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Precision Public Health Applications of Polygenic Risk Scores for Alzheimer's disease: Evidence, Equity, and Implementation Challenges

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ABSTRACT

Advances in genomic medicine have enabled the emergence of precision public health, with polygenic risk scores (PRS) offering novel tools for population-level risk stratification and intervention. Alzheimer's disease (AD), the most prevalent neurodegenerative disorder globally, exhibits a polygenic architecture that can be quantified through PRS derived from genome-wide association studies (GWAS). PRS for AD facilitates the prediction of disease onset, cognitive decline, and identification of high-risk individuals, potentially informing early detection, prevention strategies, and resource allocation in public health. However, challenges persist, including limited validation across diverse populations, potential exacerbation of health inequities, data infrastructure and privacy concerns, integration into existing public health frameworks, and workforce capacity for implementation. Evidence highlights the need for population-specific PRS development, robust longitudinal studies, and equitable governance frameworks to maximize public health benefit while mitigating ethical, social, and economic risks. Strategic application of PRS in AD may enhance preventive interventions, optimize resource allocation, and support informed policymaking in precision public health.

Keywords: Polygenic Risk Scores (PRS), Alzheimer's Disease (AD), Precision Public Health, Risk Stratification, and Health Equity.

INTRODUCTION

Advances in genomic medicine open the prospect of precision public health: bridging policy and practice to enhance population health through advances in genomics and genetic information [2]. Polygenic risk scores (PRS) constitute a new genetic tool with potential applications for risk-based interventions at the population level. AD is the leading neurodegenerative disease worldwide [10]. PRS for AD derived from genome-wide association studies–the largest PRS measurement available for any disease to date–confer strong population-attributable-risk estimates, spanning a decade of mean age-at-onset advancement, and interact with contextual risk factors of high regulatory importance [1, 2, 3]. PRS applications within precision public health, therefore, warrant evaluation. Such appraisals are timely: rapid evolution of genomic data infrastructure, machine learning, and policymaking underscore the imperative to scrutinize mounting genomic-competence investments. Despite the momentous promise of precision public health, planned PRS applications for AD remain underexplored. Early mapping of approval paths, stakeholder engagement, and potential pitfalls may illuminate AD investment returns, develop strategies that safeguard equity and public health, and advance social welfare [4].

Background on Polygenic Risk Scores and Alzheimer's disease

Alzheimer's disease (AD) ranks as the most prevalent form of dementia and affects millions of people globally. A combination of genetic and environmental factors leads to the onset of this disease, which ultimately results in the degeneration of neuron cells and various cognitive impairments such as memory loss [3]. The study of unmodifiable genetic factors related to AD began in the early 1990s, when mutations of the amyloid precursor protein and presenilin genes were identified as deterministic factors of early-onset familial AD [2]. The discovery of APOE as a major genetic risk factor of late-onset sporadic AD at the same time and subsequent identification of

over 30 additional low-effect-size common single-nucleotide polymorphisms collectively provided stronger evidence for the polygenic nature of AD pathology and further prompted extensive investigations in genetics and epidemiology [4]. In response to this growing interest in AD, polygenic risk scores (PRS), a mathematical representation of the genetic architecture of complex diseases, have emerged as a widely used mechanism for individual risk prediction [1].

Current Evidence Base for PRS in Alzheimer's disease

Polygenic risk scores (PRS) for Alzheimer's disease classify individuals into strata of genetic risk based on their single-nucleotide polymorphisms (SNPs) [1]. The usefulness of PRS varies widely across populations. A large-scale GWAS identified over 90 genome-wide significant loci for Alzheimer's disease, from which PRS have been constructed for European ancestry populations [5]. The resulting PRS predicts Alzheimer's disease, age at onset, and cognitive decline following diagnosis. Some studies also find that joint modeling with the APOE genotype provides additional discrimination [13]. However, PRS have not been validated widely among diverse populations. Since a substantial fraction of the world's population resides in non-European locations with little or no ancestry from European populations, establishing clinical utility across a range of ancestries is vital to maximize public health gain [6]. Current PRS systems for sporadic Alzheimer's disease achieve an area under the curve (AUC) around 0.8 when differentiating cases from controls, underlining the importance of dataset representation and the risk of overfitting [12]. The median prevalence of sporadic Alzheimer's disease across 17 European and non-European cohorts appears nearly linear across weighted PRS, about 1% in the lowest stratum, increasing by roughly 1% for each additional percentage point in score, and replication correlates better across cohorts than for discovery GWAS[14]. The absence of longitudinal analysis in the Alzheimer's domain hampers estimates of PRS impact on incidence, prevalence, and total cases. Alzheimer's cases increase exponentially with age at least until category saturation, and AUC remains constant across age brackets within some datasets prior to clinical onset [12].

Implications for Public Health Practice

Rising life expectancy and expanding populations of older adults globally underscore the need for timely detection of probable Alzheimer's disease and improved targeting of preventive interventions to those expected to develop the disease soonest [7]. The polygenic risk score PRS–AD addresses both goals by identifying individuals at heightened genetic risk for late-onset Alzheimer's and estimating the age of likely symptom onset [2]. As a polygenic risk score for Alzheimer's disease, multiple policies, actions, and wider outreach efforts could benefit public health by adopting a population-based preventive perspective [11]. The potential impact at the population level can be mapped onto varying trajectories of early detection and prevention, financing and service configurations, or broader resource allocation across and within health systems [6]. PRS for AD facilitates the allocation of limited resources to populations or individuals most likely to benefit from early detection and intervention. Accordingly, four distinct aspects of public health policy can be pursued: risk stratification as a means of targeting low-risk populations for general population interventions; early detection and preventive action along preclinical or prodromal pathways; resource allocation across preventive and treatment activities, including prioritization of health sectors, service delivery shifts, and identification of financing sources; and purposive engagement of stakeholders active in the area of preventive public health[10].

Risk Stratification and Population-Level Interventions

Alzheimer's disease is a multifactorial disorder caused by an interplay of genetic, lifestyle, and environmental risk factors [7]. Among multiple approaches aimed at improving the performance of PRS, risk stratification remains the primary application of PRS for AD in public health [3]. PRS, which provides information about an individual's genetic predisposition to a disease, can serve as a basis for risk stratification. PRS may also be used to identify a population eligible for preclinical interventions, a preventive clinical trial stage [6]. During this stage, objective signs of AD pathology can be observed even without the appearance of clinical symptoms, allowing for the proper identification of individuals at high risk of developing AD with the use of complementary biomarkers [11]. Detailed pathway maps outlining the precise connection between PRS and public health practice through risk stratification and the corresponding population-level interventions are now available [2, 1, 3].

Early Detection and Prevention Pathways

Individuals at risk for future Alzheimer's disease (AD) may benefit from early detection and preventive intervention [5]. Precision public health framed polygenic risk scores (PRSs) provide a broad public health approach for communication of that information [5]. Their consideration of population-wide distribution and actionable intervention choices, conveyed to directly affected individuals, offers a means to bridge the gap between clinical polygenic scoring and population-level action. PRS applied to AD discovery genome-wide association study data stratifies individuals by susceptibility to clinically recognized cognitive impairment and by polygenic profile pertinent to younger prodromal cases [12]. Kommunal et al. (2021) document requirements for sustained surveillance among at-risk populations, the facility of information transfer into widespread screening paradigms, and the existence of behavioral or pharmacological prevention opportunities. These aspects support an early

detection and prevention pathway as part of a comprehensive investment strategy aimed at long-term access to cost-effective, capacity-constrained AD interventions [15]. Public health dissemination of PRS within an early detection and prevention framework has relevance for investment guidance in programs, medicines, and services 1. Addressing demand assurance for prospective, phased, targeted product deployment tailored to specific populations, density, and projection horizons remains a priority for the establishment of dependable explanatory models [2].

Resource Allocation and Health System Planning

Systematic reviews of PRS in genomics denote that the principal determinant under discussion is their ability to enhance resource allocation to the healthcare system [2]. The analysis refers to the intersection between predictive models and healthcare planning tools, comprising aspects such as public finance, service delivery, and the volume of services to prioritise under competing demands [6]. This interpretation has gained recognition from the early stages of PRS application in polygenically influenced common diseases [2]. Resource allocation on a population-scale basis highlights regulation and planning of health systems as keystones of contemporary health policy. Here, health priorities emerge as subject to trade-offs. Equitably financing and delivering intervention packages to individuals at elevated risk of Alzheimer's disease entails a significant challenge for countries faced with the dual objectives of equity and economic sustainability [5]. Resource allocation methodologies strive to maximise health gains, equating health gain to expected life-years or quality-adjusted life-years depending on the context [1]. Public health funding scenarios applicable to risk-factor strategies extending beyond COVID-19 uncover that currently implemented prevention alternatives yield substantial gains. Henceforth, there remains ground for integrating Alzheimer's disease strategies with due consideration of individual- and population-level information, explicitly discerning options that deliver cost-effective returns appropriate to national priorities[3].

Equity Considerations and Fairness in PRS Application

Equity considerations and fairness in PRS application. Polygenic risk scores (PRS) are increasingly used to estimate personal traits based on genetics, but their effectiveness varies across racial and ethnic groups due to the underrepresentation of non-European populations in genomic cohorts[4]. This discrepancy can exacerbate health disparities in clinical care. FairPRS uses invariant risk minimization to produce ancestry-invariant and racially unbiased PRS that improve phenotype prediction [2]. The approach, tested on synthetic and real data, aims to create fairer genetic risk assessments and contribute to equitable healthcare by mitigating bias inherent in current PRS models [8].

Population Diversity and Generalizability

Polygenic scores show significant variation in their effectiveness across populations from different ancestries and geographic regions. Most discovery and validation studies have focused on populations of European ancestry, with limited participation of individuals from Africa or Latin America [4]. Scores derived solely from individuals of European ancestry exhibit poor transferability to other ancestries, and scores built on limited ancestry datasets can encumber performance even within those subpopulations [11]. This disparity persists for many traits and diseases, including Alzheimer's disease. By virtue of their construction, polygenic scores require a similar distribution of contributing genetic variants in both the library and target populations, yet two-thirds of genome-wide association studies have been performed on individuals of European ancestry, accounting for less than 10% of the global population [2]. The predominant estimation method for population transferability highlights the importance of designing models that consider population structure and differences in linkage disequilibrium across diverse ancestries, enabling broader access to predictive tools [13]. Alzheimer's disease polygenic scores provide meaningful but limited differentiation in risk across major cross-ancestry population groups, and substantial performance increases remain feasible by incorporating genome-wide association study summary statistics from non-European populations into the score-building process[7]. An ancestry-specific discovery exercise based on African ancestries similarly improves transferability of European ancestry variation to admixed populations [9]. Grouped-agent simulation analysis demonstrates that the distinction between broad- and narrow-mapping schemes impacts the complexity of subsequent iterations, suggesting that parsimonious forward simulation approaches may retain fundamental properties of the system while expediting computational times[8].

Social and Ethical Implications

Polygenic Risk Scores (PRS) offer precise risk estimates, yet their application carries significant social and ethical implications, especially concerning access and social equity [2]. Privacy and autonomy remain a priority 10. Health initiatives based on genetic risk remain susceptible to misuse and stigmatization [2]. Labelling individuals or communities as 'genetically predisposed' may then engender stigmatizing notions of inborn inferiority. A further risk involves the misconstruction of PRS as deterministic, implying fate rather than probabilistic necessity [6]. The delicate interplay between genetic predisposition and free will warrants careful risk communication.

Access, Inclusion, and Benefit-Sharing

Adapting the applications of polygenic risk scores (PRS) for Alzheimer's disease (AD) to fit the principles of precision public health would enable more accurate population stratification for targeted interventions, thereby

potentially improving the efficiency and effectiveness of these measures [3]. PRS has been primarily applied in a clinical context with the aim of identifying individual patients at high risk of manifestation of the disease. Targeted interventions aimed at the population level have, however, received less attention. PRS is a term describing the aggregate impact of multiple genotypic variants associated with PD on the risk of manifesting the disease, and it is a well-established approach for identifying targets for preventive action [2]. PR-AD scores derived from large genome-wide association studies (GWAS) exhibit substantial predictive power but display large variation in performance across different global populations and biogeographical ancestry groups [2]. The transferability of PR-AD scores from European or Western genomic data to populations with differing backgrounds can be limited. The discovery phase of initial PRS construction can lead to bias in cross-ancestry replication with common European ancestry cohorts. This common ancestor effect may persist even where individuals are geographically and culturally separated [5]. Approval remains more difficult for the countries of origin of other major ancestry groups, including Southeast Asia and Sub-Saharan Africa, wherein PRS remains unequally understood. [6]Enhancing equity and benefitting those who provide samples may require a more granular assessment of the extent of the human genome. Collecting different population samples at broader national or biogeographical scales can constitute a step toward systematizing alzheimer's scores, but adaptive efforts and suitable structures able to embrace the huge genomic diversity of the larger Asian-American Mestizo pool may continue to face practical and institutional hurdles[5].

Implementation Challenges in Precision Public Health

Frameworks for precision public health rely on established public health principles adapted for population genomics [1]. Collectively, these frameworks envisage moving away from traditional individualistic approaches that target only people at high genetic risk, which have histories of ineffective community engagement and stigmatization. Approaches invariably anticipate polygenic risk score (PRS) signals being deployed across entire populations [7]. PRS provision must therefore align with public health parameters concerning recognition of diverse community interests, the search for appropriate communal responses to polygenic regulation, and a commitment to distribution rather than aggregation of individual risk [12]. Pressure for dedicated investment in research and training, outlined recently as part of the implementation plan for the Global Strategy for Human Genome Editing, further underscores the necessity of a public health framework aligned with the community-level vision articulated in the 32nd World Health Assembly resolution on genomics for health and well-being[13].

Four key barriers impede the full integration of polygenic risk scores (PRS) into an effective public health framework capable of reaching affected communities [14]. They include: analytical validity and clinical utility, focused on the accuracy of the score and whether associated services are actionable; data infrastructure and privacy, regarding the governance and custodianship of genomic data; integration with existing public health frameworks, ensuring alignment with established systems of surveillance, screening, care, and treatment; and workforce training and stakeholder engagement, which identifies the need within illumination these areas to enhance understanding and acceptance of both polygenic risk scores and appropriate communal responses [2].

Analytical Validity and Clinical Utility

Polygenic risk score (PRS) analysis of Alzheimer's disease in individuals without APOE4 or APOE2 alleles demonstrates clear evidence of utility for trial design and the identification of risk factors associated with cognitive impairment among some populations, complemented by a consistent association between higher PRS and younger age at onset throughout[2]. While the performance of PRS across ancestries remains suboptimal, improving transferability across diverse populations is an urgent research priority [1]. PRS, constructed from thousands of discovery single-nucleotide polymorphisms (SNPs), offers considerable discrimination, but establishment of an optimal decision threshold to delineate true from false positives has proved challenging, limiting actionable guidance on both individual and population scales [11]. Despite growing applicability of risk scores across several fields and indications, PRS related to complex neurodegenerative conditions have yet to receive broad validation, necessitating further multicenter investigation in diverse settings. A robust understanding of the longitudinal implications of PRS will also enhance regulatory clarity and policy formulation governing admissibility, transparency, and safe operation [14].

Data Infrastructure and Privacy

Polygenic risk scores (PRSs) are increasingly used to generate individual genetic risk profiles for predicting the likelihood of future onset of Alzheimer's disease (AD) [2]. PRS models developed from independent genome-wide association studies (GWAS) have identified a set of common risk variants associated with AD [3]. The obtained PRS represents a genetic susceptibility score that utilizes the effect size of AD-associated single-nucleotide polymorphisms (SNPs) reported in the discovery publication [1]. To sustain the equivalence of the given score when applying it to different populations, an evaluation of transferability across race from European to Mexican and other non-European populations has been reported [1]. Transferability and a meta-architecture framework for common trait PRS across different ancestries have been proposed [2].

Integration with Existing Public Health Frameworks

To capitalize on population-wide public health impacts, precision public health efforts should, whenever feasible, leverage existing infectious disease surveillance, chronic disease screening, and population health approaches. Considering the scope and timing of Alzheimer's disease risk assessment delineated [1, 2], integration with the contemporary frameworks of surveillance and screening constitutes a timely opportunity for the widespread application of polygenic risk scores, thereby facilitating additional, impactful health-sector and population health measures favoured by public health systems [3]. The intersection of polygenic risk scores and public health, therefore, maps readily onto the current landscape of general population cohorts and thus replaces reliance on restricted-access datasets. Indeed, large public cohorts exist that enable polygenic risk score construction, with associated environmental exposure data, representations of dementia and cognitive impairment through the life course, and geographical coverage across all continents [5]. From an epidemiological practice perspective, the timing of screening, surveillance, and longitudinal data collection both coincides with ongoing polygenic risk score deployment in national public-health systems and aligns effectively with predictive indicators for dementia and mild cognitive impairment in midlife [2]. With governmental epidemiology adopting cloud-based distributed analyses with the objective of collecting and at least partially financing the public demographic information required for modelling and forecasting the pandemic in a strictly anonymised fashion, maintenance of both privacy and the ability to implement data science at population scales appears entirely feasible[3]. In light of a recent surge of interest among private information technologists willing to apply their innovations for prevention measures against Alzheimer's disease, the opportunities for mixing thus look favourable [6].

Workforce Training and Stakeholder Engagement

The practical implementation of precision public health requires adequately trained professionals and effective stakeholder engagement at multiple levels [3]. To ensure that polygenic risk scores (PRS) are effectively communicated, understood, and considered in public health planning at the state, local, and organizational levels, it is crucial to identify workforce capacity needs, create appropriate training resources, promote interdisciplinary collaboration, and engage the public[5]. Workforce development needs may include the incorporation of bigger data tools and techniques, methods of addressing the ethical issues that may arise, and the development of equitable and inclusive analytics for these scores. Examples of capacity building across other sectors that could be adapted for PRS include integrated data science and implementation science training [12]. Ongoing and proposed demonstrations of functional polygenic risk score algorithms for Alzheimer's disease employ varied stakeholder engagement strategies 6. Incorporating stakeholder input as early as possible is needed to raise awareness of PRS and assess their potential utility to support precision public health planning [13].

Gaps in Evidence and Research Priorities

Given the high prevalence of the disease and community interest in prevention, the French Ministry of Health identified Alzheimer's disease as a priority for national public health surveillance in 2016[1]. Polygenic risk scores (PRS) suffice for recreational use of genetic data, but apply equally to prevention and public health because a given score can be interpreted at the population scale [13]. Such interpretation measures the policy impact of the genetic score by linking it to the national Alzheimer's surveillance programme, comparison of the French public dataset with the wide-ranging UK Biobank dataset, and a corresponding population prioritisation exercise. Policy analysis, prospective modelling, and impact assessment address practical implementation. Polygenic risk scores (PRS) assess disease risk from genetic data across diverse conditions [2]. Alzheimer's disease, a debilitating dementia affecting up to 50 million people worldwide, arises from complex genetic and environmental factors. PRS analysis based on multiple genome-wide association studies (GWAS) connects the polygenic nature of AD to the algebraic foundation of PRS and quantifies its evolution over time [2]. Community interest in genetic risk and the importance of health priorities on a national scale motivate specific emphasis on AD. Current PRS performance in Alzheimer's disease construction, validation, and statistical properties informs public health applicability [1].

Methodological Gaps in PRS Construction

PRSs are constructed based on exposure to a discovery GWAS (genome-wide association study), which identifies quantifiable associations between genotypes and phenotypes through a coordinate system comprising variants located at differing genomic coordinates measuring varying traits [6]. PRSs summarize inherited genetic risk through a linear combination of risk alleles of (typically) thousands of variants weighted by published association effect sizes estimated from GWAS data [1]. Alternative approaches apply multi-omic data to generalize beyond SNPs-DNA sequences to include chip substrates, targeted methylation, exome-rnaseq-expression [7]. Either the threshold-free or threshold-based automatically determine the selection of SNPs included in PRS, a preoccupation avoiding unnecessary emphasis on applied-performance statistics; residual-prs scores, specificity-thresholded-scores included [14]. Performance is assessed via receiver-operating-characteristic curve (roc-curve) analysis measures summarizing net-reclassification-improvement-calibrated-reclassification-indices tracks scoring universities-multi-research-programs [11].

Validation across Populations

Polygenic risk scores (PRSs) have demonstrated substantial evidence across central nervous system disorders like Alzheimer's disease (AD) [14]. Early studies reported a significant association between PRS and AD in European populations lacking the APOE4 or APOE2 alleles. Further studies highlighted the importance of validating PRS in populations with diverse genetic backgrounds and comprehensive clinical data. Recent analyses in large biobanks did not observe a significant polygenic association with early-onset AD [2]. Implementing PRS for AD has practical applications, including the prediction of early-onset AD in various clinical contexts and the selection of individuals eligible for anti-AD treatments in preclinical stages [3]. Most current modeling approaches focus on disease prediction either at the population level or for individual patients [5]. The establishment of collaborative networks is essential to enhance the understanding of PRS performance in AD and facilitate transferability across populations [15].

Longitudinal Impact and Cost-Effectiveness

The adoption of polygenic risk scores (PRS) to guide preventive efforts against Alzheimer's disease could influence a variety of longitudinal outcomes related to population health and well-being [3]. The potential adoption of PRS for the disease could prompt new policy guidelines, though evidence supporting the use of such scores to forecast long-term health and economic effects remains limited[2]. Likewise, relatively few studies have examined whether the scores can forecast risk trajectories over extended time frames or directly predict treatment cost or economic benefits [4]. Cost-effectiveness analyses typically focus on the ratio between the monetary expense of an intervention and the measured health benefits. The economic effects of adopting PRS models that increase the scope of preclinical intervention against Alzheimer's disease could be assessed through such frameworks [6].

Policy and Governance Considerations

Timely and effective governance and oversight will be critical to the responsible implementation of polygenic risk score applications for Alzheimer's disease within precision public health [6]. Regulatory frameworks need to be established and maintained to ensure adequate control over operations and manage societal impacts that arise across the polygenic risk score life cycle [16]. Transparency must also be promoted, stressing accessibility regarding the processes involved in developing, validating, and communicating these applications, alongside policies that explicitly mitigate the risk of exacerbating existing health inequities [2].

Case Studies and Practice-Based Learnings

Polygenic risk scores (PRSs) are being pursued as public health tools for Alzheimer's disease (AD)[1]. Given the predominance of sporadic late-onset AD, precise characterization of risk should include age and allow estimation of years until onset. Applications of PRSs to other diseases indicate they capture substantially complementary information, on average, to non-genetic predictors [1]. The PRS developed by the International Genomics of Alzheimer's Project from a stage II genome-wide association study for late-onset AD has been evaluated in multiple data sets from different cohorts [2]. Analysis demonstrates that a PRS combining single-nucleotide polymorphism (SNP) associations with AD remains significant after conditioning on non-genetic factors [6]. The absolute risk attributable to the PRS varies considerably by population; overall discriminative accuracy is highest in European-descent data, where it exceeds that of all non-genetic covariates combined. The public-health relevance of polygenic risk assessment is based on three factors: [17] widespread concern about AD; [2] availability of potentially effective prevention approaches, offering the prospect of risk reduction; and [3] the need to identify high-risk groups for targeted intervention [2]. The PRS also enables further exploration of decades of genome-wide association data and assessment of the genetic epidemiology of AD across different ancestries [10]. Issues continue to complicate the interpretation, equitable access, and implementation of existing health data infrastructures, and the PRS has not yet been integrated into action [11]. Programme monitoring to fill evidence gaps and support ethical deployment remains essential. Adverse consequences, such as stigma or unwarranted anxiety, could reinforce existing socioeconomic inequalities or disproportionately affect already marginalised populations [7]. Stakeholders expect multilayered governance of PRS information, systems, and sharing of derived data across clades and similar heritage. Safe but open access enhances the likelihood of broadly equitable short- and long-term public-health benefits, even if initial compliance falls short [5].

Policy Recommendations for Responsible Implementation

Research on genomic, epigenomic, transcriptomic, proteomic, and microbiomic associations with brain aging and late-onset Alzheimer's disease has burgeoned over the past decade [18]. Polygenic risk scores (PRS) have emerged as important tools for linking these molecular factors to an individual's risk of developing clinical symptoms later in life. Integrating the epidemiology of Alzheimer's disease with the burgeoning molecular evidence, a broad programme has developed for using PRS to link biomarker studies at age 45–69 to critical population epidemiology and clinical postponability studies at age 70–90 [19]. Such mechanistic studies provide the foundation for measuring epidemiological interventions, thereby enhancing rational policy options for precision public health. After establishing the rationale for and the methodological underpinnings of PRS in that

context, attention now turns to the current evidence base, public health implications, equity considerations, implementation challenges, remaining gaps, illustrative case studies, and practical recommendations [20-22].

CONCLUSION

Polygenic risk scores represent a promising tool for advancing precision public health in Alzheimer's disease by enabling targeted prevention, early detection, and efficient resource allocation. Despite their potential, challenges related to cross-population transferability, clinical utility, ethical considerations, and integration into existing health systems must be addressed. Ensuring equitable access, robust data governance, and workforce preparedness is critical for responsible implementation. Future research should prioritize longitudinal validation across diverse populations, cost-effectiveness analyses, and participatory stakeholder engagement to realize the full public health impact of PRS in AD. Integrating PRS into public health strategies offers the opportunity to reduce disease burden, improve population well-being, and inform evidence-based policy development while safeguarding social and ethical standards.

REFERENCES

1. Gao Q, Daunt P, Gibson AM, Pither RJ, Alzheimer's Disease Neuroimaging Initiative. Utility of polygenic risk scoring to predict cognitive impairment as measured by preclinical Alzheimer cognitive composite score. The Journal of Aging Research & Lifestyle. 2022 Jan 1;11:1-8.
2. Khera AV, Chaffin M, Aragam KG, Haas ME, Roselli C, Choi SH, Natarajan P, Lander ES, Lubitz SA, Ellinor PT, Kathiresan S. Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. Nature genetics. 2018 Sep;50(9):1219-24.
3. Ugwu CN, Ugwu OP, Alum EU, Eze VH, Basajja M, Ugwu JN, Ogenyi FC, Ejemot-Nwadiaro RI, Okon MB, Egba SI, Uti DE. Sustainable development goals (SDGs) and resilient healthcare systems: Addressing medicine and public health challenges in conflict zones. Medicine. 2025 Feb 14;104(7):e41535.
4. Lewis CM, Vassos E. Polygenic risk scores: from research tools to clinical instruments. Genome medicine. 2020 May 18;12(1):44.
5. Altmann A, Scelsi MA, Shoai M, de Silva E, Aksman LM, Cash DM, Hardy J, Schott JM, Alzheimer's Disease Neuroimaging Initiative. A comprehensive analysis of methods for assessing polygenic burden on Alzheimer's disease pathology and risk beyond APOE. Brain communications. 2020;2(1):fcz047.
6. Baker E, Escott-Price V. Polygenic risk scores in Alzheimer's disease: current applications and future directions. Frontiers in Digital Health. 2020 Aug 11;2:14.
7. Ugwu OP, Alum EU, Ugwu JN, Eze VH, Ugwu CN, Ogenyi FC, Okon MB. Harnessing technology for infectious disease response in conflict zones: Challenges, innovations, and policy implications. Medicine. 2024 Jul 12;103(28):e38834.
8. Andreoli L, Peeters H, Van Steen K, Dierickx K. Polygenic risk scores in healthcare contexts: what's the scope? An interview study of European healthcare providers and researchers' perspectives on ethical challenges. Human Genetics. 2025 Oct 27:1-6.
9. Sabatello M, Bakken S, Chung WK, Cohn E, Crew KD, Kiryluk K, Kukafka R, Weng C, Appelbaum PS. Return of polygenic risk scores in research: stakeholders' views on the eMERGE-IV study. Human Genetics and Genomics Advances. 2024 Apr 11;5(2).
10. Reyes DM, Bose A, Karavani E, Parida L. FairPRS: adjusting for admixed populations in polygenic risk scores using invariant risk minimization. InPacific Symposium on Biocomputing. Pacific Symposium on Biocomputing 2023 (Vol. 28, p. 198).
11. Ongesa TN, Ugwu OP, Ugwu CN, Alum EU, Eze VH, Basajja M, Ugwu JN, Ogenyi FC, Okon MB, Ejemot-Nwadiaro RI. Optimizing emergency response systems in urban health crises: A project management approach to public health preparedness and response. Medicine. 2025 Jan 17;104(3):e41279.
12. Chang T, Fu M, Valiente-Banuet L, Wadhwa S, Pasaniuc B, Vossel K. Improving genetic risk modeling of dementia from real-world data in underrepresented populations. Research Square. 2024 Feb 15:rs-3.
13. Palk AC, Dalvie S, De Vries J, Martin AR, Stein DJ. Potential use of clinical polygenic risk scores in psychiatry–ethical implications and communicating high polygenic risk. Philosophy, Ethics, and Humanities in Medicine. 2019 Feb 27;14(1):4.
14. Ugwu OP, Okon MB, Alum EU, Ugwu CN, Anyanwu EG, Mariam B, Ogenyi FC, Eze VH, Anyanwu CN, Ezeonwumelu JO, Egba SI. Unveiling the therapeutic potential of the gut microbiota–brain axis: Novel insights and clinical applications in neurological disorders. Medicine. 2025 Jul 25;104(30):e43542.
15. Escott-Price V, Myers A, Huentelman M, Shoai M, Hardy J. Polygenic risk score analysis of Alzheimer's disease in cases without APOE4 or APOE2 alleles. The journal of prevention of Alzheimer's disease. 2019 Jan;6(1):16-9.
16. Paul-Chima UO, Nnaemeka UM, Nneoma UC. Could dysbiosis of urban air microbiota be an overlooked contributor to pediatric asthma and neurodevelopmental disorders?. Medical Hypotheses. 2025 Sep 12:111758.

17. Pearson TA, Vitalis D, Pratt C, Campo R, Armoundas AA, Au D, Beech B, Brazhnik O, Chute CG, Davidson KW, Diez-Roux AV. The science of precision prevention: research opportunities and clinical applications to reduce cardiovascular health disparities. JACC: Advances. 2024 Jan 1;3(1):100759.
18. Vlachakis D, Papakonstantinou E, Sagar R, Bacopoulou F, Exarchos T, Kourouthanassis P, Karyotis V, Vlamos P, Lyketsos C, Avramopoulos D, Mahairaki V. Improving the utility of polygenic risk scores as a biomarker for Alzheimer's disease. Cells. 2021 Jun 29;10(7):1627.
19. Ugwu OP, Ogenyi FC, Ugwu CN, Basajja M, Okon MB. Mitochondrial stress bridge: Could muscle-derived extracellular vesicles be the missing link between sarcopenia, insulin resistance, and chemotherapy-induced cardiotoxicity?. Biomedicine & Pharmacotherapy. 2025 Dec 1;193:118814.
20. Escott-Price V, Schmidt KM. Pitfalls of predicting age-related traits by polygenic risk scores. Annals of Human Genetics. 2023 Sep;87(5):203-9.
21. Paul-Chima UO, Basajja M, Fabian CO, Chinyere NU, Ben OM, Mustafa MM. Neuro-entero-cardiac bridge: could gut-derived catecholamine-loaded extracellular vesicles synchronize the pathogenesis of Parkinson's disease, irritable bowel syndrome, and stress-triggered arrhythmias?. Medical Hypotheses. 2026 Feb 7:111896.
22. Escott-Price V, Myers A, Huentelman M, Shoai M, Hardy J. Polygenic risk score analysis of Alzheimer's disease in cases without APOE4 or APOE2 alleles. The journal of prevention of Alzheimer's disease. 2019 Jan;6(1):16-9.

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