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Precision prognostics for cardiovascular disease in Type 2 diabetes: a systematic review and meta-analysis

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Abstract

Background Precision medicine has the potential to improve cardiovascular disease (CVD) risk prediction in individuals with Type 2 diabetes (T2D).

Methods We conducted a systematic review and meta-analysis of longitudinal studies to identify potentially novel prognostic factors that may improve CVD risk prediction in T2D. Out of 9380 studies identified, 416 studies met inclusion criteria. Outcomes were reported for 321 biomarker studies, 48 genetic marker studies, and 47 risk score/model studies.

Results Out of all evaluated biomarkers, only 13 showed improvement in prediction performance. Results of pooled meta-analyses, non-pooled analyses, and assessments of improvement in prediction performance and risk of bias, yielded the highest predictive utility for N-terminal pro b-type natriuretic peptide (NT-proBNP) (high-evidence), troponin-T (TnT) (moderate-evidence), triglyceride-glucose (TyG) index (moderate-evidence), Genetic Risk Score for Coronary Heart Disease (GRS-CHD) (moderate-evidence); moderate predictive utility for coronary computed tomography angiography (low-evidence), single-photon emission computed tomography (low-evidence), pulse wave velocity (moderate-evidence); and low predictive utility for C-reactive protein (moderate-evidence), coronary artery calcium score (low-evidence), galectin-3 (low-evidence), troponin-I (low-evidence). Risk scores showed modest discrimination, with lower performance in populations different from the original development cohort.

Conclusions Despite high interest in this topic, very few studies conducted rigorous analyses to demonstrate incremental predictive utility beyond established CVD risk factors for T2D. The most promising markers identified were NT-proBNP, TnT, TyG and GRS-CHD, with the highest strength of evidence for NT-proBNP. Further research is needed to determine their clinical utility in risk stratification and management of CVD in T2D.

Plain language summary

People living with type 2 diabetes (T2D) are more likely to develop problems with their heart or blood circulation, known as cardiovascular disease (CVD), than people who do not have T2D. However, it can be difficult to predict which people with T2D are most likely to develop CVD. This is because current approaches, such as blood tests, do not identify all people with T2D who are at an increased risk of CVD. In this study we reviewed published papers that investigated the differences between people with T2D who experienced CVD compared to those who did not. We found some indicators that could potentially be used to determine which people with T2D are most likely to develop CVD. More studies are needed to determine how useful these are. However, they could potentially be used to enable clinicians to provide targeted advice and treatment to those people with T2D at most risk of developing CVD.



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ndividuals with type 2 diabetes (T2D) have a 1.5 to 2-fold higher risk of developing cardiovascular disease (CVD) compared to those without T2D^{1,2}. This is particularly concerning given the high global prevalence of diabetes and the aging population. More than 500 million individuals worldwide are affected by this chronic disease, resulting in substantial human and economic costs^{3,4}. However, predicting CVD risk in T2D remains a challenge, and existing risk algorithms, such as the UK Prospective Diabetes Study (UKPDS) Risk Engine and Framingham Risk Score (FRS), have shown only modest predictive value in external validation studies^{5–7}. Thus, it is essential to identify or develop readily available and cost-effective measures that can accurately identify individuals with a higher absolute risk of developing CVD beyond the risk estimated from established risk factors.

Precision medicine provides a promising approach to optimize risk prediction by integrating multidimensional data (i.e., genetic, sociodemographic), clinical. accounting for individual differences⁸. Recognizing the potential value of precision medicine in improving diabetes prevention and care, the Precision Medicine in Diabetes Initiative (PMDI) was established in 2018 by the American Diabetes Association (ADA) in partnership with the European Association for the Study of Diabetes (EASD) and is led by global leaders in precision diabetes medicine⁹. This systematic review is written on behalf of the ADA/EASD PMDI as part of a comprehensive evidence evaluation in support of the 2nd International Consensus Report on Precision Diabetes Medicine¹⁰. As part of this broader initiative, we conducted a systematic review and meta-analyses addressing precision prognosis for CVD outcomes.

While previous systematic reviews of biomarkers for prediction of CVD have been conducted in the general population^{11–25}, this review focused on patients with T2D. We sought to answer two questions: (1) Which novel markers predict CVD in people with T2D? (2) Is there any evidence that these markers enhance risk prediction beyond current practice? Addressing these questions may inform the development of more effective strategies for detecting and predicting CVD in individuals with T2D, ultimately leading to improved management and prevention of this complication.

Therefore, to identify those biomarkers with most promising clinical utility for CV risk assessment, we followed a rigorous stepwise approach, including evaluation of the incremental value of each biomarker beyond traditional risk factors (i.e. with evaluation of improvement in different metrics such as c-statistic and net reclassification improvement – NRI), as recommended by the statement from the American Heart Association for identification of novel markers for CV disease²⁶.

In summary, employing a stringent study selection process, this systematic review and meta-analysis identified four prognostic factors with high predictive utility, supported by moderate to high-strength evidence. Furthermore, three prognostic factors demonstrated moderate predictive utility, backed by low to moderate-strength evidence, and six prognostic factors showed low predictive utility, with evidence levels ranging from low to moderate. Risk scores demonstrated modest discrimination on internal validation, with diminished performance in external validation, particularly in cohorts diverging from the original population.

Methods

As a reporting guidance, we followed the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) statement²⁷. Figure 1 presents the PRISMA flow diagram, illustrating the process that led to the final selection of studies for review. Prior to data collection, the proposed systematic review and meta-analysis was registered on PROSPERO (Registration number: CRD42021262843).

Inclusion and exclusion criteria. This review included longitudinal studies (prospective or retrospective cohorts, including secondary analyses of cohorts from randomized controlled trials) of participants with T2D (youth-onset and adult-onset). Inclusion criteria included observational studies published from 1990-2021 that reported on the association between a prognostic factor or risk score and one or more CVD outcomes among participants with T2D. During the period of our review, the diagnostic criteria for T2D underwent some modifications (e.g. change in fasting glucose threshold, addition of hemoglobin A1C). We accepted studies that reported the inclusion of participants with T2D as defined in each individual study. Exclusion criteria included cross-sectional studies, studies utilizing surrogate endpoints for cardiovascular (CVD) outcomes such as carotid intima-media thickness, endothelial dysfunction, and arterial stiffness, and studies including only participants with pre-diabetes or only participants with type 1 diabetes. Studies with mixed populations of diabetes were included only if results were reported separately for participants with T2D. Supplemental Table 1 summarizes the Participant Intervention Comparison Outcomes and Studies (PICOS) framework.

Outcomes. Only studies reporting outcomes on fatal or non-fatal coronary heart disease (CHD) or cardiovascular mortality (either alone or as individual component of composite outcomes) were included. A broad definition of CHD, including any outcomes defined by terms such as myocardial infarction, ischemic heart events, cardiac events, coronary artery disease, and major cardiovascular events was used.

Search strategy. We conducted a comprehensive search on Medline and Embase of studies published from January 1990 to March 2021 using keywords and MeSH (Medical Subject Headings) terms relevant to T2D and CVD (see Supplemental Note 1). In addition, we searched the reference lists of eligible studies and systematic reviews to identify any further relevant studies. The search strategy was designed by a multi-professional team of researchers with expertise in precision medicine, clinical diabetes, cardiovascular disease, biomarker development and evaluation, genetic markers, and predictive analytics, supported by two librarians with expertise in conducting systematic reviews and meta-analyses. References identified were exported to EndNote (Clarivate Analytics) and imported to Covidence, where studies were assessed for eligibility. After the removal of duplicates, 14 authors participated in screening each title/abstract, and full-text articles were obtained if abstracts were considered eligible by at least one author. Each full-text article was assessed for inclusion independently by two authors (among 12 total authors), and disagreements were resolved by consensus.

Data extraction. All data were extracted and coded by one author and reviewed by a second author to ensure data accuracy. After undergoing training to ensure consistency in the process, thirteen authors participated in the data extraction process (A.A., C.T., L.L., M.F.G., M.L.M., N.M., R.C.W.M., S.K., C.H., G.Y., Y.Z., M.D.P., S.C.T.). To minimize inter-reviewer variability and ensure consistency in data extraction, all authors underwent training sessions via video conferences and participated in mock assessments.

During data extraction, studies were classified into three categories based on the primary type of prognostic factors

reported, namely biomarkers, genetic markers, and risk scores. Biomarkers were broadly defined as non-genetic laboratory tests, clinical conditions, socio-demographics, vital signs, diagnostic procedures, and imaging tests. Genetic markers included specific DNA sequences or variations, such as single nucleotide polymorphisms (SNPs), restriction fragment length polymorphisms (RFLP), or short tandem repeats (STR). Risk scores were defined as predictive models, algorithms, or risk calculation tools that estimated the overall likelihood or category of cardiovascular disease (CVD) based on a set of risk factors. When multiple genetic variants were combined to predict risk (using SNPs), the study was classified as a genetic marker (i.e., genetic risk score) rather than a risk score. Additional details about the included studies can be found in Supplemental Note 2.

The following data were extracted from each article using a standardized data form in Covidence and Excel data tables: study characteristics (country or countries of the study population, study start and end year, study design, inclusion/exclusion criteria, study setting, data sources), participant characteristics (years of follow-up, follow-up duration, total number of participants, race/ethnicity/ancestry, and baseline characteristics), prognostic factor(s) characteristics (name, prognostic factor type, units of measurement, units and cut-offs in regression analyses, transformation methods, effect measures [hazard ratio, odds ratio, c-statistic, net reclassification improvement (NRI), integrated discrimination index (IDI), etc.] and 95% confidence intervals, adjusted covariates), and outcomes (CVD outcome definition, number of events and non-events), and validation methods. For genetic markers, we collected risk variants, risk alleles, and closest gene (locus).

For continuous variables, we collected mean and standard deviation or median and interquartile range as reported in the study. We collected fully adjusted effect measures (HR, RR, OR, c-statistic) and their corresponding 95% CIs reported in the original articles. When studies reported multiple multivariate-adjusted effect measures, we collected the estimate from the most fully adjusted model. We did not contact primary authors to obtain data that were not reported. Furthermore, data were collected to evaluate the risk of biases in each study as summarized in Supplemental Table 2 and described in the quality assessment paragraph.

Quality assessment. We used a modified Newcastle-Ottawa Scale (NOS) to assess quality and risk of biases. The scale assesses studies based on six common domains, including representativeness of the exposed and non-exposed cohorts, ascertainment of exposure and outcome, and adequacy of study follow-up for primary and secondary CVD events, as well as the adequacy of cohort follow-up²⁸. For biomarker studies, we added two additional domains to the NOS to address bias due to confounding by evaluating the number of covariates and established CVD risk factors included in the adjusted models. Each study was given a score for each domain and an overall quality evaluation was determined by adding up these scores. The possible range of scores for non-genetic biomarkers, based on 8 domains, was 2 to 28, while for genetic biomarkers and risk scores, scores ranged from 2 to 18 based on 6 domains. Two authors assessed study quality independently, and a third author resolved any disagreements.

We reported the overall risk of bias based on the distribution of scores in each prognostic factor category, with higher scores representing lower risk of bias. Studies in the top, second, and lowest tertiles (according to the distribution specific for each type of study, i.e. non-genetic biomarkers, genetic biomarkers and risk scores) were considered to have low, medium, and high risk of bias, respectively. The score of each domain was also classified as low, medium, or high risk of bias for graphical purposes, as clarified in Supplemental Table 2.

Statistical analysis. A random-effects model was used to pool the overall effect estimates in all meta-analyses, only if the heterogeneity test was statistically significant. For studies reporting the same effect measure (e.g. HR), we calculated the pooled effect estimate with 95% CIs for each biomarker or genetic marker and assessed heterogeneity between studies using the Cochran's Q statistic (p < 0.1), the I^2 index >75%, and τ^2 . Due to the limited number of studies per prognostic factor, subgroup analyses by population characteristics or outcomes were not performed. We performed sensitivity analyses by excluding studies with high risk of bias. As the number of studies per prognostic factor was always less than 10, we were unable to assess publication bias using funnel plots. We used R, version 4.2.3 (R Project for Statistical Computing), with the "meta", "metafor", and "forestplot" packages for all analyses²⁹. Two-sided statistical tests were used with a significance threshold of <0.05.

Strength of the evidence. We considered aspects of the GRADE approach³⁰ and the JBI critical appraisal tools³¹ in grading the strength of evidence for individual biomarkers and genetic markers/risk scores. We applied relevant GRADE criteria, including indirectness, inconsistency, and imprecision, throughout the study. Since we only included studies that involved patients with T2D and a "hard" clinical CVD outcome, the evidence is considered direct by definition. We analyzed the results from T2D patients with and without baseline CVD and specified all relevant CVD outcomes to assess the applicability of individual biomarkers in specific populations and outcomes. To ensure robustness and validity of our findings, we established strict eligibility criteria, excluding studies that did not adjust for established CVD risk factors (listed in Supplemental Table 3). Furthermore, we scored studies based on the adequacy of adjustment for covariates, including the total number of covariates and established CVD risk factors, in accordance with the JBI criterion for statistical adjustment of confounders.

We used the American Heart Association scientific consensus report for stepwise evaluation of novel markers for CVD risk²⁶ to identify promising biomarkers and genetic markers based on their strength of evidence progressing from measures of association, discrimination, improvement in discrimination, net reclassification index (NRI) or integrated discrimination index (IDI). This approach is summarized in Supplemental Table 4. For biomarkers and genetic markers, we progressed from those with significant adjusted association in at least one study to those with net positive number of studies showing significant association in a consistent direction. The net positive number of studies was calculated by summing up all studies with positive association and subtracting studies with no association (e.g., three studies showing positive association and two studies with no association yielded a net positive number of one). We identified biomarkers that improved prediction performance when added to established models, based on improvement in at least one of c-statistic, NRI (the probability that a person is appropriately classified into either high- or low-risk), or IDI (quantification of predicted probabilities of events and non-events based on inclusion of the biomarker in the model), and further narrowed down the list to those with improvement in all three indicators.

Accordingly, for each of the prognostic factors that passed our evidence-based screening criteria, predictive utility was classified as high (3 points), moderate (2 points), or low (<2 points) based on three criteria: number of studies with all three performance

indicators satisfied (1 point if >0 studies, 0 points if 0 studies), number of pooled meta-analyses showing significant association (1 point if >0, 0 points if 0 studies), non-pooled analysis showing \geq 75% of studies had a significant association (1 point if yes, 0 points if no). Strength of Evidence was classified as high (4 points), moderate (2 or 3 points), or low (<2 points) based on four criteria: at least one meta-analysis was conducted regardless of outcome (1 point if yes, 0 points if no), exclusion of high risk of bias studies did not alter inferences from meta-analyses (1 point if unaltered, 0 points if altered), exclusion of high risk of bias studies did not alter inferences from non-pooled analyses (1 point if unaltered, 0 points if altered), and consistencies in the definition of the prognostic marker used in analyses (1 point if yes, 0 points if no).

For the risk scores, we provide a complete assessment of risk of bias and pooled c-statistics; however, we decided not to conduct a corresponding stepwise approach to evidence grading as explained above for biomarkers/genetic markers due to the complexity in verifying specifications of each model over time and across comparisons. Inferences from the risk score results are here meant to guide future work that would permit analyses to handle this complexity.

Inclusion and ethics statement. This research is a part of a broader initiative, Precision Medicine in Diabetes Initiative (PMDI), that was established by the American Diabetes Association (ADA) in partnership with the European Association for the Study of Diabetes (EASD) and is led by global leaders in precision diabetes medicine. Therefore, researchers from multiple countries and continents have contributed to this study. The roles and responsibilities of co-authors were collaboratively agreed upon before the start of the review process. This study is exempt from ethical review due to the use of publicly available data.

Reporting summary. Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Results

Study selection and characteristics. Out of 9380 studies identified from databases/registries (N = 9332) and other sources (N = 48), there were 9316 unique studies after removing 64 duplicates. Of these, 615 articles were selected for full-text review, and finally, 416 articles were considered appropriate for inclusion in the analysis^{5,32-446}. Outcomes were reported for 321 biomarker studies, 48 genetic marker studies, and 47 risk score/model studies, as shown in Supplemental Data 1, 2, and 3. Figures 1 and 2 provide an overview of the screening and selection process.

Predominant ancestry in the studied populations were European (57.1%), East Asian (19.7%), South Asian (5.5%) and Hispanic or Latin American (4.2%). Geographically, the United States, United Kingdom, China, Japan, and Italy were the top five represented countries with regards to origin of study participants and author affiliation in the included studies. Figure 3 and online interactive figures (https://hugofitipaldi.shinyapps.io/T2D_prognostic/) offer a detailed breakdown of ethnic and geographic distributions⁴⁴⁷.

CVD outcomes. There was heterogeneity in the CVD outcomes evaluated across the analyzed studies (see Supplemental Fig. 1). The median duration of follow-up reported across studies was 5 years (IQR 3.1 to 7.8 years). The most frequently reported outcomes were coronary heart disease, cardiovascular mortality, and stroke, either individually or combined. The vast majority (87%)

of studies had a clearly defined outcome based on ICD-10 codes, clinical documentation, or adjudication, with 9% relying on registry or record linkage, and 4% using either patient self-report or having an unclear definition. We classified primary prevention as the prediction of CVD in individuals without a history of the disease, secondary prevention as the prediction of recurrent CVD events or CVD progression in those already diagnosed with the disease, and mixed populations as a combination of both primary and secondary prevention.

Biomarkers. Among 416 included studies, 321 (77.2%), 48 (11.5%), and 47 (11.2%) were studies of non-genetic biomarkers, genetic biomarkers, and non-genetic risk scores, respectively. Among the 321 studies of non-genetic biomarkers, 70 (21.8%) evaluated established CVD risk factors and were excluded, while 30 studies (9.3%) were included because they used a novel approach (e.g., variability, setting) for an established risk factor (Fig. 2). Further, three studies did not adjust for any CVD risk factors and were excluded, leaving 218 studies consisting of 195 unique biomarkers in the analysis.

Among these 195 biomarkers analyzed, 134 (69%) had a significant adjusted association for predicting CVD, based on a net positive number of studies (Fig. 4 and Supplemental Data 4). Out of these, 12 (9%) showed improvement in c-statistic, NRI, or IDI in more than one study: N-terminal pro b-type natriuretic peptide (NT-proBNP), C-reactive protein (CRP), troponin T (TnT), coronary artery calcium score (CACS), coronary computed tomography angiography (CCTA), single-photon emission computed tomography (SPECT) scintigraphy, pulse wave velocity (PWV), galectin-3 (Gal-3), troponin I (TnI), carotid plaque, growth differentiation factor-15 (GDF-15), and triglyceride-glucose (TyG) index. The following biomarkers showed prediction performance but in only one study: SPECT, TnI, TyG, 25-hydroxyvitamin D, poly (ADP-ribose) polymerase (PARP), and interleukin-6 (IL-6).

Biomarkers with all three prediction performance indicators satisfied in more than one study were NT-proBNP, TnT, and CCTA, with results summarized in Table 1. For NT-proBNP, 5 studies reported improvement in c-statistics ranging from 0.01 to 0.07, significant increase in NRI ranging from 0.04 to 0.50, and significant rIDI ranging from 0.012 to 0.48 (in four studies). For TnT, 3 studies reported improvement in c-statistics ranging from 0.02 to 0.10, significant NRI ranging from 0.150 to 0.44, and rIDI ranging from 0.03 to 0.05. For CCTA, 3 studies reported improvement in c-statistics ranging from 0.08 to 0.35, with one study reporting statistically significant improvements in NRI of 0.55 and rIDI of 0.046. Of these three biomarkers, NT-proBNP showed the strongest incremental predictive value based on the magnitude of these indicators. Supplemental Data 5 shows the degree of variation in measurement methods used for each of these biomarkers.

Forest plots in Fig. 5a show the HRs for 11 studies evaluating NT-proBNP, conducted in heterogeneous populations (2 primary, 5 mixed, and 4 secondary), outcomes, units in regression analyses (i.e., SD, SD of log), and laboratory units (ng/L, pg/mL). Nonetheless, all studies except one showed a significant association with a CVD outcome. Eight out of 11 (73%) studies were assessed to be at low risk of bias. Figure 6a and Supplemental Figs. 2a, b show the meta-analysis of NT-proBNP as a continuous variable per logarithmic and per 1 SD unit increase, confirming the highly significant association with CVD (pooled HR 1.53, 95% CI 1.26-1.85 per log increase; pooled HR 1.59, 95% CI 1.27–1.99 per SD increase) after accounting for heterogeneity with the random effects models (I² 90% and I² 83%, respectively). Interestingly, although our review excluded studies

T2D CVD Prognostics



Fig. 1 PRISMA flow diagram detailing the process that led to final study inclusion for review. Flowchart illustrating the screening of studies through title and abstract review, screening, and inclusion. *n* number of studies.

focusing exclusively on heart failure patients, among three studies that incorporated EF as a covariate in their models, NT-proBNP was shown to have predictive value for cardiovascular outcomes independent of $\text{EF}^{241,326,397}$ (Supplemental Data 5).

Forest plots in Fig. 5b show the HRs for 8 studies evaluating TnT, conducted primarily for mixed or secondary populations with variable CVD outcomes. Studies differed with respect to cutoffs and categories for TnT, units of measurement (ng/ml, ng/L) and analysis (per log, per 1 SD log). Among these studies, all but one showed a positive association. Notably, the study by Lepojarvi 2016 was an outlier in its magnitude of effect and confidence intervals. Overall, for TnT, study quality was good with 6 out of 8 (75%) assessed to be at low risk of bias²²⁷. A significant association for TnT was observed in studies where the biomarker was evaluated as a continuous variable per 1 log increase with pooled HR 1.64 (95% CI 1.23, 2.18) and I² 59% (Fig. 6b and



Fig. 2 Selection of studies to be included for evaluating the associations of biomarkers, genetic markers and non-genetic risk scores with cardiovascular outcomes. This figure shows the selection criteria used to identify included biomarkers, genetic biomarkers, and non-genetic risk scores. No. number. *See Supplemental Table 3.

Supplemental Fig. 3a); similarly, when treated as a binary or categorical variable, the pooled HR was 2.64 (95% CI 1.03, 6.72) with $I^2 = 95.9\%$ (Fig. 6b and Supplemental Fig. 3b). However, when treated as a continuous variable per 1 SD, there was no longer a significant association in a random effects model (Fig. 6b and Supplemental Fig. 3c).

Forest plots in Fig. 5c show the HRs for 5 studies evaluating CCTA conducted primarily for primary CVD prevention with variable CVD outcomes. Studies differed significantly with respect to CCTA definition of subclinical or clinical CHD. All 5 studies showed a significant association; however, 2 of the 5 studies (40%) were assessed to be at a high risk of bias.

Apart from these three biomarkers, SPECT, TnI, TyG, 25hydroxyvitamin D, poly(ADP-ribose) polymerase (PARP), and interleukin-6 (IL-6) showed prediction performance in all three performance indicators but in only one study. Forest plots for the remaining 9 biomarkers that showed improvement in at least one performance indicator in more than one study (CACS, carotid plaque, CRP, gal-3, GDF-15, PWV, SPECT scintigraphy, TnI, and TyG) are shown in Supplemental Figs. 4–6. Again, there was substantial heterogeneity with respect to study populations, outcomes, and units of analysis for these biomarkers. Biomarkers showing positive association in at least 75% of studies included CACS, carotid plaque, gal-3, PWV, SPECT scintigraphy, TnI, and TyG. While CRP did not meet the threshold of 75% of studies showing an association, when meta-analyzed as a binary or categorical variable, it showed a significant pooled association; PWV and TyG also demonstrated significant association in pooled analysis (Supplemental Fig. 7).

Genetic markers. Among the 48 genetic studies analyzed (Supplemental Data 2), 79 genetic biomarkers were examined for their association with incident CVD events (Supplemental Data 6), mainly in populations of European (65%) or Asian (26%) ancestries, with sparse representation of populations of other ancestries (e.g., African 12% or Hispanic 3%), with 12% of associations being tested in mixed populations. Most of the studies (70 out of 79) used single variants as distinct genetic biomarkers (exposure), while 9 studies used a combination of different SNPs into genetic risk scores (GRS) as the exposure. Remarkably, most of these exposures were tested only in one study, and external validation was performed in only 4 out of 48 studies, with only one study using a longitudinal cohort as a validation set, i.e., GRS for CHD. Overall, among the 79 genetic biomarkers, 33 (41.8%) had at least one study showing significant association, out of which 29 had a net positive number of studies showing significant association. Out of these 29 genetic biomarkers, two were tested in more than one study (rs10911021 on GLUL, GRS for CHD [GRS-CHD]), one had improvement in any performance indicator in a single study (isoform e4 in APOE), and one had improvement in all three performance indicators in a single study (GRS-CHD) (Fig. 7).



Fig. 3 Global distribution of origin and ancestry of the study populations and countries of affiliation and gender distribution of authors of the included studies. Panel **A** shows the top 20 countries of origin and ancestry of the study populations evaluated in the included studies. Panel **B** shows the top 20 countries of affiliation and gender distribution of authors of the included studies. The data used for this visualization was obtained from PubMed and PubMed Central through manual curation and by applying text mining functions developed using R software version 4.1.2. The final proportions of ancestries were calculated for each unique study and then aggregated as described in detail here⁴⁴⁸.

Notably, the rs10911021 variant in *GLUL* was the only single variant that showed an association with CVD in several studies. This variant was initially identified in T2D patients using a genome-wide approach and subsequently confirmed for its association with CVD in selected populations from two additional studies. For GRS-CHD, four separate studies investigated the combination of up to 204 CHD variants from 160 distinct loci derived from the general population. These studies had distinct but overlapping and increasing numbers of loci and variants

tested in more recent investigations. The most recently performed GRSs were externally validated and demonstrated significant improvements in CVD risk reclassification (cNRI) as well as notable enhancements of 8% in relative IDI (rIDI). However, these findings were identified in subjects of European ancestry and ancestry-specific analyses showed consistency in Asian subjects but not in other ancestral backgrounds. Forest plots for variants located on the GRS-CHD and *GLUL* are shown in Fig. 8, while their meta-analyses can be found in Supplemental Fig. 8.



Fig. 4 Sankey diagram showing the funneling of identified non-genetic biomarkers through sequential filtering steps. The number of biomarkers passing or not passing each step (based on the criteria specified at the bottom of the diagram) is depicted at the top of the colored bars, with biomarkers passing all steps having the strongest predictive performance value.

Risk scores/models. Forty-seven studies reported results of 27 unique CVD risk scores (Supplemental Data 3 and 7). Supplemental Figs. 9 and 10 provides the c-statistics from internal and external validation analyses, respectively. On both internal and external validation, discrimination was modest. Most risk scores were developed in the United States, Europe, and East Asia and 61.1% of the internal validation studies were assessed to be at a high risk of bias. Model performance tended to decline when validated in countries that differed from the development cohort (Supplemental Fig. 11). For example, the FDS study achieved high c-statistics (>0.80) when validated in an Australian cohort, but lower ones (0.58-0.69) when tested in European countries. In line with previous studies^{5–7}, discrimination for the UKPDS and FRS was generally poor on external validation. Most prediction models focused on baseline characteristics and did not account for time-varying factors that may modify CVD risk (e.g., statin, SGLT-2i, GLP-1 RA). An exception was the BRAVO risk engine, published in 2020 and validated in trials of SGLT-2i patients, showing that this risk engine effectively predicted CV health benefits through improvements in common clinical measures (e.g., A1C, SBP, and BMI)³⁴³.

Supplemental Figs. 12, 13 provide the pooled c-statistics from external validation studies on those risk scores for which the analysis was possible: ADVANCE, CHS, CVD-EDIC, NDR, NZ DCS and UKPDS risk scores. All risk scores exhibited modest discrimination (pooled c-statistics ranging from 0.63 to 0.68), with no individual risk score substantially outperforming the others.

Supplemental Fig. 14a, b provide a histogram of the total number of adjusted covariates and number of adjusted traditional CVD risk factors in each of the studies, respectively. Supplemental Fig. 15 is a network figure representing the connections of the adjusted covariates in the 416 included studies.

Sensitivity analyses. The results of sensitivity analyses excluding studies with high risk of bias from meta-analyses of biomarkers, genetic risk score, and for risk scores where pooled analyses were possible, respectively, are shown in Supplemental Figs. 16–18.

Synthesis. Table 2 provides a summary of findings of studies assessing the most promising biomarkers and genetic markers/ scores for precision prognosis of CVD in T2D, along with our conclusions regarding their predictive utility and strength of evidence. In our synthesis of the evidence, we took into account the results from the sensitivity analyses described in the previous paragraph. The highest predictive utility was observed for NTproBNP (high-evidence), TnT (moderate-evidence), TyG (highevidence), and GRS-CHD (moderate-evidence). Prognostic factors with moderate predictive utility were CCTA (low-evidence), SPECT scintigraphy (low-evidence), and PWV (moderate-evidence). Prognostic factors with low predictive utility included CRP (moderate-evidence), CACS (low-evidence), Gal-3 (lowevidence), TnI (low-evidence), carotid plaque (low-evidence), and GDF-15 (low-evidence). Supplemental Figs. 19-22, 23, 24 provide the quality assessment for the included biomarker, genetic marker, and risk score studies, respectively.

Discussion

Our systematic review of prognostic markers for CVD in individuals with T2D has revealed several notable findings. First, among the numerous studies that investigated the prognostic significance of CVD risk markers, only a few have been consistently found to be significantly associated with cardiovascular risk. Namely, NT-proBNP, TnT, TyG, and GRS-CHD demonstrated the highest predictive utility, with NT-proBNP having the strongest evidence. However, most of the remaining markers have not been adequately tested or compared against established CVD risk factors. Finally, even though some markers have demonstrated the capability of predicting cardiovascular events beyond what current risk factor-based models can offer, their application in clinical practice remains limited, as there is inadequate evidence of their contemporary clinical utility.

During the search process, a considerable number of studies were found ineligible for inclusion in our systematic review. Available studies were primarily cross-sectional in design, and only a limited number of them focused specifically on individuals with T2D and examined the early utility of risk factors and

Table 1 Perforn	nance of the pred	liction of 3 biomarkers with the most evi	idence.					
Biomarker	Study	Clinical factors / biomarkers to be	Improveme	ent in C-statistics	NRI		Ī	
		compared	Yes /No	Estimate (95% CI) and <i>P</i> -value	NRI (95% CI)	P-value	IDI (95% CI)	P-value
NT-proBNP	Sharma 2020	Age, sex, SBP, history of HF, duration of diabetes, prior MI, hypertension, hypertlinidemia smoking eGFR	Yes	0.05 (NR)	0.39 (0.30-0.47)	NR	0.09 (0.08-0.10)	<0.05
	Wolsk 2017	Prior MJ, BMI, NSTEMI (index event), heart rate, HbA _{1c} , percutaneous coronary intervention at the index event, cerebrovascular disease, AF, prior HF, sodium concentration, macroalbuminuria, PAD, age, and LDL	Kes	0.01 (CI NR), P < 0.05	0.11 (5.7-16.6)	<0.05	0.08 (0.03-1.6)	<0.05
	Wong 2019 Scirica 2016	concentration. Age ≥ 65 years, Male, T2D, Hypertension Treatment arms, age, SBP, sex, history of HF-, duration of diabetes, prior MI, history of hypertension, history of	Y Y es	0.03 (CI NR), P = 0.001 0.07 (CI NR), P < 0.001	0.35 (0.24-0.45) 0.040 (0.03-0.04)	<0.001	0.01 (0.01-0.02) 0.48 (0.41-0.55)	<0.001<<0.05 0.05</td
	Van der Leeuw 2016	hyperlipidemia, smoking, and eGFR Female sex, age at diabetes diagnosis, duration of diabetes, HbA _{1c} , square of HbA _{1c} , SBP, square of SBP, TC/HDL ratio, urinary ACR, current smoking status, history of major macrovascular	Yes	0.02 (0.00-0.04), P-value NR	0.2 (0.10-0.44)	<0.05	N N	х Х
	Van der Leeuw 2016	disease Female sex, age at diabetes diagnosis, duration of diabetes, HbA _{te} , systolic blood pressure, TC/HDL ratio, eGFR, current smoking status, history of	Yes	0.02 (0.00-0.05), P-value NR	0.50 (0.26-0.73)	<0.05	Z	N N
ТлТ	Lepojarvi 2016	major macrovascular disease Age, sex, history of acute MI, BMI, Canadian Cardiovascular Society grading of angina pectoris, left ventricular ejection fraction and mass index, HDL cholesterol, ACR, HbA _{1c} and type of glucose metabolism	Yes	0.10 (Cl and <i>P-</i> value NR),	0.231 (0.067-0.394)	-0.01	0.05 (0.03-0.08)	100.0>
	Scirica 2016	disorder Treatment arms, age, SBP, sex, history of HF, duration of diabetes, prior MI, history of hypertension, history of	Yes	0.07 (CI NR), P < 0.001	0.440 (0.380-0.510)	<0.05	0.03 (0.02-0.03)	<0.05
	Rørth 2019	hyperlipidemia, smoking, and eGFK Natural logarithm of NT-proBNP, age, sex, treatment effect, ejection fraction, NYHA class, BMI, heart rate, SBP, creatinine, LDL, prior angina pectoris, AF and pacemaker implantation.	Kes	0.02 (CI NR), P = 0.02	0.150 (0.051-0.261)	0.007	0.03 (0.01-0.06)	<0.001

biomarkers in predicting future cardiovascular events. A major limitation in many studies was inadequate adjustment for established CVD risk factors; and even if studies considered adjustments, only a small fraction evaluated clinical utility beyond the use of established risk factors. These findings emphasize the need for better-designed studies to improve our understanding of the prognostic value of markers for CVD in T2D.

Most studies included in the final analysis were conducted in people of European, East or South Asian ancestry, with the top-5 countries of recruitment being the United States, UK, China, Japan and Italy. African ancestry and countries were underrepresented. A skewed geographical distribution was also evident regarding countries of author affiliation, with the same top-5 countries dominating the volume of publications. Although the geographical and ancestral imbalance reported here for biomarker studies is less pronounced than what was recently reported for GWAS studies⁴⁴⁸, it highlights the pressing need to enhance data collection, biomarker discovery and validation, as well as the development of population-specific cardiovascular risk prediction models in underrepresented populations and ancestries to hopefully help reduce healthcare disparities⁴⁴⁹.

In our analyses, the novel biomarker emerging as the best predictor was NT-proBNP; indeed, it fulfilled all criteria of predictive and clinical utility with multiple studies showing improvement in all prediction performance indicators, with consistency of results across studies and meta-analyses. Notably, this biomarker had also been found to be useful as a prognostic marker for incident CVD in the general population⁴⁵⁰. Our findings suggest that NT-proBNP, beyond its established role in the diagnosis and management of patients with heart failure, might also be used as a marker to predict CVD. Another biomarker found in the general population to improve primary CVD risk prediction among asymptomatic middle-aged adults is highsensitivity CRP (hs-CRP). In our review, CRP was found to have low predictive utility with moderate strength of evidence, which may be due to variability in cut-offs used for this marker, the relatively small numbers of studies, differential effects in diabetes, or less sensitive to detect low-grade vascular inflammation (compared with hs-CRP).

Despite numerous genetic studies probing the link between polymorphisms and cardiovascular outcomes in diabetes, few genetic markers have been consistently examined in longitudinal studies or reliably found to be associated with these outcomes. Only one study from the systematic review utilized a genomewide association study (GWAS) approach, identifying the rs10911021 variant near GLUL to be associated with CV outcome in diabetes, at genome-wide significance. The variant at GLUL was subsequently confirmed in two independent studies¹⁷². A more recent GWAS conducted among Chinese patients with T2D identified a variant at PDE1A for CHD in T2D, which was not included in our systematic review as it fell beyond our study inclusion period⁴⁵¹. Polygenic risk scores also appear to emerge as promising tools, and GRS constructed from variants associated with CHD in the general population seem helpful for cardiovascular risk stratification in diabetes²⁵⁷.

Based on these limited findings, it becomes clear that we need a greater number of adequately powered GWAS to identify genetic markers associated with CVD in T2D. Nevertheless, we found several examples of studies that evaluated the utility of applying polygenic risk scores, or genome-wide polygenic risk scores, derived from the general population, for CVD risk stratification in T2D. In general, these have fair performance and a similar ability to stratify as in patients without diabetes. Considering the substantially larger sample sizes in currently published metaanalyses of GWAS for CHD in the general population, this approach will probably be more fruitful for the integration of

3iomarker	Study	Clinical factors / biomarkers to be	Improven	nent in C-statistics	NRI		Ō	
		compared	Yes /No	Estimate (95% CI) and <i>P</i> -value	NRI (95% CI)	P-value	IDI (95% CI)	P-value
CTA	Lee	Age, male sex, HTN, smokers,	Yes	0.07 (CI NR),	0.550	<0.0001	0.05	0.0006
	2017	hyperlipidemia, eGFR, and HbA _{1c}		P = 0.03	(0.343-0.757)		(0.02-0.07)	
	Halon	UKPDS and log CAC Score	Yes	0.35 (CI NR),	0.63	NR	0.65	NR
	2016			P = 0.021	(CI NR)		(CI NR)	

First author	Year	Study population	DM pop N	Event N	Outcome	No. of covariates	Risk of bias				Per unit increase	Hazard ratio [95% Cl]
vonScholten	2015	Primary	200	40	3p MACE, HF	10	Medium				per 1 SD of the logarithms (ng/L)	1.70 [1.13, 2.56]
Colombo	2018	Primary	2105	144	CHD, Stroke	16	Low		-		per 1 SD (pg/mL)	1.94 [1.54, 2.45]
McMurray	2011	Mixed	4038	1010	3p MACE, HF	29	Low		⊢ ∎i		per 1 logarithm (pg/mL)	1.30 [1.15, 1.46]
Bruno	2013	Mixed	1825	175	CVM	13	Low		, — I	•	per 1 logarithm (pg/mL)	1.69 [1.39, 2.05]
Bruno	2014	Mixed	1645	149	CVM	11	Low		⊢		per 1 SD of the logarithms (pg/mL)	1.84 [1.52, 2.22]
Resl	2016	Mixed	746	171	CHD, Stroke, HF, PAD, ACM	4	Low				per 1 logarithm (pg/mL)	1.17 [1.07, 1.27]
Scirica	2016	Mixed	12310	NR	3p MACE, HF	13	Low		⊢ •		per 1 SD of the logarithms (pg/mL)	1.62 [1.50, 1.74]
Savonitto	2018	Secondary	7226	210	CVM	7	High		H		per 1 logarithm (pg/mL)	1.83 [1.60, 2.09]
Rørth	2019	Secondary	759	NR	CHD, CVM, HF, ACM	13	Low		⊢		per 1 logarithm (pg/mL)	1.85 [1.54, 2.23]
Lorenzo-Almoros	2020	Secondary	232	56	CHD, Stroke	15	Low	⊢−−−−			per 1 SD (pg/mL)	0.95 [0.68, 1.33]
Sharma	2020	Secondary	5380	837	3p MACE, HF	14	Medium		H H -1		per 1 logarithm to the base 2 (pg/mL)	1.24 [1.18, 1.31]
							0.5			2 25		

HR [95% CI]

N terminal pro B type natriuretic peptide (NT-proBNP)

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First author	Year	Study population	DM pop N	Event N	Outcome	No. of covariates	Risk of bias							Per unit increase / Cutoff for biomarker	Hazard ratio [95% Cl]
McMurray	2011	Mixed	4038	1010	3p MACE, HF	29	Low	-	-				2	>0.028 ng/mL vs. ≤0.028 ng/mL	1.50 [1.06, 2.13]
Keller	2018	Mixed	1034	377	3p MACE	17	Med.						(Q4 (>90 ng/L) vs Q1 (≤35 ng/L)	2.10 [1.49, 2.95]
Resl	2016	Mixed	746	171	CHD, Stroke, HF, PAD, ACM	10	Low	F	-				ş	per 1 logarithm (ng/L)	1.43 [1.13, 1.81]
Scirica	2016	Mixed	12310	NR	3p MACE, HF	13	Low		-				F	per 1 SD of the logarithms (pg/mL)	1.41 [1.32, 1.51]
Everett	2015	Secondary	1984	198	3p MACE, ACM	18	High						10	≥14 ng/L vs. <14 ng/L	1.56 [1.22, 1.99]
Lepojarvi	2016	Secondary	1053	37	CHD, CVM, HF	11	Low						• >	>14 ng/L vs. ≤14 ng/L	15.50 [5.12, 46.90]
Rørth	2019	Secondary	759	NR	CHD, CVM, HF, ACM	13	Low		⊢■				3	per 1 logarithm (ng/L)	1.91 [1.45, 2.51]
Lorenzo-Almoros	2020	Secondary	232	NR	CHD, Stroke	15	Low	-					1	per 1 SD (ng/mL)	1.02 [0.84, 1.23]
								_					-		
							(0.75	1.5	5	10	20 40	Ċ.		
										HR [95%	CIJ				

Troponin T (TnT)

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Coronary computed tomography angiography (CCTA)

First author	Year	Study population	DM pop N	Event N	Outcome	No. of covariates	Risk of bias		Per unit increase / Cutoff for biomarker	Hazard ratio [95% Cl]
									obstructive CAD >50%	
Lee	2017	Primary	933	94	CHD, Revasc, ACM	7	Medium		vs. <50%	3.83 [2.45, 5.98]
Halon	2019	Primary	630	24	CHD	4	Low	·•	mild plaque calcification <50% vs. other plaques	2.60 [1.13, 5.97]
Halon	2016	Primary	630	24	CHD, CVM, Angina	3	High		per 1 quartile of Gensini score	2.50 [1.67, 3.74]
Tian	2019	Mixed	164	20	CHD, CVM, Revasc, Angina	9	Medium	,,	obstructive CAD vs. no CAD	7.79 [1.75, 34.70]
							(9 2 3 4 5 7 9 15 30		
								HR 195% CII		

Fig. 5 Forest plots for three biomarkers (NT-proBNP, TnT, and CCTA) with the most evidence for prediction of CVD outcomes. Panel a (NT-proBNP); Panel b (TnT); Panel c (CCTA). HR hazard ratio, CI confidence interval, DM pop N, sample size for diabetes population; Event N, number of individuals developed CVD outcomes; 3p MACE, 3-point major adverse cardiovascular events; HF heart failure, CHD coronary heart disease, CVM cardiovascular mortality, PAD peripheral artery disease, ACM all-cause mortality.

genetic markers into risk stratification of cardiovascular complications. In the limited studies that have evaluated the added benefit of polygenic risk scores above clinical markers, there is, in general, a modest but significant improvement in prediction. Whether polygenic risk scores will become viable options for future risk stratification would partly depend on the availability of these tools, and the cost-effectiveness of adding these measures into clinical practice.

Beyond individual prognostic markers, our review identified several studies that evaluated CVD risk prediction models. While the UKPDS risk engine (developed among subjects with newly diagnosed T2D the UK) and the Framingham risk equation (developed from the general population in the US) were the most widely studied, they do not perform well in contemporary studies of people with T2D. This suggests difficulties in applying certain risk models to current healthcare settings. Nevertheless, our literature review shows that clinical risk models are perhaps the "readiest" for implementation in clinical practice to improve risk stratification in diabetes. On external validation, newer risk scores generally achieved higher discrimination compared to UKPDS and FRS, with Fremantle Diabetes Study 2 (FDS-2) having the highest c-statistic of 0.81 (developed and validated in different populations in Australia). We found that risk models performed better when validated in cohorts similar to the derivation cohort, with c-statistics of 0.699 \pm 0.015 and 0.668 \pm 0.006 (95% CI) (P = 0.018) for concordant and discordant studies, respectively.

In an era when electronic medical record (EMR)-based prediction models are being increasingly used, our results suggest that researchers should focus on the development of populationspecific risk models that are intended to be deployed in the same

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Variable type in analys (Per unit increase)	is	DM pop N	Event N	ľ	Heterogene τ ²	ity test P _Q				Fixed-effects Pooled HR [95% Cl]	model P	Random-effects Pooled HR [95% Cl]	<u>s model</u> P
Continuous (per 1 logarit	thm)	14594	>1566	90.09%	0.041	2.19e-09		·		1.39 [1.32, 1.47]	3.04e-31	1.53 [1.26, 1.85]	1.19e-05
Continuous (per 1 SD)		16492	>389	82.6%	0.048	0.00818				1.64 [1.53, 1.74]	3.94e-51	1.59 [1.27, 1.99]	4.3e-05
b							0.8	1 1.5 2 HR [95% CI]	2.5				
						Trop	onin T (Tn	т)					
Variable type in analysis (Per unit increase)	DM pop N	Event N	Hete I ²	rogeneity test τ ²	Pa					<u>Fixed-effe</u> Pooled HR [95% Cl]	cts model P	<u>Random-effe</u> Pooled HR [95% Cl]	<u>ets model</u> P
Binary / categorical	8109	1622	95.9%	0.827	0.000532					1.76 [1.48, 2.09]	9.35e-11	2.64 [1.03, 6.72]	0.0422
Continuous (per 1 logarithm)	1505	>171	58.96%	0.025	0.119	H				1.62 [1.35, 1.94]	1.5e-07	1.64 [1.23, 2.18]	0.000627
Continuous (per 1 SD)	12542	NR	89.85%	0.047	0.0017					1.36 [1.28, 1.45]	1.85e-21	1.21 [0.89, 1.67]	0.228
						0.7 0.9	2	3 4	567				

N terminal pro B type natriuretic peptide (NT-proBNP)

Fig. 6 Meta-analysis of NT-proBNP and TnT for predicting cardiovascular outcomes. Panel **a** (NT-proBNP); Panel **b**: TnT; *PQ* is the *p*-value obtained from the Cochran's Q test. HR, hazard ratio; CI, confidence interval; DM pop *N*, sample size for diabetes population; Event *N*, number of individuals developed CVD outcomes.

HR [95% CI]



Fig. 7 Sankey diagram showing the funneling of identified genetic biomarkers through sequential filtering steps. The number of biomarkers passing or not passing each step (based on the criteria specified at the bottom of the diagram) is depicted at the top of the colored bars, with biomarkers passing all steps having the strongest predictive performance value.

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Senetic risk scores (GRS) derived from coronary artery disease loci known from general population

First author	Year	Study I population	Population ancestry	No. of variants	DM pop N	Event N	Outcome	No. of covariates	Risk of bias			Per unit increase	Hazard Ratio [95% Cl]
Cox	2014	Primary I	European American	30	983	101	CVM	7	Medium		.	per 1 SD	1.46 [1.08, 1.97]
Mccaffery	2015	Mixed	Multi-ethnic	153	4016	NR	3p MACE, Angina	7	High	,_ . _	e.	per 1 SD	1.17 [1.08, 1.26]
Morieri	2018	Mixed I	Non-Hispanic Whites	204	5104	675	CHD	9	Medium			per 1 SD	1.17 [1.08, 1.27]
Morieri	2018	Mixed	Non-Hispanic Whites	204	1931	163	CHD	9	Medium			per 1 SD	1.32 [1.13, 1.55]
Morieri	2018	Mixed	African-Americans	204	1398	122	CHD	9	Medium	·		per 1 SD	0.95 [0.79, 1.14]
Morieri	2018	Mixed	Hispanics	204	529	61	CHD	9	Medium			per 1 SD	1.20 [0.92, 1.57]
Morieri	2018	Mixed	Asians	204	469	25	CHD	9	Medium			per 1 SD	1.98 [1.31, 2.99]
b										0.75 1	1.5 2 HR [95% CI]	2.5 3	
							rs10911	1021 at GL	JL				
First author	Year	Study populatio	Population on ancestry	DM poj N	p Event N	Out	come N c	o. of ovariates	Risk of bias			Comparison group vs. reference group	Odds ratio [95% Cl]
Qi	2013	Primary	White (female	s) 1326	350	CHE	2		Low	·	-	C allele vs. T allele 1.	34 [1.10, 1.63]
Qi	2013	Primary	White (males)	984	319	CHE	2		Low			C allele vs. T allele 1.	49 [1.20, 1.86]
Baeney	2016	Primary	White/Europea	an 1537	160	CHE) 1		Medium	·	_	C allele vs. T allele 1.	25 [0.94, 1.67]

Fig. 8 Forest plots of genetic risk scores and GLUL variant rs10911021 for predicting cardiovascular outcomes. Panel a: Genetic risk scores; Panel b: GLUL variant rs10911021; HR, hazard ratio; CI, confidence interval; DM pop N, sample size for diabetes population; Event N, number of individuals developed CVD outcomes; 3p MACE, 3-point major adverse cardiovascular events.

population from which they were developed since the goal should be to achieve the highest predictive accuracy rather than to find a generic model that performs modestly well in all settings. Despite their potential utility and low implementation costs, we found a paucity of evidence showing integration of risk engine calculators into clinical practice. We are aware of several notable exceptions. For example, the Joint Asia Diabetes Evaluation (JADE) program has incorporated several risk prediction algorithms derived from Asian patients with diabetes into a web-based e-health portal, together with a graphical interface and decision support⁴⁵², and has been evaluated in different clinical settings, including in randomized clinical trials^{453–456}. Many EMR systems offer quick calculations of CVD risk using the American College of Cardiology/American Heart Association (ACC/AHA) Pooled Cohort Equations based on inputs available in the patient's record, and we recommend that future risk scores found to have high predictive accuracy be made easily accessible to clinicians within their EMR workflow.

Given the limitations and gaps that emerged from this review, we recommend that future studies follow several guidelines to improve the quality and impact of studies on precision prognostics in diabetes. First, studies attempting to identify a risk marker should be conducted in prospective or longitudinal cohorts or trials, to provide more robust and reliable data. Second, studies should have sufficient sample size and duration of follow-up (at least 3 years for primary CVD events and at least 1 year for secondary CVD events) to ensure adequate statistical power. Third, studies must adjust for a minimal set of established clinical cardiovascular risk factors, to ensure that known risk factors do not confound any observed associations. Finally, studies must attempt to explore the added utility of biomarkers by comparing against prediction using established risk factors or models, or available risk engines for cardiovascular events. This would include evaluation of the change in c-statistics after adding risk markers/biomarkers of interest but also consider including additional metrics such as NRI and IDI. We believe that if journals make these requirements mandatory when evaluating such studies, it will help ensure that research funders are made aware and future studies are best suited for informing advances in this area especially in resource-limited countries. As in any other research field, harmonization of protocols, methods, and analysis pipelines should be encouraged to allow comparisons across studies and for clinical translation.

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1 75

1 25 OR [95% CI]

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There are several unique strengths of this work. To our knowledge, this represents one of the most comprehensive overviews of the current status of knowledge about risk stratification of cardiovascular outcomes in T2D. We included studies from 1990 onwards, to capture some of the older studies, as well as more contemporary studies. Our inclusion of "biomarkers" in the broadest term allowed us to provide an objective overview of the different approaches currently being explored for better risk stratification. Limiting the analyses to studies using longitudinal cohorts allowed us to focus on studies that would inform prognostication. Limiting analyses to "hard" cardiovascular endpoints, rather than also including surrogate endpoints such as carotid intima-medial thickness, allowed us to focus on endpoints that would be of greatest clinical relevance. However, while this approach allows us to maximize the translational approach of our analyses, future studies focused on identification of biomarkers associated with early disease-informative endpoints (i.e. subclinical markers of atherosclerosis or minor cardiovascular disease) might identify different novel biomarkers for early-stage cardiovascular complications.

Our study does have limitations. We had to omit a considerable number of cross-sectional studies due to the extensive scope of the systematic review and the explained focus on longitudinal studies. We included only English language publications. Our search terms, potentially more sensitive towards detecting studies on clinical risk factors and biomarkers than genetic factors, may have led to fewer genetic studies being identified. However, we managed to supplement this by reintegrating some missing articles using the identified literature and the investigators' expertise.

In conclusion, our systematic review on prognostic markers for cardiovascular endpoints in T2D identified several findings, which to the best of our knowledge, have not been previously reported, and has revealed some important knowledge gaps. We

Table 2 Conclus	ion and strength of th	ie evidence.						
	A	в	υ	۵	ш	Ŀ	U	т
Prognostic Biomarker	No. of studies with all 3 performance indicators satisfied	No. of pooled meta- analyses showing significant association	No. of pooled meta-analyses showing significant association (excluding high risk of bias)	Non-pooled analyses showed that >=75% of studies had significant association	Persistent association on sensitivity analysis for non-pooled analyses (excluding high risk of bias)	Consistency in definition of prognostic biomarker used in analysis	Conclusion (predictive utility)	Strength of Evidence
NT-proBNP	m	2/2	2/2	Yes	Yes	Yes	High	High
CRP	0	1/2	1/2	No	No	No	Low	Moderate
TnT	4	2/3	1/3	Yes	Yes	No	High	Moderate
CACS	0	0	0	Yes	No	No	Low	Low
CCTA	2	0	0	Yes	No	No	Moderate	Low
SPECT	-	0	0	Yes	No	No	Moderate	Low
PWV	0	1/1	1/1	Yes	Yes	No	Moderate	Moderate
Gal-3	0	0	0	Yes	Yes	No	Low	Low
Tnl	-	0	0	No	No	No	Low	Low
Carotid	0	0	0	Yes	Yes	No	Low	Low
plaque								
GDF-15	0	0	0	No	No	No	Low	Low
TyG	-	1/1	NA	Yes	No	Yes	High	Moderate
GRS-CHD	-	1/1	1/1	Yes	No	No	High	Moderate
Table includes genetic an (3 point) moderate (2 po. points) based on criteria (Column E: exclusion of hi	d non-genetic biomarkers showing ints) or low (<2 points) based on i defined in columns B, C, E and F (C igh risk of bias studies did not altu	i improvement in prediction perfor the criteria defined in columns A, column B: at least one meta-analy cer inferences from non-pooled ar	mance (i.e. at least one of c-statist B and D (Column A: >0 = 1 point; sis conducted [regardless of outco nalyses [YES] =1 point; Column F	tic, NRI, IDI) and in more than 1: ; Column 8: >0 = 1 point, Colum me1 = 1 point, Column C: exclus : "yes" = 1 point).	tudy (corresponding to all markers n D: "Yes" =1 point). Strength of Ei ion of high risk of bias studies did n	in green boxes in Fig. 4 and Fig. 5 vidence was classified as High (4 iot alter inferences from meta-an	 Notes: Predictive utility was cl t points), moderate (2 or 3 point alyses [same number as in colur 	sssified as high s) and low (<2 nn B] = 1 point;

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found that NT-proBNP, TnT, TyG, and GRS-CHD had high predictive utility beyond traditional CVD risk factors, with the highest strength of evidence for NT-proBNP. Among genetic markers, there was only sufficient evidence for the polygenic risk score for CHD, and among risk scores, predictive utility was modest on external validation. Given the relatively low number of studies analyzing these novel prognostic factors using a rigorous approach, these findings support the need for future studies testing these markers with convincing demonstration of incremental predictive utility. NT-proBNP appears to be the only biomarker ready to be tested prospectively to evaluate its utility in modifying clinical practice for prediction of CVD risk.

Data availability

The protocol for this systematic review and meta-analysis is publicly available through the International Prospective Register of Systematic Reviews (PROSPERO), with the registration number CRD42021262843. Comprehensive search strategies that can be reproduced are outlined in Supplemental Note 1. Any further details required are available from the corresponding author upon reasonable request. Complete lists of the publications where data were extracted for this study are provided as Excee files in Supplemental Data 1 (list of studies on non-genetic biomarkers), Supplemental Data 2 (list of studies on genetic biomarkers), supplemental Data 3 (list of studies on non-genetic risk scores). Supplemental Data 4, 6, and 7 provide source data used to generate forest plots and meta-analyses. The data presented in Fig. 3 is also available as online interactive figures (https://hugofitipaldi.shinyapps.io/T2D_prognostic/) and in a data repository (https://zenodo.org/records/10277173)⁴⁴⁷.

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Drs. M.F.G., R.C.W.M., and N.M. had full access to all the data in the study and take full responsibility for the integrity of the data and the accuracy of the data analysis. Concept and design: R.C.W.M., N.M., M.F.G., A.A.M., A.A., L-L.L., R.W.K., S.C.T., C.H.T., M.D-P., F.C., S.S. Acquisition, analysis, or interpretation of data: R.C.W.M., N.M., A.A., M.F.G., M.D-P., C.H.T., R.W.K., F.C., S.C.T., L-L.L., S.S., A.A.M., T.C., M.P., M.L.M., H.F., S.K., G.Y., Y.Z., C.H. Drafting of the manuscript: R.C.W.M., N.M., M.F.G., A.A., M.L.M., L-L.L., C.H.T., H.F., S.K. Critical revision of the manuscript for important intellectual content: R.C.W.M., N.M., M.F.G., A.A., J.-L.L., M.L.M., C.H.T., F.C., T.C., M.D-P., H.F., C.H., S.K., S.S., R.W.K., A.A.M., S.C.T., G.Y., Y.Z., M.P., D.S., R.JdS, D.K.T. Statistical analysis: C.H.T., M.L.M., N.M. A.A., L-L.L., M.L.M., C.H.T. contributed equally to this work and are considered co-first authors. M.F.G., R.C.W.M., and N.M. supervised all aspects of this work and are considered co-senior authors.

Competing interests

The authors declare the following competing interests: L-L.L. has served as an advisory committee member for Bayer, Boehringer Ingelheim, Novo Nordisk, Procter & Gamble Health, and Viatris; and as a speaker for Abbott, AstraZeneca, Boehringer Ingelheim, Merck Sharp & Dohme, Novo Nordisk, Roche, Sanofi, Servier, and Zuellig Pharma Therapeutics. She has also received research grants from Abbott, AstraZeneca, and Boehringer Ingelheim. M.L.M. received lecture fees, consultancy, or advisory board fees from Amarin, Amgen, Eli Lilly, Merck Sharp & Dohme, Mylan, Novo Nordisk, Servier, and SlaPharma, all not directly related to this manuscript. R.W.K. has received consulting fees from Novo Nordisk. M.F.G. has received financial and non-financial (in kind)

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