International Journal of Community Medicine and Public Health
Ludhiadch A et al. Int J Community Med Public Health. 2026 Aug;13(8):4720-4729
https://www.ijcmph.com
pISSN 2394-6032 | eISSN 2394-6040

DOI: https://dx.doi.org/10.18203/2394-6040.ijcmph20262766

Review Article

Bridging human genetics and community medicine: emerging applications for precision public health

Abhilash Ludhiadch[1]*, Raman Zaildar[2], Saurabh Kumar[3], Shiv K. Giri[3]

[1]Department of Community and Family Medicine, AIIMS, Bathinda, Punjab, India
[2]Department of Community Medicine and School of Public Health, Post Graduate Institute of Medical Education and Research, Chandigarh, India
[3]Department of Biotechnology, School of Basic and Applied Sciences, Maharaja Agrasen University, Solan, Himachal Pradesh, India

Received: 30 April 2026
Revised: 20 July 2026
Accepted: 23 July 2026

***Correspondence:**
Dr. Abhilash Ludhiadch,
E-mail: aludhiadch@gmail.com

ABSTRACT

Historically, human genetics and community medicine have evolved as separate disciplines. The domain of genetics has been on molecular mechanisms of disease and community medicine has traditionally been on prevention at the population level and health systems. Over the last two decades, advances in genomic technologies, falling sequencing costs and the expansion of large-scale biobanks have made it possible to integrate genetic insights into public health. This convergence has led to the development of precision public health, which seeks to improve disease prevention, risk stratification and health interventions at the population level. Moreover, in countries such as India, the distinct genetic diversity resulting from endogamy and founder effects points to the necessity of population-specific genomic approaches within public health frameworks. This review summarizes the existing evidence for the incorporation of human genetics into community medicine in the following areas: genetic epidemiology, population risk prediction, genetic screening across the life course, infectious disease genomics, pharmacogenomics, and genetic determinants of non-communicable diseases. It shows the potential of tools such as polygenic risk scores, pathogen genome sequencing and pharmacogenomic testing to enhance early detection, targeted prevention and rational therapeutics. The review also discusses the Indian context, with examples of national initiatives such as the Genome, India Project and the National Sickle Cell Elimination Mission as examples of translating genomic science to public health practice. Crucially, it addresses implementation challenges such as ancestry bias, ethical considerations, health system readiness, and the need for culturally sensitive community engagement.

Keywords: Precision public health, Human genetics, Community medicine, Public health genomics

INTRODUCTION

Human genetics and public health have traditionally developed in distinct spheres, genetics aimed to identify biological factors of disease, whereas community medicine focused on population-level prevention, environmental influences, and health systems.[1] In the last twenty years, the worldwide landscape has transformed significantly with the advent of public health genomics, a field that incorporates genetic findings into policies and initiatives designed to enhance population health. The global decline in sequencing costs, progress in analytics, and access to extensive biobanks (including UK Biobank, All of Us in the USA, FinnGen, and Genomics England) have facilitated unparalleled understanding of the genetic framework of complex disorders. These programs have illustrated how genomics can enhance precision prevention, risk stratification, pharmacogenomics, and population-level infectious disease control.

Genomic tools have been integrated into public health systems worldwide (Figure 1). Newborn screening (NBS) for genetic and metabolic disorders is standard in affluent nations, HPV testing via molecular assays is now the WHO-recommended primary screening method for cervical cancer and precision medicine initiatives increasingly employ polygenic risk scores (PRS) to customize preventive interventions. Furthermore, pathogen genomics was essential during the COVID-19 pandemic, allowing nations to monitor variants and inform real-time policy decisions.[2] The endorsement of CRISPR/Cas9 therapeutics for sickle cell disease and β-thalassemia in 2023–2024 represents a significant advancement, establishing gene editing as a feasible and scalable intervention for prevalent genetic disorders globally.

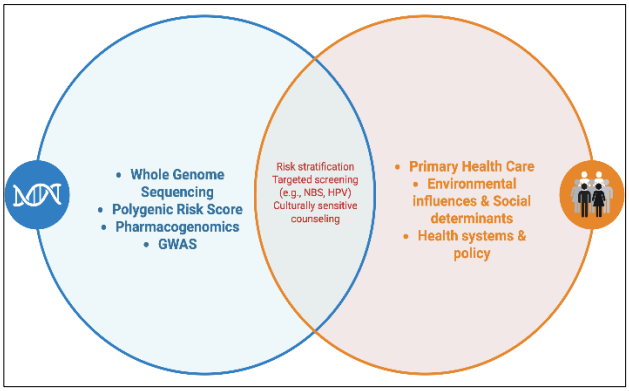

Figure 1: Roles of human genetics and community medicine in precision public health.

India reflects these global trends but encounters distinct challenges owing to its remarkable genetic diversity.[3] Endogamy, founder effects, and sociocultural stratification have led to disease burdens that are specific to certain populations, such as thalassemia, sickle cell disease, congenital hearing loss related to GJB2, and G6PD deficiency. These genetic conditions significantly impact morbidity and are unevenly distributed among caste, tribal, and regional groups, rendering genomics particularly pertinent for community-level public health planning.[4] The GenomeIndia Project has greatly improved India's genomic capabilities. Its goal is to create a complete Indian reference genome panel that will help with disease variant interpretation, pharmacogenomics, and polygenic risk prediction.[5]

India's use of CRISPR-based therapy to treat sickle cell disease is a major national achievement. The first Indian patient was treated in 2023–2024 with help from research groups from around the world. This is very important because sickle cell disease affects tribal communities that are already at a risk, and India has started the National Sickle Cell Elimination Mission (2023–2030) to bring together genomic screening, counselling, and advanced therapies.[6] Another important step forward is the creation of an HPV DNA testing kit that was made in the country and is cheap and good for screening large groups of people.[7] This breakthrough is in line with WHO's plan to eliminate cervical cancer around the world. It also lets India switch from VIA to molecular HPV testing in its national programs.[8] These changes in India and around the world show how human genetics and public health are coming together more and more. Genomic tools are becoming an important part of watching for diseases, screening for them, figuring out who is at risk, and customizing prevention. Simultaneously, community medicine offers the systems, implementation frameworks, and community involvement essential for the equitable dissemination of genomic innovations to varied populations. Therefore, it is crucial to meticulously consider the application of new findings in human genetics within community medicine and the influence of public health frameworks on the equitable, ethical, and effective utilization of genomic technology. This review synthesizes the latest studies on the convergence of human genetics and community medicine. It emphasizes practical applications, implementation challenges, and prospective developments critical for population health, particularly in low- and middle-income nations.

ROLE OF HUMAN GENETICS IN COMMUNITY MEDICINE

Genetic epidemiology and population risk assessment

Genetic epidemiology has historically functioned as a fundamental link between molecular genetics and community medicine by measuring the impact of inherited variation on disease distribution among populations.[9] Classical genetics remains tethered to familial disorders, whereas genetic epidemiology situates susceptibility within a population context, amalgamating allele frequencies, gene-environment interactions, and social determinants of health to guide prevention strategies. This field has progressed over the last twenty years from candidate-gene associations to genome-wide and population-scale analyses, rendering it directly pertinent to public health planning. In India, genetic architecture that is specific to a certain population is especially important. Extensive endogamy, founder effects, and regional stratification have led to the clustering of pathogenic variants within specific communities. Well-documented instances encompass GJB2 mutations significantly associated with congenital non-syndromic hearing loss, particularly within North and South Indian demographics. Founder BRCA1/2 variants identified in specific ethnic and religious communities.[10] The elevated occurrence of hemoglobinopathies, including sickle cell disease and β-thalassemia, in the central, western, and tribal regions of India.[4] These patterns illustrate the ineffectiveness of population-agnostic genetic models in Indian contexts and the necessity of locally sourced epidemiological data for precise risk assessment and screening design.[11] From a community medicine standpoint, this type of genetic information at the population level makes it possible to make smart decisions about which screening programs to

focus on first. Carrier screening for hemoglobinopathies, targeted newborn screening for congenital hearing loss, and cascade testing for hereditary cancers exemplify practical applications where genetic epidemiology informs public health initiatives.[12,13] These interventions are effective solely when integrated into community-based counseling frameworks that consider literacy, stigma, and cultural context domains typically addressed by community medicine. In recent years, PRS have become a strong addition to genetic epidemiology.[14] They let us measure the total genetic risk for common diseases that have many causes. PRS combine the effects of hundreds to millions of variants, each of which poses a small risk, to place people on a scale of how likely they are to get sick. Strong evidence now shows that PRS can find groups of people who are at a much higher risk for coronary artery disease, type 2 diabetes, obesity, stroke, and mental health problems, sometimes even higher than the risk levels seen in monogenic conditions.[14] When combined with standard risk factors like age, body mass index, diet, physical activity, and socioeconomic status, PRS enhance risk prediction beyond conventional models. From the perspective of community medicine, the significance of PRS resides not solely in individualized precision medicine, but in precision prevention. Using PRS to divide people into groups can help public health systems with limited resources set different screening intervals, start lifestyle changes earlier, and give priority to people who are at high risk.[15] For instance, people in the highest PRS decile for coronary artery disease might benefit from earlier lipid screening and intensive lifestyle counseling. On the other hand, people with a higher genetic risk of type 2 diabetes might be better off with structured community-based prevention programs. However, the applicability of PRS in India and other low- and middle-income countries requires careful consideration. Most PRS come from datasets with European ancestry, which makes them less accurate when used on people from different backgrounds. This limitation has significant equity ramifications, as uncritical acceptance of such scores may exacerbate health disparities. The GenomeIndia Project and GenomeAsia are two examples of projects that are starting to create genomic reference data for specific populations. This data is expected to greatly improve the calibration, validity, and interpretability of PRS for Indian populations. As these datasets grow, they will help make ancestry-informed PRS that are better for use in communities. To sum up, genetic epidemiology, along with new tools like polygenic risk scores, gives community medicine a data-driven way to figure out how risky a population is. When used wisely and ethically, these methods can help with targeted lifestyle changes, starting screening early, culturally appropriate counselling, and focusing on high-risk groups.[16] This will make the preventive side of public health stronger without going against its goal of fairness.

Genetic screening and early detection platforms

One of the most useful and important ways to use human genetics in community medicine is genetic screening. It helps doctors find people or families who are at risk for inherited or preventable diseases before they cause permanent damage. Screening is different from diagnostic testing because it tests a whole group of people instead of just one. This means that it needs to be carefully planned, with community involvement, ethical oversight, and strong ties to the health system. Community medicine is important for making genetic screening useful for public health programs.[17] It does this by making sure that the right people are chosen, that there is a lot of coverage, that there is counselling support, and that care continues.[18] Figure 2 illustrates the life-course approach to genetic screening, with a focus on important times from before birth to adulthood. It shows how screening methods change over time, from screening for inherited and metabolic disorders in pregnant women and newborns to screening for carrier status, hereditary cancer syndromes, and other genetic conditions that start in adults, all of which help prevent problems before they happen and give the right kind of help when they do.

Newborn screening

Newborn screening is seen as a very important part of keeping kids healthy around the world, and it is a great example of how genomics can be used in public health. Over the past ten years, NBS programs have grown a lot in India. Some states now use public health facilities to test for congenital hypothyroidism, G6PD deficiency, and other metabolic disorders. Early detection through biochemical screening, followed by genetic confirmatory testing, enables the swift initiation of hormone replacement or dietary management, thereby preventing intellectual disability, metabolic crises, and long-term disability. Evidence from Indian pilot and state-level programs demonstrates that the incorporation of NBS into standard postnatal services is both feasible and cost-effective when supported by referral networks and parental counselling.[19] From a community medicine perspective, the effectiveness of NBS relies on both laboratory accuracy and the execution of follow-up protocols—enabling the recall of screen-positive infants, confirmatory testing, initiation of treatment, and ongoing monitoring.[20] This shows how important it is to link genetic screening to maternal and child health services, training for health workers, and counselling that includes the whole family.

Hemoglobinopathies

Hemoglobinopathies, particularly β-thalassemia and sickle cell disease, rank among the most prevalent genetic disorders in India.[21] They demonstrate the utility of population-based genetic screening. There are programs for screening before marriage, during pregnancy, and in schools in places where there are a lot of cases, especially in the western, central, and tribal belts. These programs focus on identifying carriers, providing genetic counselling, and making informed reproductive choices to prevent the birth of children with serious diseases.[22] Studies conducted in India consistently show that the

effectiveness of hemoglobinopathy screening markedly enhances when genetic testing is incorporated into community health systems and augmented by structured counselling in primary care settings.

The National Sickle Cell Elimination Mission (2023–2030) just started, and it shows how important community medicine is for linking genetic screening with outreach, counselling, and access to higher-level care. This is especially true for tribal groups that don't get enough care.

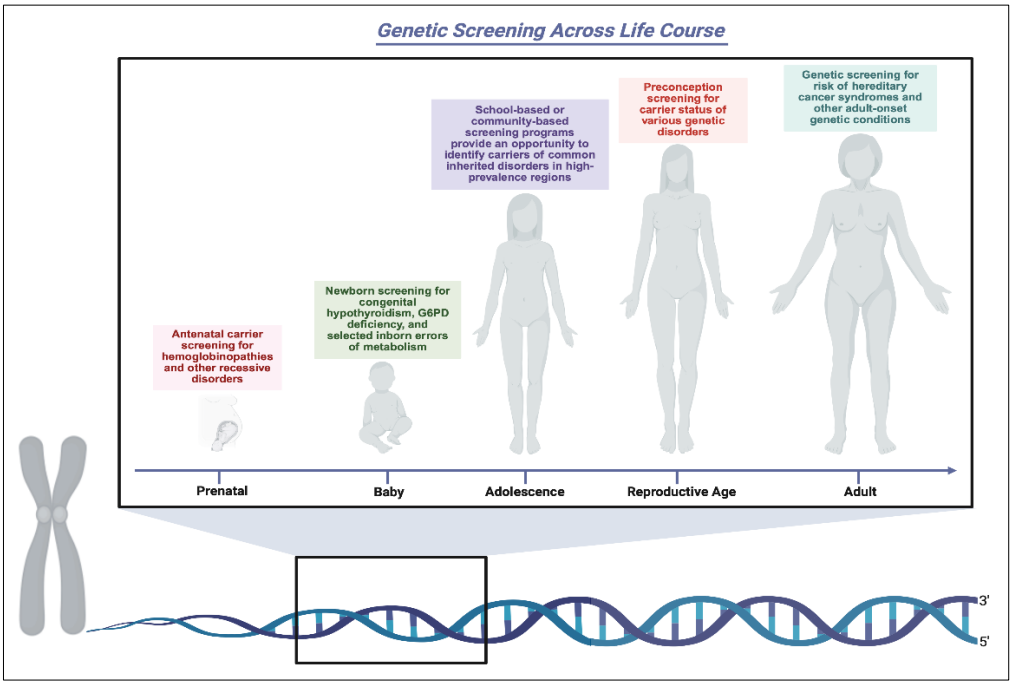

Figure 2: Genetic screening across the life course.

Hereditary cancers

Screening for hereditary cancer syndromes, such as BRCA1/2-related breast and ovarian cancer and Lynch syndrome-related colorectal cancer, constitutes an emerging area of genetic screening in public health. Traditionally confined to tertiary centers, there is an increasing recognition that community-based identification of high-risk families employing structured family history tools followed by targeted genetic testing can significantly reduce cancer morbidity and mortality through early surveillance and preventive interventions. Pilot programs in India that link genetic screening with community-based cancer awareness campaigns and outreach led by ASHA have shown promise in finding families at risk and making cascade testing easier. Community medicine helps by making sure that risk communication is culturally sensitive, fighting the stigma that comes with cancer genetics, and encouraging people to stick with long-term surveillance.

Implementation consideration

Evidence consistently shows that genetic screening works best when it is part of strong public health systems that offer counseling before and after the test, ethical oversight, ways to refer people, and communication that is sensitive to different cultures. Community medicine provides the essential implementation framework to harmonize technological advancements with equity, acceptability, and sustainability. As genetic screening expands to encompass rare diseases and prevalent multifactorial conditions, community medicine will increasingly be pivotal in assessing the efficacy of these emerging technologies in enhancing public health.

Genomics in infectious disease surveillance and control

The incorporation of genomics into infectious disease surveillance signifies one of the most significant advancements in contemporary public health. Traditionally, community medicine depended on clinical case definitions, culture-based diagnostics, and descriptive epidemiology to comprehend disease transmission and inform control measures.[22] These methods are still important, but they don't always give clear and timely results. Genomic technologies, which include both host and pathogen genomics, have completely changed this field by making it possible to track transmission dynamics in high resolution, find drug resistance early, and better assess risk during outbreaks. Genomics has changed the way we control infectious diseases in public health from a mostly reactive model to one that supports more and more proactive and targeted actions. This change has been most clearly seen during the COVID-19 pandemic, but it is also important for tuberculosis, antimicrobial resistance (AMR), influenza, dengue, and other infections that are already common or are starting to appear.

Host genetics and susceptibility to infection

Host genetic variation significantly influences susceptibility to infection, disease severity, and clinical outcomes, although this role is frequently overlooked.[23] Gene variants implicated in pathogen entry, immune recognition, and inflammatory responses such as ACE2, TMPRSS2, HLA alleles, and elements of the type I interferon pathway have been demonstrated to affect the host's response to viral infections, including SARS-CoV-2, influenza, and dengue. Evidence gathered over the last ten years indicates that variations among individuals and populations in these pathways partially elucidate the observed heterogeneity in infection rates and disease severity during outbreaks. In community medicine, the significance of host genomics is not solely in individualized prediction, but in population-level risk stratification.[24] Understanding genetic susceptibility patterns can help determine which people should get vaccinated first, which should get preventive care, and which should go to the hospital first, especially when resources are limited during an epidemic. Although widespread routine host genetic screening is not currently viable, findings from population-based studies are progressively shaping public health policy, particularly when integrated with age, comorbidities, and social vulnerability indicators.

Pathogen genomics and transmission dynamics

Pathogen genomics has likely had the most direct and noticeable effect on controlling infectious diseases. Whole-genome sequencing (WGS) enables accurate differentiation among strains, facilitating the reconstruction of transmission networks that remain undetectable by traditional epidemiological methods. WGS has become an important tool for finding drug-resistant Mycobacterium tuberculosis, telling the difference between reactivation and reinfection, and finding ongoing transmission in communities. Several studies have shown that genomic data can greatly improve the efficiency of contact tracing when used with field epidemiology. This can help plan targeted interventions.

The COVID-19 pandemic made it even clearer how important genomic surveillance is. Rapid sequencing and global data sharing made it possible to find variants of concern, figure out how easily they spread and how well they can avoid the immune system, and quickly change containment and vaccination plans. In India, national genomic surveillance networks showed how pathogen genomics can be used in a large and varied public health system, as long as labs, epidemiologists, and policymakers work together.

Genomics and antimicrobial resistance

Antimicrobial resistance (AMR) is a slowly growing but very serious public health problem, especially in countries with low or middle incomes. Genomic methods have changed how we watch for AMR by making it possible to find mutations and mobile genetic elements that cause resistance, often before phenotypic resistance shows up in the clinic. Genomic AMR surveillance enables the monitoring of resistant clones across hospitals, communities, and regions, thereby facilitating evidence-based antibiotic stewardship and infection control initiatives. Genomic AMR data give community medicine useful information that works well with syndromic surveillance and prescription audits.[25] When combined with regular surveillance systems, these data can help create treatment guidelines for the region, find places where resistance is growing, and promote the smart use of antibiotics in primary care.

Role of community medicine in genomic surveillance

Genomics is very advanced technology, but its effect on public health depends on how well it is put into practice. Community medicine is still very important in this area. Field epidemiology, systematic sample collection, outbreak investigation, and the interpretation of genomic findings within local sociocultural and environmental contexts are critical for converting sequence data into public health initiatives. Community medicine professionals are also very important for risk communication, getting people involved in their communities, and making sure that genomic surveillance doesn't just stay in labs but also helps with prevention strategies in the real world. In short, genomics has changed the way we watch for infectious diseases by making it more accurate, faster, and better at predicting what will happen.[26] However, it can only be useful for public health if there are strong community medicine frameworks that combine genomic insights with traditional epidemiology, health systems, and community engagement. The future of controlling infectious diseases does not depend solely on genomics; rather, it hinges on the synergistic integration of genomic science and population-based public health practices.

Pharmacogenomics in primary health care

Pharmacogenomics serves as a practical intersection of human genetics and community medicine, as it directly impacts the safety and efficacy of medications commonly prescribed in primary health care.[27] Inter-individual variability in drug response long recognized in clinical practice is now understood to be substantially driven by genetic variation in drug-metabolizing enzymes, transporters, and immune-related genes. Pharmacogenomics presents an opportunity to enhance outcomes on a large scale by tailoring drug selection and dosage to a patient's genetic profile, particularly in primary care settings that handle a significant share of chronic diseases, mental health disorders, and infectious diseases.

In the past, pharmacogenomic applications were only used in specialized centers. However, more and more evidence shows that they are also useful in community-based care.[28]

Changes in CYP2C9 and VKORC1, for example, account for a large part of the differences in warfarin dose requirements between people. Numerous studies have shown that dosing based on genotype speeds up the time it takes to get stable anticoagulation and lowers the risk of bleeding problems. These are important outcomes in primary care, where anticoagulation is often started and monitored.[29] Polymorphisms in CYP2D6 significantly affect the metabolism of frequently prescribed antidepressants, antipsychotics, and opioid analgesics.[30] People who metabolize drugs slowly or very quickly may not respond to treatment or have bad reactions to drugs at normal doses. Because there are so many people in the community with mental health problems and chronic pain, CYP2D6-guided prescribing could help people respond better to treatment and stick with it, while also cutting down on trial-and-error prescribing. The public health importance of pharmacogenomics is most apparent in severe adverse drug reactions. The robust correlation between the HLA-B*15:02 allele and carbamazepine-induced Stevens–Johnson syndrome and toxic epidermal necrolysis in South and Southeast Asian populations exemplifies a significant instance of genomics mitigating catastrophic consequences.[31] In many Asian countries, it is now recommended to do genetic testing for this allele before giving a prescription.[32] This shows how one genetic test can save lives, especially in places where carbamazepine is still widely used to treat epilepsy and neuropathic pain. Changes in TPMT and NUDT15 are another good example because they affect how thiopurines are broken down and the risk of severe myelosuppression.[33] Thiopurines are usually started in specialist settings, but primary care doctors often keep an eye on patients and change their doses as needed. Using pharmacogenomic information to help make treatment decisions can greatly lower the risk of side effects, hospital stays, and long-term problems. From a community medicine standpoint, the potential of pharmacogenomics extends beyond personalized precision medicine to encompass population-level safety and rational drug utilization. Adverse drug reactions are a major cause of illness, death, and high health care costs that can be avoided, especially in low- and middle-income countries.[34] Pharmacogenomics provides a preventive framework by identifying high-risk individuals prior to exposure, closely aligning with the preventive principles of primary health care. However, careful thought must go into putting it into practice in community settings. Some of the biggest problems are making tests available, paying for them, teaching providers, and figuring out how to use genetic information in clinical workflows.[35]

It is very important to create pharmacogenomic data that is specific to certain populations, especially those that are not well represented, in order to make sure that everyone gets the same benefit.[36] As national genomic projects grow and digital health systems get better, pharmacogenomics is about to become an important part of safe prescribing and patient safety in primary health care.

Genetic determinants of non-communicable diseases

NCDs are the leading cause of illness and death worldwide and present a particularly intricate challenge in low- and middle-income countries, where swift epidemiological transitions have occurred amid enduring social and environmental disparities.[37] Major NCDs like type 2 diabetes, cardiovascular disease, stroke, and common mental disorders are now known to be caused by a combination of genetic risk factors and lifestyle choices that can be changed, such as diet, exercise, smoking, stress, and exposure to harmful substances in the environment. Consequently, human genetics has advanced non-communicable disease research beyond rudimentary concepts of "genetic determinism" to a sophisticated comprehension of risk gradients among populations.

Metabolic disorders and type 2 diabetes

T2DM has been one of the most thoroughly investigated non-communicable diseases from a genetic epidemiology standpoint. Variants in genes like TCF7L2, SLC30A8, and FTO have been consistently linked to a higher risk of diabetes in many groups of people, including South Asians. It is important to note that these variants do not function independently; their effects are significantly influenced by obesity, physical inactivity, and dietary habits.[38] From the perspective of community medicine, these findings underscore the principle that genetic risk enhances rather than supplants the influence of behavioural and environmental determinants. Genetic risk information can be utilized at the population level to pinpoint individuals or subgroups that may gain from earlier screening, enhanced lifestyle intervention, or more rigorous metabolic monitoring. Evidence from prospective cohorts indicates that individuals with a high genetic risk significantly benefit from lifestyle modifications, highlighting the potential of genetics to inspire preventive measures rather than fatalism when effectively communicated.

Cardiovascular disease and polygenic risk

Cardiovascular diseases, such as coronary artery disease (CAD) and ischemic stroke, illustrate the polygenic characteristics of prevalent NCDs. Large-scale genome-wide studies have shown that PRS can divide groups of people into different risk groups. People in the highest PRS percentiles have a risk level that is similar to that of people with rare monogenic mutations. When used with other risk factors like diabetes, blood pressure, lipid levels, smoking, and diabetes, PRS slightly but consistently makes risk prediction better. For community medicine, PRS is important for precise prevention, not just for individualized therapy.[39] Using PRS to stratify populations could help start preventive measures earlier, like lifestyle counselling and drug treatments like statins, especially for people who would otherwise be considered at intermediate risk. It is also important to recognize the limitations of ancestry bias and equity, especially in countries like India

where European-derived PRS may not work as well.[40] It is therefore very important to keep working on making ancestry-informed risk scores using genomic datasets from indigenous people.

Mental health and genetic susceptibility

Mental health disorders, especially major depressive disorder (MDD), significantly impact the global NCD burden but are insufficiently acknowledged in public health frameworks. Genetic research has pinpointed several susceptibility loci, encompassing genes associated with serotonergic and glutamatergic pathways. Variants in TPH1, which affects serotonin synthesis, and DAOA, which is involved in glutamatergic neurotransmission, have been linked to susceptibility to depressive disorders and associated endophenotypes (125). From a community medicine standpoint, genetic insights into mental illness present opportunities to reconceptualize depression as a biologically influenced yet alterable condition potentially diminishing stigma and enhancing help-seeking behavior (147). Although genetic testing for depression is not presently advised in standard practice, population-level genetic research enhances risk models, facilitates early identification strategies, and fosters the creation of targeted preventive interventions, especially when integrated with psychosocial risk assessment.

Stroke and emerging sex-specific genetic risk

Stroke exemplifies a domain in which genetic epidemiology is advancing swiftly, especially concerning sex-specific genetic influences. New evidence shows that some genetic variants have different effects on stroke risk in men and women.[41-46] This is because of interactions between sex hormones, vascular biology, and genetic architecture. This has significant ramifications for public health, as stroke prevention strategies have historically employed a sex-neutral framework, notwithstanding established disparities in incidence, age of onset, and outcomes. Systematic synthesis of sex-stratified genetic data such as through meta-analyses of genome-wide and candidate gene studies holds promise for refining risk prediction and tailoring prevention strategies. From a community medicine perspective, integrating sex-specific genetic insights corresponds with overarching initiatives aimed at equity-sensitive and life-course-oriented non-communicable disease prevention.

Implications for community-based prevention

In the realm of NCDs, genetics primarily enhances community medicine through risk stratification, targeted prevention, and the facilitation of improved health communication. When genetic risk information is combined with behavioural and environmental data, it can help people stick to lifestyle changes, encourage earlier screening, and make prevention more personal without getting in the way of population-wide efforts. Community medicine also plays a big role in making sure that genetic information is shared in a way that is fair, doesn't make people feel bad about themselves, and is used to give people and communities power instead of putting them in a box. In short, genetic factors that cause NCDs add to our understanding of public health strategies, but they don't replace them. The task ahead is to turn what we know about genetics into interventions that are fair, scalable, and strengthen existing NCD programs while also taking into account the complicated social situations in which these diseases happen. Figure 3 represents a stepwise model that uses genomic inputs like monogenic variants and PRSto divide a population into low, intermediate, and high-risk groups. Which further helps public health officials decide what actions to take, and these actions are backed by policy, ethical governance, health systems, and community involvement to make sure they are fair and can be used by everyone.

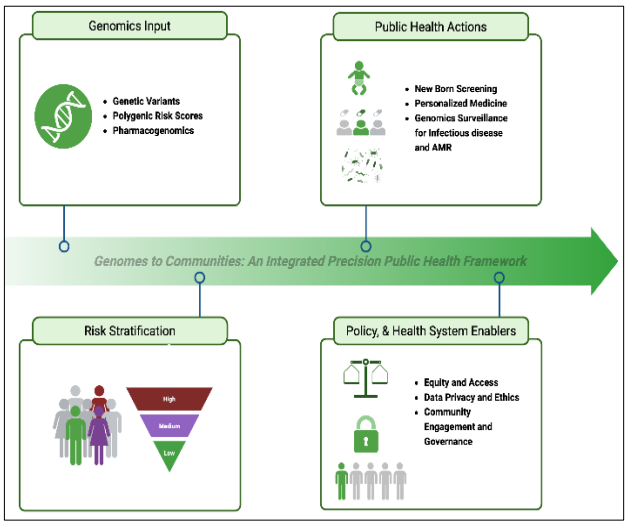

Figure 3: Integrated precision public health framework.

FUTURE DIRECTIONS

The future of community medicine depends on how well "precision medicine" and "precision public health" work together. We need to go beyond biological reductionism and adopt a socio-genomic framework that combines multi-ancestry PRSwith actual social determinants of health (SDOH). A critical priority is the democratization of genomics; researchers must prioritize the inclusion of underrepresented populations in global biobanks to ensure that predictive models are valid for the Global South, thereby preventing a "genomic divide".

The next ten years should also be about Implementation Science 2.0, which uses AI-driven platforms to put pharmacogenomics and pathogen surveillance right into primary care workflows. Finally, it's important to set up strong ethical guidelines for community-led data sovereignty to build trust and make sure that new technologies, like CRISPR-based therapies, stay fair and available to everyone.

CONCLUSION

The integration of human genetics and community medicine signifies a revolutionary phase for global health, shifting the discipline from a reactive framework to one of precision public health. This review emphasizes that genomic tools such as polygenic risk scores, pathogen sequencing, and pharmacogenomic screening are no longer limited to specialized laboratories; they are becoming essential for population-level risk stratification and the control of infectious diseases. But to move forward, we need to be very committed to fairness and implementation science. We need to actively reduce ancestry biases in genomic datasets so that new technologies don't make health disparities worse. We can move from care that focuses on individuals to a sustainable, proactive model by putting these advanced molecular insights into the strong frameworks of primary health care and community engagement. In the end, the combination of genomic science and social determinants of health is what will give communities the power they need to lower the global burden of both communicable and non-communicable diseases.

Funding: No funding sources
Conflict of interest: None declared
Ethical approval: Not required

REFERENCES

1. Khoury MJ, Burke W, Thomson EJ. Genetics and public health: A framework for the integration of human genetics into public health practice. Genetics and Public Health in the 21st Century: Using Genetic Information to Improve Health and Prevent Disease, Oxford Monographs on Medical Genetics (New York, 2000; online edn, Oxford Academic. 2009.
2. Jimenez-Silva C, Rivero R, Douglas J, Bouckaert R, Villabona-Arenas CJ, Atkins KE, et al. Genomic epidemiology of SARS-CoV-2 variants during the first two years of the pandemic in Colombia. Commun Med. 2023;3(1):97.
3. Basu A, Sarkar-Roy N, Majumder PP. Genomic reconstruction of the history of extant populations of India reveals five distinct ancestral components and a complex structure. Proc Natl Acad Sci U S A. 2016;113(6):1594-9.
4. Sinha S, Seth T, Colah RB, Bittles AH. Haemoglobinopathies in India: estimates of blood requirements and treatment costs for the decade 2017–2026. J Community Genet. 2020;11(1):39-45.
5. Bhattacharyya C, Subramanian K, Uppili B, Biswas NK, Ramdas S, Tallapaka KB, et al. Mapping genetic diversity with the GenomeIndia project. Nat Genet. 2025;57(4):767-73.
6. National Sickle Cell Anaemia Elimination Mission. Guidelines & Training Materials. Available at: https://sickle.nhm.gov.in/home/guidelines. Accessed on 12 May 2026.
7. Union Minister Dr. Jitendra Singh convenes a joint meeting of Department of Biotechnology, AIIMS New Delhi, BIRAC, ICMR and Industry partners to review the indigenously developed HPV test kits for Cervical Cancer screening in India Calls Scientific Review of Indigenously Developed HPV Test Kits for Cervical Cancer Screening. Available at: http://www.pib.gov.in/PressReleseDetail.aspx?PRID=2123856&reg=3&lang=2. Accessed on 12 May 2026.
8. World Health Organization. WHO guideline for screening and treatment of cervical pre-cancer lesions for cervical cancer prevention. 2021. Available at: https://www.who.int/publications/i/item/9789240030824. Accessed on 12 May 2026.
9. Khoury MJ. Genetic Epidemiology and the Future of Disease Prevention and Public Health. Epidemiol Rev. 1997;19(1):175-80.
10. Singh J, Thota N, Singh S, Padhi S, Mohan P, Deshwal S, et al. Screening of over 1000 Indian patients with breast and/or ovarian cancer with a multi-gene panel: prevalence of BRCA1/2 and non-BRCA mutations. Breast Cancer Res Treat. 2018;170(1):189-96.
11. Moreno-Grau S, Vernekar M, Lopez-Pineda A, Mas-Montserrat D, Barrabés M, Quinto-Cortés CD, et al. Polygenic risk score portability for common diseases across genetically diverse populations. Hum Genomics. 2024;18(1):93.
12. Jha RK, Kaple M, Ambad RS, Dhok A, Anjankar A. Comprehensive Neonatal Screening for Genetic Disorders in Tribal Populations of Central India. J Pharm Bioallied Sci. 2024;16(Suppl 4):S4021-5.
13. Pandharipande A, Radhakrishnan N, Verma S, Chauhan VK, Baby EP, Srivastava A. Barriers to cascade screening and prenatal testing in families with genetic haematological diseases. J Rare Dis. 2025;4(1):18.
14. O'Sullivan JW, Ashley EA, Elliott PM. Polygenic risk scores for the prediction of cardiometabolic disease. Eur Heart J. 2023;44(2):89-99.
15. Rout M, Wander GS, Ralhan S, Singh JR, Aston CE, Blackett PR, et al. Assessing the prediction of type 2 diabetes risk using polygenic and clinical risk scores in South Asian study populations. Ther Adv Endocrinol Metab. 2023;14:20420188231220120.
16. Kachuri L, Chatterjee N, Hirbo J, Schaid DJ, Martin I, Kullo IJ, et al. Principles and methods for transferring polygenic risk scores across global populations. Nat Rev Genet. 2024;25(1):8-25.
17. CDC. ACCE Model Process for Evaluating Genetic Tests. 2022. Available at: https://archive.cdc.gov/www_cdc_gov/genomics/gtesting/acce/index.htm. Accessed on 12 May 2026.
18. World Health Organization. Cancer - Screening and early detection. Available at: https://www.who.int/europe/news-room/fact-sheets/item/cancer-screening-and-early-detection-of-cancer. Accessed on 12 May 2026.

19. Raveendran A, Chacko TJ, Prabhu P, Varma R, Lewis LE, Rao P, et al. Need and Viability of Newborn Screening Programme in India: Report from a Pilot Study. Int J Neonatal Screen. 2022;8(2):26.
20. Friedman JM, Cornel MC, Goldenberg AJ, Lister KJ, Sénécal K, Vears DF, et al. Genomic newborn screening: public health policy considerations and recommendations. BMC Med Genomics. 2017;10(1):9.
21. Jena RK, Sethy S, Dash PK, Behera M, Palande B, Dave U. Hemoglobin Variant Analysis and Its Comparison between Conventional High-performance Liquid Chromatography Using Whole Blood versus Dried Blood Spot: High-performance Liquid Chromatography. Indian J Public Health. 2025;69(3):280.
22. Mami DM, Romba M, Patrick M. The Surveillance in Infectious Disease Control Role of Genomic. Int J Adv Multidisc Res Stud. 2025;5(4):1608-15.
23. van der Made CI, Netea MG, van der Veerdonk FL, Hoischen A. Clinical implications of host genetic variation and susceptibility to severe or critical COVID-19. Genome Med. 2022;14(1):96.
24. Sun N, Lu Y, Li C, Jiang A, Liu L, Guo J. Genetic Risk of Different Populations in COVID-19 Susceptibility and Severity. Infect Drug Resist. 2025;18:5499-505.
25. Sulis G, Sayood S, Gandra S. Antimicrobial resistance in low- and middle-income countries: current status and future directions. Expert Rev Anti Infect Ther. 2022;20(2):147-60.
26. Grubaugh ND, Ladner JT, Lemey P, Pybus OG, Rambaut A, Holmes EC, et al. Tracking virus outbreaks in the twenty-first century. Nat Microbiol. 2019;4(1):10-9.
27. Rigter T, Jansen ME, de Groot JM, Janssen SWJ, Rodenburg W, Cornel MC. Implementation of Pharmacogenetics in Primary Care: A Multi-Stakeholder Perspective. Front Genet. 2020;11:10.
28. Kabbani D, Akika R, Wahid A, Daly AK, Cascorbi I, Zgheib NK. Pharmacogenomics in practice: a review and implementation guide. Front Pharmacol. 2023;18:14.
29. Johnson JA, Gong L, Whirl-Carrillo M, Gage BF, Scott SA, Stein CM, et al. Clinical Pharmacogenetics Implementation Consortium Guidelines for CYP2C9 and VKORC1 genotypes and warfarin dosing. Clin Pharmacol Ther. 2011;90(4):625-9.
30. Jukic MM, Smith RL, Haslemo T, Molden E, Ingelman-Sundberg M. Effect of CYP2D6 genotype on exposure and efficacy of risperidone and aripiprazole: a retrospective, cohort study. Lancet Psychiatry. 2019;6(5):418-26.
31. Nakkam N, Konyoung P, Amornpinyo W, Saksit N, Tiamkao S, Khunarkornsiri U, et al. Genetic variants associated with severe cutaneous adverse drug reactions induced by carbamazepine. Br J Clin Pharmacol. 2022;88(2):773-86.
32. Tiwattanon K, John S, Koomdee N, Jinda P, Rachanakul J, Jantararoungtong T, et al. Implementation of HLA-B*15:02 Genotyping as Standard-of-Care for Reducing Carbamazepine/ Oxcarbazepine Induced Cutaneous Adverse Drug Reactions in Thailand. Front Pharmacol. 2022;13:867490.
33. Matsuoka K. NUDT15 gene variants and thiopurine-induced leukopenia in patients with inflammatory bowel disease. Intest Res. 2020;18(3):275-81.
34. Sultana J, Cutroneo P, Trifirò G. Clinical and economic burden of adverse drug reactions. J Pharmacol Pharmacother. 2013;4(Suppl 1):S73-7.
35. Haga SB, Burke W, Ginsburg GS, Mills R, Agans R. Primary care physicians' knowledge of and experience with pharmacogenetic testing. Clin Genet. 2012;82(4):388-94.
36. Sirugo G, Williams SM, Tishkoff SA. The Missing Diversity in Human Genetic Studies. Cell. 2019;177(1):26-31.
37. Hay SI, Ong KL, Santomauro DF, A B, Aalipour MA, Aalruz H, et al. Burden of 375 diseases and injuries, risk-attributable burden of 88 risk factors, and healthy life expectancy in 204 countries and territories, including 660 subnational locations, 1990–2023: a systematic analysis for the Global Burden of Disease Study 2023. The Lancet. 2025;406(10513):1873-922.
38. Qi L, Cornelis MC, Zhang C, van Dam RM, Hu FB. Genetic predisposition, Western dietary pattern, and the risk of type 2 diabetes in men. Am J Clin Nutr. 2009;89(5):1453-8.
39. Khera AV, Emdin CA, Drake I, Natarajan P, Bick AG, Cook NR, et al. Genetic Risk, Adherence to a Healthy Lifestyle, and Coronary Disease. N Engl J Med. 2016;375(24):2349-58.
40. Wang Y, Namba S, Lopera E, Kerminen S, Tsuo K, Läll K, et al. Global Biobank analyses provide lessons for developing polygenic risk scores across diverse cohorts. Cell Genomics. 2023;3(1):100241.
41. Howard DM, Adams MJ, Clarke TK, Hafferty JD, Gibson J, Shirali M, et al. Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. Nat Neurosci. 2019;22(3):343-52.
42. Chen D, Liu F, Yang C, Liang X, Shang Q, He W, et al. Association between the TPH1 A218C polymorphism and risk of mood disorders and alcohol dependence: evidence from the current studies. J Affect Disord. 2012;138(1–2):27-33.
43. Khoodoruth MAS, Estudillo-Guerra MA, Pacheco-Barrios K, Nyundo A, Chapa-Koloffon G, Ouanes S. Glutamatergic System in Depression and Its Role in Neuromodulatory Techniques Optimization. Front Psychiatry. 2022;13:886918.
44. Lebowitz MS. The Implications of Genetic and Other Biological Explanations for Thinking about Mental Disorders. Hastings Cent Rep. 2019;49 Suppl 1(Suppl 1):S82-7.

45. Baek CH, Kim HJ, Park HY, Seo HY, Yoo H, Park JE. Influence of Biogenetic Explanations of Mental Disorders on Stigma and Help-Seeking Behavior: A Systematic Review and Meta-Analysis. J Korean Med Sci. 2022;38(3):e25.
46. Traylor M, Rutten-Jacobs LCA, Holliday EG, Malik R, Sudlow C, Rothwell PM, et al. Differences in Common Genetic Predisposition to Ischemic Stroke by Age and Sex. Stroke. 2015;46(11):3042-7.

Cite this article as: Ludhiadch A, Zaildar R, Kumar S, Giri SK. Bridging human genetics and community medicine: emerging applications for precision public health. Int J Community Med Public Health 2026;13:4720-9.