

Towards the identification of blood biomarkers for acute stroke in humans: a comprehensive systematic review

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WHAT IS ALREADY KNOWN ABOUT THIS SUBJECT

Stroke is the largest single cause of disability in the UK. While tests based upon biomarkers have been around for decades, interest in the applications of biomarkers has increased greatly in recent years. Biomarkers released into the bloodstream following a stroke are useful not only for understanding the pathogenesis of stroke, but also play a significant role in the development of personalised medicine. The efficacy of current clinical models and imaging techniques for the diagnosis and prognosis of acute stroke could be improved when used in conjunction with blood biomarkers. While several studies have proposed a number of biomarkers associated with acute stroke in humans, there is conflicting information about the significance of implicated markers, and their clinical relevance is unclear.

WHAT THIS STUDY ADDS

In an attempt to consolidate the plethora of data in this field, we have conducted a comprehensive systematic review and meta-analysis of proteomic and metabolomic blood biomarkers associated with acute stroke. Our meta-analysis has found eight biomarkers that are significantly associated with the diagnosis and prognosis of acute stroke. Interestingly we also found that CRP, a protein commonly implicated as a strong biomarker of inflammation and stroke, may not have sufficient sensitivity and specificity to be of clinical value. Thus while the biomarkers identified through our study are likely to be biologically informative about the mechanisms of vascular disease, their clinical potential for a blood-based test warrants further investigation.

AIMS

Identification of biomarkers for stroke will aid our understanding of its aetiology, provide diagnostic and prognostic indicators for patient selection and stratification, and play a significant role in developing personalized medicine. We undertook the largest systematic review conducted to date in an attempt to characterize diagnostic and prognostic biomarkers in acute ischaemic and haemorrhagic stroke and those likely to predict complications following thrombolysis.

METHODS

A comprehensive literature search was carried out to identify diagnostic and prognostic stroke blood biomarkers. Mean differences (MDs) and 95% confidence intervals (CIs) were calculated for each biomarker.

RESULTS

We identified a total of 141 relevant studies, interrogating 136 different biomarkers. Three biomarkers (C-reactive protein, P-selectin and homocysteine) significantly differentiated between ischaemic stroke and healthy control subjects. Furthermore, glial fibrillary acidic protein levels were significantly different between haemorrhagic stroke and ischaemic stroke patients (MD 224.58 ng l⁻¹; 95% CI 25.84, 423.32; *P* = 0.03), high levels of admission glucose were a strong predictor of poor prognosis after ischaemic stroke and symptomatic intracerebral haemorrhage post-thrombolysis, glutamate was found to be an indicator of progressive (unstable) stroke (MD 172.65 μmol l⁻¹, 95% CI 130.54, 214.75; *P* = 0.00001), D-dimer predicted in-hospital death (MD 0.67 μg ml⁻¹, 95% CI 0.35, 1.00; *P* = 0.0001), and high fibrinogen levels were associated with poor outcome at 3 months (MD 47.90 mg l⁻¹, 95% CI 14.88, 80.93; *P* = 0.004) following ischaemic stroke.

CONCLUSIONS

Few biomarkers currently investigated have meaningful clinical value. Admission glucose may be a strong marker of poor prognosis following acute thrombolytic treatment. However, molecules released in the bloodstream before, during or after stroke may have potential to be translated into sensitive blood-based tests.

Introduction

Stroke is the second most common cause of death after ischaemic heart disease and is a major cause of disability worldwide [1]. Every year, over 150 000 people in the UK suffer from a stroke, costing the NHS over £2.8 billion, with this figure likely to increase in today's ageing population [2, 3].

Stroke is characterized by the sudden loss of cerebral blood circulation, resulting in a corresponding loss of neurological function. Two principal subtypes exist, namely ischaemic stroke caused by thrombosis or embolism, representing over 80% of all strokes, and haemorrhagic stroke caused by rupture of an artery. Despite the two subtypes sharing similar risk profiles [4], they exhibit distinct molecular mechanisms in the acute phase [5–8].

It is important to distinguish between stroke subtypes and other mimics, such as migraine, focal epilepsy and structural brain lesions [9], which can account for up to a third of patients with stroke-like symptoms [10]. Owing to its accessibility and speed, computed tomography (CT) has been the mainstay of stroke imaging. However, as acute ischaemic stroke is often isodense on CT its initial usefulness is often limited to excluding a haemorrhage. Thus, at present, stroke diagnosis is frequently made upon probability rather than certainty. Diffusion magnetic resonance imaging (MRI) is a more reliable tool for acute diagnosis, but has the disadvantage of being expensive and less readily available.

Biotechnology and pharmaceutical companies are actively engaged in developing new drugs for ischaemic stroke for use particularly at the acute stage (<24 h from onset) in order to reverse and/or protect the rapidly developing necrotic brain region. However, use of these drugs requires a confident diagnosis of stroke, the lack of which has been one reason for the poor uptake of recombinant tissue plasminogen activator thrombolysis [11, 12]. The failure of the neuroprotective agent NXY-059 in the SAINT-II trial, despite rigorous STAIR (Stroke Therapy Academic Industry Round table) guidelines, supports the necessity to adopt a biomarker-based system to drug development that should increase the likelihood of success in both preclinical and clinical trials through proof of concept [13]. Drug discovery processes that are based upon these biomarker strategies are also likely to be more efficient and cost-effective [14].

Stroke biomarkers of high specificity and sensitivity should be able to diagnose and differentiate between intracerebral haemorrhage (ICH) and acute ischaemic stroke (AIS), to predict prognosis after stroke and to facilitate patient stratification for therapeutic intervention. The ideal biomarker test for acute ischaemic stroke would act as a prehospital screening tool, allowing rapid diagnosis without the necessity for neuroimaging.

The development of successful diagnostic tests through biomarker identification has proved to be a challenge to

biomedical scientists. Many protein and metabolic biomarkers have been implicated in the pathophysiology of stroke, but their clinical relevance is unclear. In order to provide the scientific community with some clarity in this disparate field, we have performed a comprehensive systematic review of proteomic and metabolomic blood biomarkers studied in acute stroke, including those used for either diagnostic or prognostic purposes, as well as those that attempt to predict outcome from pharmacological interventions such as thrombolysis. To the best of our knowledge, this is the largest such analysis conducted to date.

Methods

Data sources and extraction

Electronic databases MEDLINE, EMBASE and Google Scholar were searched on 19 November 2010 up to 1 January 2011 for all studies detailing the use of blood biomarkers for stroke in humans. Search retrieval was maximized by using four terms for thrombolysis (thrombolysis, thrombolytic therapy, plasminogen activator and alteplase), seven for haemorrhagic stroke (cerebral, intracranial, parenchymal, intraventricular, infratentorial, supratentorial h[a]emorrhage and bleeding), 14 for ischaemic stroke (ischaemic, ischemic, cerebral, intracranial, parenchymal, intraventricular, infratentorial, supratentorial, cerebrovascular, infarction, stroke, thrombus, occlusion and embolus), three for generic biomarkers (biological, biochemical marker and biomarker) and 780 specific biomarker terms with 'and/or' used as a Boolean operator (Supporting Materials S1). References from all relevant papers were hand searched for additional studies, and the MEDLINE 'Related Articles' option was used to identify further articles. The search was restricted to the English language. Searches and study screening were performed independently by N.H. and P.McC.; data extraction was conducted by N.H. alone.

Inclusion criteria were set using Cochrane guidelines [15]. For the evaluation of diagnostic biomarkers, studies were required to have reported markers that discriminated between ischaemic and haemorrhagic stroke and non-stroke subjects (healthy, stroke mimics or other neurological diseases). Where more than one cohort was examined, data for each population were extracted separately. Studies were eligible for inclusion if blood had been drawn within 24 h of stroke onset, and prognostic biomarkers measured using death, disability or handicap scales. No minimal sample size was set for study inclusion, but only papers reporting continuous measures of biomarker activity or concentration (mean/median and standard deviation/range) were chosen for meta-analysis. Papers reporting only the risk of subsequent stroke or risk of stroke in a nonstroke population were not included. Papers examining subarachnoid haemorrhage were excluded. Observational studies were reviewed using STROBE criteria; the quality of

diagnostic and prognostic studies was reviewed using modified QUADAS criteria [16] and a quality questionnaire implemented by Whiteley *et al.* [17], respectively. The Quorum Statement [18] was also consulted.

Statistical analysis

A meta-analysis was performed on each biomarker for which data were available for more than two studies comparing the same cohorts. Data were analysed using the Review Manager v5.0 software (Cochrane Collaboration, Syracuse, NY, USA). In instances when a biomarker was reported in different units between studies, the units were adjusted for consistency. Where values were reported as medians and ranges, the mean and standard deviation were estimated using a variety of models dependent upon sample size, as described by Hozo *et al.* [19]. Data variability reported as standard error or confidence intervals was also converted to a standard deviation value. Mean difference (MD) was calculated for each biomarker using a random-effects model, as well as 95% confidence intervals (CIs) to measure the strength of association. Tests for heterogeneity with iterative analyses were conducted for each meta-analysis ($P < 0.05$) and, where appropriate, funnel plots and Egger regression (two-tailed) were used to assess publication bias in Comprehensive Meta-Analysis version 2 software.

Results

The primary search identified 819 studies for ischaemic stroke (diagnostic and prognostic), 673 for haemorrhagic stroke (diagnostic and prognostic) and 256 for prognosis after thrombolysis. Of these, 189, 116 and 47 studies met the inclusion criteria, respectively. A total of 136 different biomarkers were identified (Supplementary Table S1).

Of the 189 manuscripts identified for ischaemic stroke, data for meta-analysis could be extracted from 53 reporting diagnostic biomarkers and 47 reporting prognostic biomarkers, as these were the studies reporting continuous data. Of the 116 studies identified for haemorrhagic stroke, data could be extracted from 14 reporting diagnostic biomarkers and eight reporting prognostic biomarkers (Preferred Reporting Items for Systematic Reviews and Meta-Analyses flow diagram [20]; Figure 1).

Diagnostic biomarkers for ischaemic and haemorrhagic stroke

Of the markers measured for differentiation between ischaemic stroke and healthy control subjects, only three (C-reactive protein (CRP), P-selectin and homocysteine) were found to be of statistical significance in our meta-analysis (CRP, MD 2.03 mg l⁻¹, 95% CI 1.11, 2.94; $P = 0.0001$, Figure 2; P-selectin, MD 56.75 ng ml⁻¹, 95% CI 10.60, 102.90; $P = 0.02$; and homocysteine, MD 4.76 mmol l⁻¹, 95% CI 2.82,

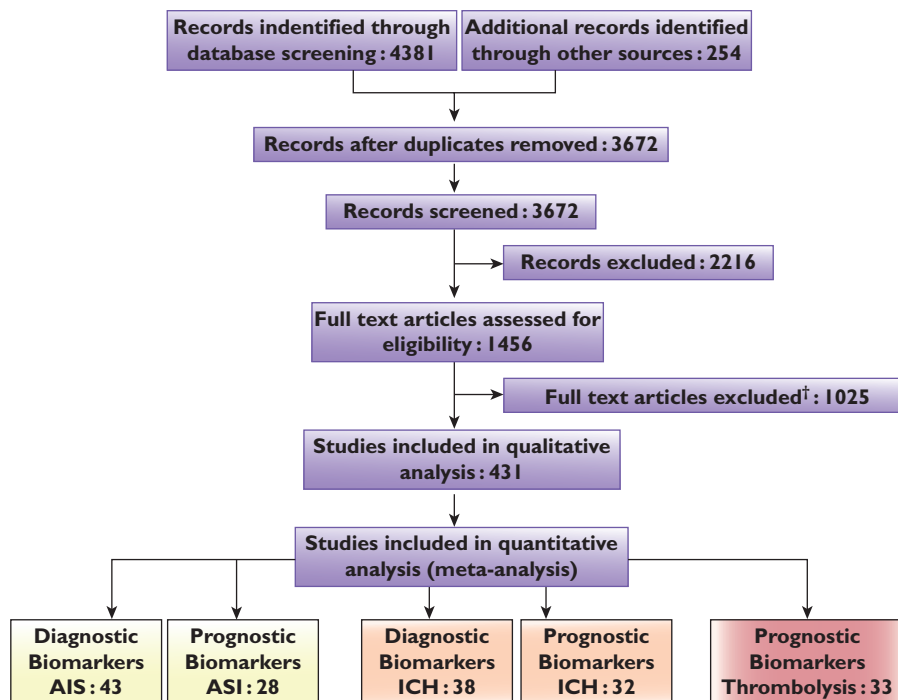


Figure 1

Preferred Reporting Items for Systematic Reviews and Meta-Analyses statement flow diagram illustrating the search strategy and number of studies included in the meta-analysis. Abbreviations: AIS, acute ischaemic stroke; and ICH, intracerebral haemorrhage. †Full text articles excluded because: duplicate studies, report risk not diagnosis/prognosis, data not reported in desired format

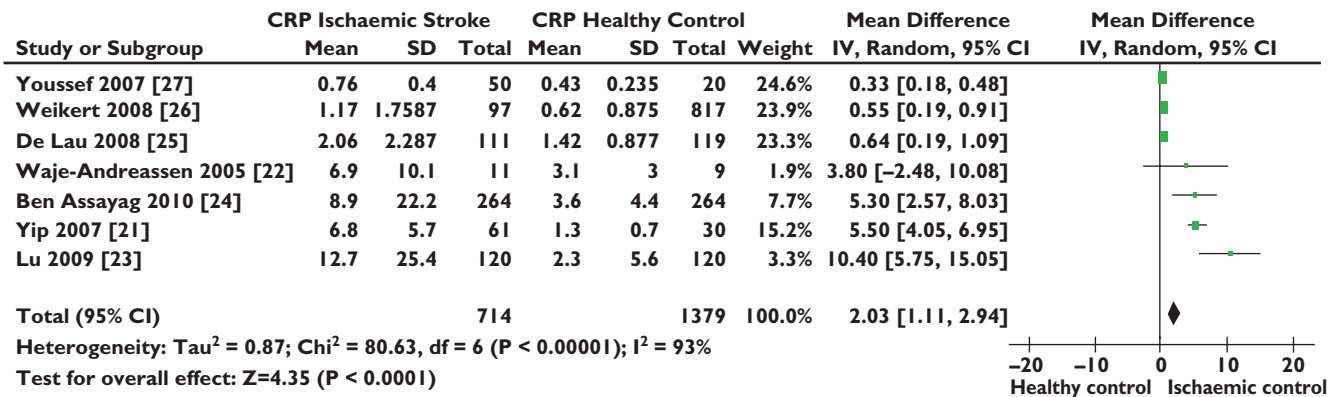


Figure 2

Forest plot comparing C-reactive protein (CRP) levels in acute ischaemic stroke and a healthy population. High CRP levels show a significant association with the presence of ischaemic stroke

6.71; $P = 0.00001$); however, the high level of heterogeneity ($P < 0.00001$) between papers reporting these markers lends uncertainty to the quality and value of the results.

Separate analysis of hs (high sensitivity)-CRP [21–24] and CRP levels [25–27] removed the high heterogeneity present in the combined analysis (combined, $I^2 = 93\%$, $P = 0.00001$; hs-CRP only, $I^2 = 32\%$, $P = 0.22$; and CRP only, $I^2 = 22\%$, $P = 0.28$), but found little difference in the distinguishing power of hs-CRP over CRP assays (hs-CRP, MD 5.94 mg l⁻¹, 95% CI 4.11, 7.78; $P = 0.00001$; and CRP, MD 0.42 mg l⁻¹, 95% CI 0.24, 0.60; $P = 0.00001$).

Only one protein, glial fibrillary acidic protein (GFAP), was able to differentiate statistically between ischaemic and haemorrhagic stroke (MD 224.58 ng l⁻¹, 95% CI 25.84, 423.32; $P = 0.03$), with no significant heterogeneity between studies, although this is based on only three studies. One study, by Dvorak *et al.* [28], reported measurements of GFAP taken at regular intervals up to 24 h following stroke. These investigators showed that serum GFAP levels are much higher in haemorrhagic stroke than in ischaemic stroke, increasing steadily up to 12 h post-stroke and then declining, while GFAP levels are barely measurable before 12 h in ischaemic stroke patients, and continue to increase up to 24 h. Following an iterative analysis, we found that measurement of GFAP levels within a 3–4 h time window gave the best differentiation between the two stroke types.

Prognostic biomarkers for ischaemic and haemorrhagic stroke

Studies reported a number of outcome measures post-stroke (Supplementary Table S1). Many of these outcomes were measured at differing time points (in hospital, 48 h, 3 months or several years later) and used a variety of outcome scores {modified Rankin Scale (mRS) [29, 30], Canadian Stroke Scale (CSS) [31, 32], Barthel Index [33, 34] and National Institute of Health Stroke Scale (NIHSS) [35]}.

We identified prognostic biomarkers of significant value in three different outcomes of ischaemic stroke: progressive (decrease > 1 CSS)/stable stroke within 48 h), in-hospital survival/death and good (mRS 0–2)/poor (mRS 3–6) outcome at 3 months. For all of these outcomes, high admission glucose levels were found to be a strong predictor of poor prognosis (MD 3.17 mmol l⁻¹, 95% CI 1.60, 4.74; $P = 0.0001$; MD 1.85 mmol l⁻¹, 95% CI 0.61, 3.15; $P = 0.003$; and MD 0.98 mmol l⁻¹, 95% CI 0.48, 1.48; $P = 0.0001$, respectively). In addition, glutamate was found to be an indicator of progressive stroke (MD 172.65 μmol l⁻¹, 95% CI 130.54, 214.75; $P = 0.00001$); D-dimer predicted in-hospital death (MD 0.67 μg ml⁻¹, 95% CI 0.35, 1.00; $P = 0.0001$) and high fibrinogen levels were associated with poor outcome at 3 months post-stroke (MD 47.90 mg l⁻¹, 95% CI 14.88, 80.93; $P = 0.004$) following iterative analysis and exclusion of one paper [36] that accounted for high heterogeneity.

None of the candidate molecules reported to be of prognostic value following haemorrhagic stroke showed statistical significance in the meta-analysis.

Prognostic biomarkers following thrombolysis

Studies reported a number of outcomes following thrombolysis, including death, oedema, dramatic recovery, poor outcome (NIHSS, mRS), occurrence of haemorrhagic transformation and/or symptomatic haemorrhage and efficiency of recanalization. Of these, only one outcome, risk of post-thrombolysis symptomatic haemorrhage, was found to have a biomarker, admission glucose, of statistical significance after conducting a meta-analysis of observational studies (MD 0.85 mmol l⁻¹, 95% CI 0.37, 1.35; $P = 0.0006$; Figure 3).

Discussion

Numerous molecules have been suggested as biomarkers that are useful in the accurate diagnosis of ischaemic and

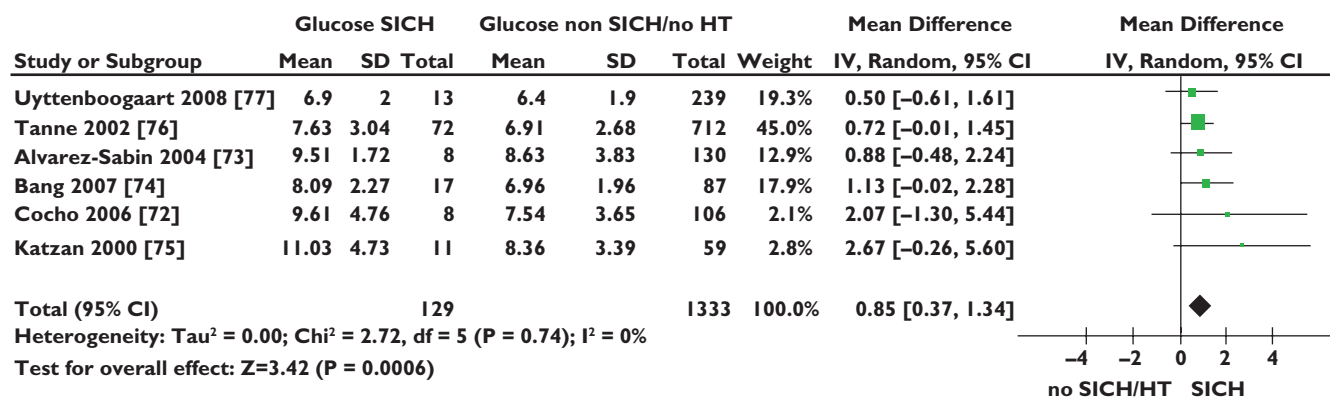


Figure 3

Forest plot showing association of high admission glucose levels with risk of ischaemic stroke patients developing symptomatic intracerebral haemorrhage (SICH) post-thrombolysis

haemorrhagic stroke; however, our study finds that at present few can significantly differentiate between patients with ischaemic and haemorrhagic stroke, or between stroke patients and healthy or patient control subjects. Of 136 molecular variables measured for stroke management, only eight (four diagnostic: CRP, P-selectin, homocysteine and GFAP; and four prognostic: glucose, glutamate, D-dimer and fibrinogen) were found to be supported by statistical analyses (Table 1).

Diagnostic and prognostic biomarkers for stroke

Biomarkers implicated in the differentiation between ischaemic stroke patients and control subjects include acute phase and inflammatory proteins CRP and P-selectin. Notably, only one biomarker identified as being significantly associated with stroke, GFAP, is a solely brain-derived molecule, although it is likely that the dysregulation of proteins involved in cell adhesion (e.g. intracellular adhesion molecule 1, fibronectin and matrix metalloproteinase-9) and increased plasma DNA levels in blood samples of stroke patients are a direct result of tissue damage within the brain. Being highly expressed by astroglial cells, which maintain the protective function of the blood-brain barrier, it has been suggested that enhanced GFAP levels are associated with the blood-brain barrier injury [37]. Foerch and colleagues [38] found that GFAP was detectable in 81% of patients with haemorrhagic stroke, compared with only 5% having ischaemic stroke.

The amino acid glutamate is the most abundant neurotransmitter in the brain, and it is likely that high levels are an indication of the extent of neuronal damage and therefore prognosis following stroke [39]. Homocysteine is another amino acid with a well-established relationship with vascular disease, linked with atherosclerosis, oxidative damage and vascular smooth muscle cell proliferation.

With this in mind, it is not surprising that higher homocysteine levels can distinguish ischaemic stroke patients from healthy control subjects [40].

Prognostic biomarkers for thrombolysis

Intravenous recombinant tissue plasminogen activator has revolutionized acute stroke management since its approval by the US Food and Drug Administration in 1996, and is the standard thrombolysing agent across the world.

Whilst 50% of patients receiving intravenous recombinant tissue plasminogen activator achieve complete or partial recanalization of the middle cerebral artery, a third of these patients also experience neurological worsening or delayed ischaemic injury [41–43]. Furthermore, risk of developing symptomatic ICH is one key reason why clinicians are reluctant to thrombolysise a patient and accounts for low treatment rates in the UK [44]. As not all forms of ICH are symptomatic or detrimental, a biomarker that is able to predict poor outcome following thrombolysis would improve patient selection, stratification, uptake of treatment and management.

One marker repeatedly found to be associated with poor prognosis after stroke and after thrombolysis was glucose. Post-stroke hyperglycaemia is a common phenomenon, with up to 50% of patients in two-thirds of ischaemic stroke subtypes having blood glucose levels of above 6.0 mmol l⁻¹. There is ample evidence to suggest that hyperglycaemia is detrimental in cerebral ischaemia [45].

Clinical relevance of statistically significant markers

In complex conditions, such as acute ischaemic stroke, there is a large degree of heterogeneity between patients,

Table 1

Summary of statistically significant biomarkers

Biomarker	Number of studies	Number of subjects	Mean difference	95% Confidence interval	P value	Interstudy heterogeneity (χ^2 ; P value)
Ischaemic stroke						
Diagnosis						
Acute ischaemic stroke vs. healthy control subjects						
C-Reactive protein (mg l ⁻¹)	8 [21–27]	2326	1.6	0.92, 2.27	0.00001	$\chi^2 = 97.00$; $P = 0.00001$
P-Selectin (ng ml ⁻¹)	2 [56, 57]	179	56.75	10.60, 102.90	0.02	$\chi^2 = 50.46$; $P = 0.00001$
Homocysteine (mmol l ⁻¹)	3 [27, 58, 59]	759	4.76	2.82, 6.71	0.00001	$\chi^2 = 42.70$; $P = 0.00001$
Prognosis						
Good outcome (mRS 0–2) vs. poor outcome (mRS 3–6)						
Glucose (mmol l ⁻¹)	4 [60–63]	1696	0.98	0.48, 1.48	0.0001	$\chi^2 = 15.25$; $P = 0.002$
Fibrinogen (mg l ⁻¹)	4 [36, 60, 62, 63]	1642	47.90	14.88, 80.93	0.004	$\chi^2 = 9.23$; $P = 0.010$
Progressive (dec > 1 CSS in 48 h) vs. stable stroke						
Glucose (mmol l ⁻¹)	3 [64–66]	572	3.17	1.60, 4.74	0.0001	$\chi^2 = 29.12$; $P = 0.00001$
Glutamate (μ mol l ⁻¹)	3 [64, 65, 67]	341	172.65	130.54, 214.75	0.00001	$\chi^2 = 14.45$; $P = 0.0007$
Survival in hospital vs. death in hospital						
Glucose (mmol l ⁻¹)	2 [68, 69]	1295	1.85	0.61, 3.15	0.003	$\chi^2 = 0.26$; $P = 0.61$
D-Dimer (μ g ml ⁻¹)	2 [69, 70]	566	0.67	0.35, 1.00	0.0001	$\chi^2 = 0.64$; $P = 0.42$
Haemorrhagic stroke						
Diagnosis						
Intracerebral haemorrhage vs. acute ischaemic stroke						
Glial fibrillary acidic protein (ng l ⁻¹)	3 [28, 38, 71]	258	224.58	25.84, 423.32	0.03	$\chi^2 = 5.70$; $P = 0.06$
Prognosis following thrombolysis						
Symptomatic intracerebral haemorrhage vs. no/asymptomatic haemorrhage						
Glucose (mmol l ⁻¹)	6 [72–77]	1462	0.85	0.37, 1.34	0.0006	$\chi^2 = 2.71$; $P = 0.74$

with biochemical profiles likely to be altered by the site, intensity and duration of ischaemia [46]. The additional effects of ethnicity, comorbidities, analytical techniques and interpretation of results limit reproducibility between studies [47]. The analysis of small sample populations has made it difficult to ascertain the true relationship between a marker and patient diagnosis/prognosis; the analysis of samples from large patient cohorts, stratified by known risk factors, should minimize the influence of clinical confounding variables [48].

With these experimental variations in mind, it is important that the parameters of data collection and classification are clearly outlined in every study report. The REMARK (Reporting Recommendations for Tumour Marker Prognostic Studies) guidelines, proposed by McShane *et al.* [49] suggests 20 items that should be reported in every biomarker study, including detailed descriptions of the patient population, basis for study design and assumptions of the model used to analyse data. While these recommendations were devised for tumour studies, they perhaps should be applied to all biomarker investigations.

A recent review has commented upon the risk of individual studies exaggerating biomarker associations and the caution needed in interpreting the reported results [50]. Hence, although our meta-analysis has established eight biomarkers of statistical significance likely to be

indicative of the pathophysiology of stroke, these markers may have only marginal translational value. A difference in means between two populations does not eliminate the possibility of considerable overlap between the two distributions, leading to high rates of false positives and false negatives at set thresholds [51]. This concept can be illustrated by plotting distribution curves based upon biomarker levels found in two clinically distinct populations. Figure 4b demonstrates that CRP levels in ischaemic stroke and healthy control populations from studies included in our meta-analysis lack the sensitivity and specificity required for effective discrimination between the two populations, raising doubt about the clinical value of CRP as a biomarker [52]. Conversely, glucose levels after ischaemic stroke appear to be more promising in characterizing patients with stable prognosis or progressive worsening (Figure 4c).

Multimarker panel tests

To date, no individual biomarker has proved to have adequate sensitivity and specificity for a clinical diagnostic test. A number of studies have attempted a multimarker panel approach in order to improve sensitivity and specificity [53–55]; however, thus far none has been suitably successful in a clinical setting.

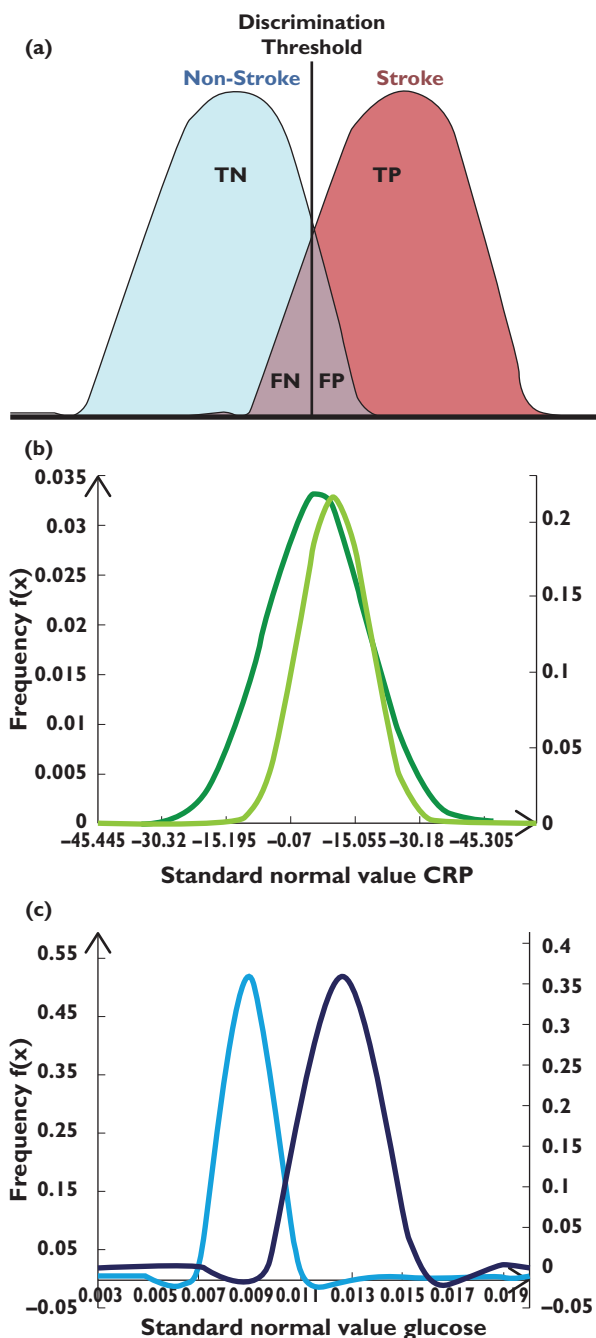


Figure 4

Biomarker distribution profiles for determining discrimination limits. (a) Biomarker discrimination limits are dependent upon the separation of distributions between two populations, affecting the numbers of true positives (TPs), true negatives (TNs), false positives (FPs) and false negatives (FNs) that can be distinguished. (b) C-Reactive protein distributions in ischaemic stroke patients and healthy control subjects, based upon data from studies in our meta-analysis. An arbitrary cut-off value could result in high rates of FPs and FNs. (c) Admission glucose levels in ischaemic stroke patients based upon studies included in our meta-analysis show good separation between distribution curves; hence, admission glucose could be a good indicator of progressive worsening compared with stable prognosis. (b) Ischaemic Stroke (—); Healthy (—). (c) Stable (—); Progressive (—)

This emphasizes a requirement for the identification of novel candidate biomarkers to develop a clinically relevant plasma-based test. As results from our meta-analysis suggest, the incorporation of routine biochemical variables, such as glucose and fibrinogen, into a marker panel could also enhance the accuracy of such a test. Importantly, this holds great implications for the development of a blood-based test for stroke, because the use of routine markers provides a simple and effective method of assessment, removing the need for a test based upon proteins that could potentially require longer and more complex laboratory analysis.

Limitations

It is important that the findings of this systematic review are considered in light of its limitations. Considerable heterogeneity between study design and data analysis precluded the inclusion of many studies into a meta-analysis and restricts the interpretation of our findings. Papers reporting threshold values for biomarker concentrations were excluded to reduce bias, as were papers that reported odds ratios without detailing the mean/median and variability of each data set. It is probable that the timing of a blood sample taken after stroke affects the concentrations of the biomarkers measured, although this could not be explored owing to the paucity of data. Despite the presence of heterogeneity, a number of measures have been taken to limit its impact, e.g. the use of the random-effects model and subgroup analysis. However, it is difficult to avoid publication bias when conducting a meta-analysis. Notwithstanding this inevitability, we have tried to account for this by manually searching abstracts and letters and by performing funnel plots and Egger regression asymmetry tests (Supporting Materials S2; Supporting Information Figures S1 and S2).

It is also important to consider that the meta-analysis was conducted collectively to maintain high statistical power, rather than splitting studies based upon their sample of measurement (plasma/serum/whole blood). However, iterative analysis found that inclusion/exclusion of certain sample types did not make significant differences to the results achieved. For example, exclusion of two studies reporting serum homocysteine levels in diagnosing between ischaemic stroke and healthy control subjects did not significantly affect analysis (collective, MD 1.60, 95% CI 0.92, 2.27; $P = 0.00001$; and plasma studies only, MD 1.34, 95% CI 0.69, 2.00; $P = 0.0001$). Finally, our work was limited to studies mainly of European origin. Although this restriction may not allow a detailed assessment of other ancestral groups, the extent of heterogeneity would in all likelihood have been too great to incorporate such diverse populations into the pooled odds ratio for each biomarker.

Conclusion

Even though stroke biomarkers studied are likely to be biologically informative about the mechanisms of vascular disease, their clinical value as sensitive diagnostic and prognostic tests remains uncertain. While many such biomarkers have been evaluated, few stand up to statistical scrutiny. However, admission glucose levels could be a strong predictor of poor prognosis and symptomatic ICH following thrombolytic treatment for ischaemic stroke. Proteins involved in metabolic pathways that are released into the blood before, during or after stroke do have the potential to be incorporated into clinically useful tests.

Competing Interests

There are no competing interests to declare.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Material S1

Search strategy for extraction of relevant papers for review.

Material S2

Funnel plot and Egger Regression results to assess publication bias associated with results in Figures 2 and 3.

Figure S1

Funnel plot assessing publication bias for studies comparing C-reactive protein (CRP) levels in acute ischaemic stroke and healthy population. Egger Regression intercept probability value = 3.453; standard error = 0.799; *P* value (two-tailed) = 0.111. Performed using Comprehensive Meta-Analysis version 2 software.

Figure S2

Funnel plot showing association of high admission glucose levels with risk of ischaemic stroke patients developing symptomatic intracerebral haemorrhage (SICH)

post-thrombolysis. Egger Regression intercept probability value = 1.167; standard error = 0.610; *P* value (two-tailed) = 0.128. Performed using Comprehensive Meta-Analysis version 2 software.

Table S1

List of all biomarkers identified in literature search that met inclusion criteria. Results from RevMan meta-analysis output are detailed, and biomarkers of significance are highlighted in yellow.

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