(%0) 0
NCDs	11	85 (10–7091)	3 (27.3%)	4 (36.4%)	2 (18.2%)	(%0)0	1(9.1%)	4 (36.4%)
Pharmacogenomics	5	990 (100–11,495)	0 (0%)	2 (40.0%)	(%0) 0	3 (60.0%)	(%0)0	(%0) 0
Rare diseases	99	32 (1–5314)	14 (21.2%)	18 (27.3%)	42 (63.6%)	3 (4.5%)	2 (3.0%)	1 (1.5%)

In case of multiple sequencing techniques were performed, the listed sequencing techniques derive from the main sequencing techniques used for each study. Abbreviations: GWAS, genome-wide association study; NCD, non-communicable diseases; WES, whole-exome sequencing: WGS, whole-genome sequencing.

Others: mitochondrial DNA,

or combined technique (targeted sequencing, WES, and WGS)

^aTotal number of included articles (n = 387).

^bCountry of the articles is determined by setting of study, that is, country of individuals or patients taking part in the study.

^cIncluding main diseases of NCD defined by WHO, that is, cardiovascular disease, stroke, chronic respiratory disease, and diabetes.

^dIn the year 2022, articles were included before October 2022, as of the search that was conducted.

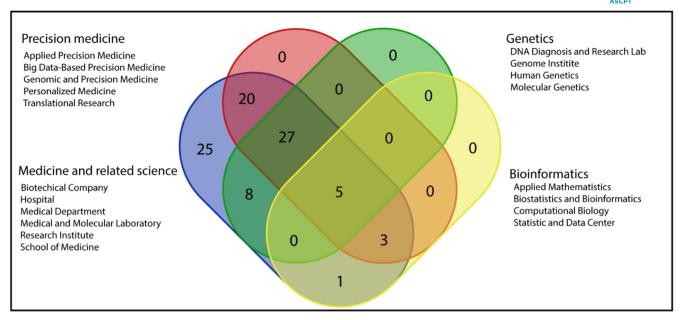


FIGURE 2 Venn diagram showing the intersection between the disciplines of the included studies.

Thailand Center for Excellence for Life Science (TCELS). The primary objectives of the initiative encompass the establishment of a comprehensive population-level genome database and the facilitation of genomic integration into the fabric of national health policies. Currently, Genomics Thailand is constructing a reference database to capture Thai genetic variations with an initial target of 50,000 samples, and subsequently expanding this repository to include 100,000 samples. Given the vast amount of sequencing data, the installation of high-performance computing (HPC) infrastructure was necessary to build sufficient storage and a reliable backup. The experts are certain that these initiatives would play a pivotal role in establishing an ecosystem conducive to precision medicine research through the enhancement of technological infrastructure and the fostering of collaborations.

Critical barriers of precision medicine in Thailand

The experts pointed out the challenges for developing and implementing precision medicine in Thailand. The challenges and critical enablers are summarized in Table 3.

Political will

Consistent government support, including substantial budgets for technology and computational infrastructure, is crucial for successful clinical implementation. Promoting genetic literacy within the community is necessary to address issues of misinterpretation and the unethical use of individuals' genetic information. Cost-effectiveness research can accelerate healthcare coverage decisions by policymakers.

Collaboration and data sharing

Establishing a standardized format and protocol is crucial for effectively generating and gathering high-quality genomic data and clinical information within the scientific community. In the past, many countries lacked governance and legislation over personal genetic data. However, recent agreements under the Personal Data Protection Act (PDPA) have facilitated data sharing while ensuring privacy. A transparent and collaborative datasharing framework can advance genomics research and precision medicine while maintaining ethical standards and privacy protection for individuals contributing data.

Computational infrastructure

The data storage infrastructure is efficiently managed by local laboratories, the National Biobank of Thailand, and the private sector. The private sector is often preferred due to its affordability in terms of subscription costs and lower maintenance expenses. The development of national digital healthcare platforms, such as "Mor Prom" shows promise in overcoming the issue of computer security by offering secure authentication and data protection measures. Such digital healthcare platforms can facilitate

TABLE 3 Challenges and critical enablers for precision medicine implementation in Thailand.

Theme	Challenge	Critical enabler
Political wills	 Imbalance of governmental funding Unregulated genomic study activity Missing of fundamental research Limited financial accessibility for healthcare services 	 Consistent and sustainably-driven policy Expanding coverage and reimbursement Economic evaluation of precision medicine Increasing genomic literacy
Collaboration and data sharing	 Unstructured data Silo of dataset Ownership of genomic data	 Statement of collaboration in the memorandum of understanding (MOU) Incentives for stakeholder Collaboration manager
Computational infrastructure	 Insufficient of high technology computational infrastructure Obsolete of technology Data security 	 Leveraging of existing infrastructure Wide spread of electronic medical records (EMR) adoption Digital health innovation
Bioinformatic workforce	 Limited bioinformatic workforce Underdeveloped career path for bioinformaticians Limited access to advance genomic analysis Lacking accreditation in the bioinformatic training 	 Formal and informal of bioinformatic training. Promoting conducive working environment Developing industry-academic partnership

the safer sharing of health data, fostering collaboration among providers and researchers while protecting sensitive information.

Bioinformatic workforce

Thailand faces a shortage of bioinformaticians due to limited interest and incentives. To address the scarcity of bioinformaticians, biologists or geneticists equipped with the skills and knowledge in bioinformatics could proficiently conduct routine genetic analyses using existing command-line tools or software with user-friendly interfaces. However, dedicated bioinformaticians could significantly enhance analysis efficiency, especially for complex research requiring algorithm development. Their expertise could lead to deeper insights into genomics. Advancements in bioinformatic tools and automated sequencing technology could lessen the need for a large bioinformatic workforce.

Bioinformatics is an interdisciplinary field encompassing biology, mathematics, statistics, and computer science. To meet the increasing demand for skilled professionals, integrating bioinformatics into undergraduate curricula is crucial. This can be achieved through standalone courses or modules within existing ones. Entrusting bioinformatics training to the Medical Technology Council (MTC) is advisable. Non-profit academic organizations and the private sector also offer short training courses in bioinformatics. This collaborative effort ensures that medical technologists acquire the necessary skills, aligning with the importance of genomic data analysis and precision medicine in healthcare. Enhancing workforce capabilities

bridges the gap between genomics research and practical implementation, leading to improved patient care.

DISCUSSION

The study combined the scoping review with in-depth interviews with experts in Thailand to provide a comprehensive overview of the progression and challenges of precision medicine in Asia. Here, we demonstrated that robust evidence of precision medicine has been made by NGS technologies in Asia, with precision oncology at the forefront of the included studies. From 2014 to 2022, 90% of the included articles were published after 2018, thus reflecting when the NGS technologies were widely available. Articles from Southeast Asia, exemplified by countries such as Singapore, Malaysia, and Thailand, were outnumbered by articles originating from East Asia. This discrepancy in publication output between the two regions reflected the variations in the research economies in setting the priorities of funding availability through national support.

Our findings showed that the main theme of precision medicine in Asia was cancer, consistent with previously reported proportions worldwide. Given the increasing burden of cancer deaths, the funding and resources of precision medicine research have primarily focused on cancer. However, infectious diseases remain a significant healthcare burden, particularly in low- and middle-income countries. Additionally, the application of genomic studies in infectious diseases included pathogen identification, host genetic susceptibility factors, treatment selection, antimicrobial-resistant marker screening, vaccine development, epidemiological investigations, and biochemical

functional analysis. The adoption of high-throughput genetic testing for infectious disease management was recommended in research and public health utilities; for instance, dengue fever, 40 malaria, and neglected tropical diseases. 41 In the context of rare and undiagnosed diseases, clinical WES and WGS exhibited substantial promise in disease management, precise diagnosis, and addressing perplexing cases that could pose challenges for both patients and healthcare practitioners.⁴² Likewise, the declining costs associated with sequencing technologies have contributed to the increasing accessibility of WGS, thus positioning it as a pivotal genetic screening tool for rare diseases as well as for pharmacogenomics.⁴⁰ With the aging population and the process of modernization, NCD has emerged as a significant burden not only in developing nations. ¹³ The widespread prevalence of NCD could be attributed to the intricate interplay between individual and population genetic factors, as well as global phenomena like aging populations, rapid urbanization, and the global proliferation of unhealthy lifestyles. Collectively, future endeavors in the realm of precision medicine would be poised to play a pivotal role in addressing the clinical complexities associated with these emerging diseases and health conditions.

In addition, the strengths of precision medicine initiatives in Thailand for rare diseases have been highlighted in the scoping review and further elucidated through interviews. Despite the numerous strengths that have been identified, the experts' perspectives also revealed certain gaps within the precision medicine landscape. Firstly, it was emphasized that politics played a pivotal role in shaping the trajectory of the implementation of the healthcare system, including that of precision medicine. The Genomics Thailand initiative stands as a clear example of Thailand's commitment to precision medicine, thereby providing a defined direction. The initiative aims to support the computational infrastructure, adopt cutting-edge technologies, and foster workforce development, all with the overarching goal of enhancing the foundational aspects of clinical implementation. However, consistent with the findings from other studies, political commitment emerges as a critical initial catalyst. 40 In contrast to developed countries where the healthcare industry or private funding plays an important role, the investment in genomic research in Thailand is intricately linked to the national healthcare system's budget, 43 which in turn dictates sustainability and alignment with universal health coverage targets. Secondly, collaboration and data sharing are stated to be limited within the scientific community. Without explicit statements in the memorandum of understanding (MOU), there exists a certain level of withholding of clinical and genetic information within the community. Achieving impactful research would necessitate a scalable sample size through the collection and

tracking of valuable clinical information, particularly for rare diseases with a low incidence rate. Since maximizing data sharing could be systematically accomplished by allocating additional resources to disseminate results⁴⁴ and promoting an open data policy for publications.⁴⁵ Thirdly, the burden of computational infrastructure might not heavily rely on technologies such as HPC⁴⁶ or cloud data storage infrastructure due to collaboration with private sector services. Nonetheless, challenges related to computational infrastructure would involve limited implementation and underutilization of electronic medical records,⁴⁷ and unstructured bioinformatics and clinical data,⁴⁸ as well as security challenges using cloud computing.⁴⁹

Lastly, the bioinformatics workforce would be a key strategic element for the successful implementation of precision medicine. We have demonstrated that the articles included in our study were conducted using an interdisciplinary approach. Only 10% of the included articles were affiliated with bioinformatics, indicating a strong integration of bioinformatics science into precision medicine research. Qualitative analysis has also revealed that bioinformatics analysis practices have been well integrated within precision medicine, clinical genetics research, and healthcare communities. Nevertheless, the current number of professionals in this field is still insufficient to fully meet the demands, which aim to reach 500 in the workforce soon. 10 In fact, providing bioinformatics education would be challenging due to its cross-disciplinary nature. Consequently, experts have suggested that the augmentation of the service workforce should be effectively achieved through standalone courses or integrated learning modules within existing programs. However, there would be a need for a stronger foundation and a more focused mathematical and statistical curriculum to enhance bioinformatics capabilities. This enhancement would be essential for the development of in-demand bioinformatic tools and applications. 50

To successfully implement precision medicine in Thailand, the research design and funding should be directed toward embedding equity into the existing health-care systems. The shortening of the listing period for clinical use of precision medicine in BRCA to the universal coverage reimbursement was an example of the country's benefit. Moreover, distributional cost-effectiveness analysis would be the approach to put equity first in determining the innovation and real-life evidence that innovation utilization should follow. The funding priorities of Genomics Thailand and the Health Systems Research Institute need urgent comprehensive planning to alleviate the stifled supply side of precision medicine research.

Several limitations of the present study were realized. Firstly, due to the prespecified eligibility criteria for the literature to be in English, some essential papers in other languages were excluded. Secondly, even though we



explicitly selected eligible articles, there might be some selection bias, and the strength of the evidence might vary due to the study design. Thirdly, it would be worth noting that the chosen articles may not offer a comprehensive portrayal of the entire precision medicine landscape. Given the stringent inclusion criteria related to NGS technology, certain domains of research could be potentially underrepresented. Additionally, we extrapolated the researchers' disciplines from the affiliation, which might not directly reflect the actual roles of the researchers. To better recognize the researchers' contributions, an extended contributorship model was proposed that could potentially improve the representation of the contribution in our further research. Furthermore, the extended inclusion criteria for case reports, conference abstracts, and unpublished data could reflect the real-life implementation of precision medicine in routine practice. Lastly, while the experts involved in the qualitative analysis may not represent the entirety of precision medicine researchers and practitioners in Thailand, their insights remain valuable. With a diverse array of professions actively participating in the genomic community in Thailand, their suggestions could offer a portrayal of the current landscape and highlight any existing gaps in precision medicine within the Thai context. Therefore, it would be crucial to recognize that their expertise was primarily grounded in the Thai context. Expanding the pool of experts to include individuals from diverse Asian countries would also contribute to a more comprehensive and nuanced understanding of precision medicine within the broader Asian context.

Collectively, in the Asian context, significant strides have been achieved in the field of precision medicine through the advancements in NGS technologies. In the pursuit of expanding the application of precision medicine beyond cancer, our study has showcased the effective navigation of various challenges. These challenges encompassed critical areas such as securing adequate funding, ensuring the availability of substantial sample sizes, fostering seamless interdisciplinary collaborations, bolstering computational infrastructure, and cultivating a skilled workforce. By addressing these multifaceted challenges head-on, our research would contribute to the broader mission of advancing precision medicine in both research endeavors and clinical implementation.

AUTHOR CONTRIBUTIONS

C.P., J.N., P.P., S.P.O., and S.P.A. designed the research. C.P., J.N., P.P., and J.R. performed the research. C.P., J.N., and J.R. analyzed the data. C.P. and J.N. wrote the manuscript.

ACKNOWLEDGMENTS

We would like to acknowledge the experts for sharing their perspectives and experiences with us.

FUNDING INFORMATION

This work has been supported by the National Science, Research, and Innovation Fund (NSRF, grant no. R2566B001).

CONFLICT OF INTEREST STATEMENT

The authors declared no competing interests in this work.

INFORMED CONSENT

All participants gave their informed consent to take part in this study.

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SUPPORTING INFORMATION

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How to cite this article: Phanthunane C, Pongcharoen S, Pannarunothai S, Roboon J, Phanthunane P, Nontarak J. Precision medicine in Asia enhanced by next-generation sequencing: Implications for Thailand through a scoping review and interview study. *Clin Transl Sci*. 2024;17:e13868, doi:10.1111/cts.13868