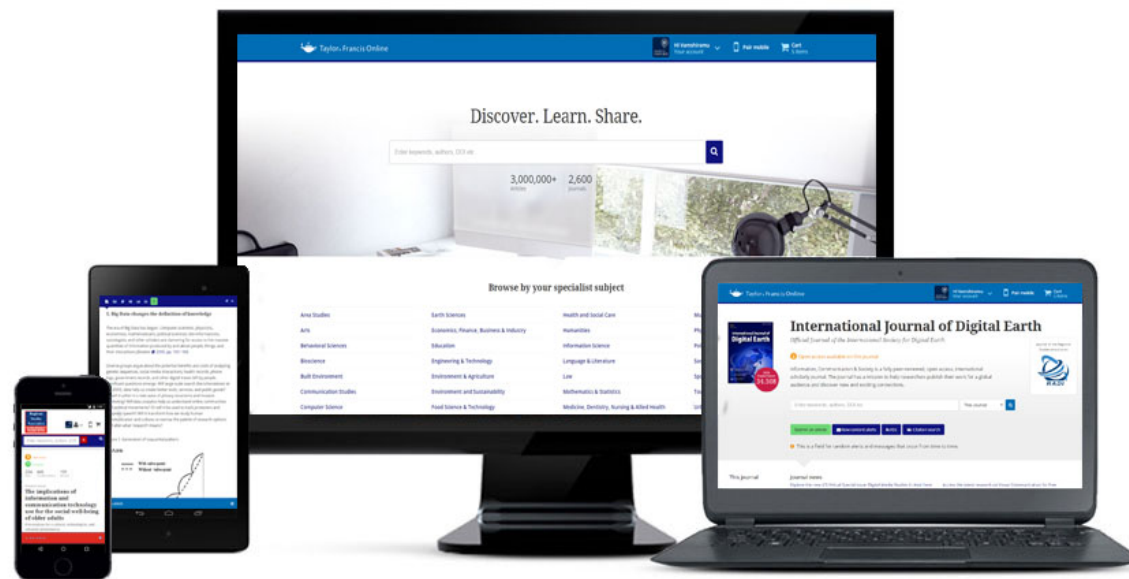




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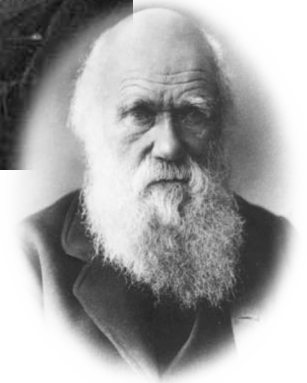
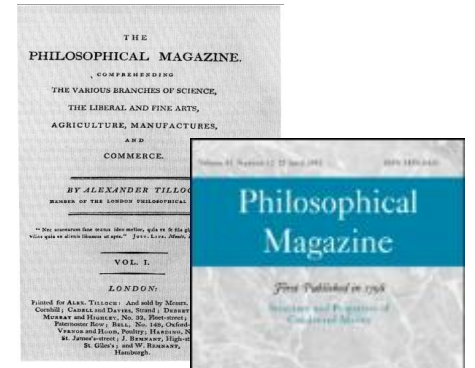
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Research Article

Social Capital, Credit Access and Household Nonfarm Enterprises in Nigeria: A new Empirical Evidence

Emmanuel O. Nwosu , Anthony Orji , Nathaniel E. Urama, Chisom Emecheta, Queen O. Chukwuma & Joseph Nnaemeka Chukwuma

Received 20 Dec 2019, Accepted 11 Sep 2020, Published online: 07 Oct 2020

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Abstract

1. Introduction

2. Brief Survey of Literature

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Abstract

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This paper investigates the effects of social capital on access to credit by household nonfarm small enterprises in Nigeria. Specifically, the paper tries to ascertain how social capital determines ability of household small businesses to borrow from formal and informal sources and the amount of credit accessed. The study uses data from the General Household Survey to estimate probit and Heckman selection model that form the basic models of the study. Specifically, the results show that belonging to informal groups increases the probability of accessing credit by 1.88%, and also has significant positive impact on the probability of using the loan to operate the enterprise. Also, membership of cooperatives significantly increases the probability of accessing enterprise loan. The results show that belonging to cooperatives and informal groups are the only social capital variables that have statistically significant impact on the amount borrowed.

Keywords: Household, nonfarm enterprise, social capital, credit
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1. Introduction



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- Materials and methods
- Results
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- Supplemental material
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- Disclosure statement

Abstract

Objective: The object of the present study was to estimate the relationship between maternal vitamin D deficiency during pregnancy and low birth weight by systematically review prevalence studies.

Methods: We collected data from relevant studies published up to April 2019 using predefined inclusion/exclusion criteria. And all the studies were searched in PubMed, Embase, Cochrane Library, and Web of Science.

Results: A total of 16 studies met the criteria and were included in the meta-analysis. When compared with normal serum levels of vitamin D, the maternal vitamin D deficiency had an increased risk of low birth weight (OR = 2.39; 95%CI 1.25–4.57; $p = .008$), and same results were found in the comparison of the mean (the total mean birth weight decreased by 0.08 kg; 95%CI -0.10 to -0.06; $p < .001$).

Conclusion: The evidence from this meta-analysis indicates a consistent association between vitamin D deficiency during pregnancy and an increased risk of low birth weight, and preventing maternal vitamin D deficiency may be an important public health strategy to help decrease the risk of low birth weight.

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ORIGINAL ARTICLE

RETRACTED ARTICLE: Serum protein biomarkers screening in patients with ischemic stroke by LC-MS/MS*

Xue-jun Wei,^{1,2} Feng Li,^{1,2} Feng-yong Yang,^{1,2} and Chong-hao Duan^{1,2}

¹Department of Intensive Care Unit and, ²Department of Emergency, The People's Hospital of Liaoyi City, Liaoyi, Shandong Province, P. R. China

Background: The purpose of this study was to investigate the serum protein biomarkers by liquid chromatography-mass spectrometry (LC-MS/MS) to identify mass spectrometry (MS) for the diagnosis of ischemic stroke (IS). **Methods:** In the study period, sera from 40 IS patients and 40 normal controls were collected for screening study. The selected protein associations with disease risk were identified using an enzyme-linked immunosorbent assay (ELISA) testing of the remaining stroke cases and 20000 peptides for biomarkers diagnosis were associated through receiver operating characteristic (ROC) curve analysis. **Results:** serum protein levels differences were suggested for 19 proteins (normal $P < 0.05$, $F_{(1,39)} = 4.26$), with these proteins having a false discovery rate < 0.05 . The association of mannose-binding lectin (MBL) with disease ($p = 0.001$) was confirmed using ELISA in multicolor studies. Based on the ROC curve, the optimal concentration of MBL as a surrogate marker to support the diagnosis of ischemic stroke (IS) was found to be 1000 $\mu\text{g/L}$, which yielded a sensitivity of 81.0% and a specificity of 80.2%. The area under the curve (AUC) was 0.724–0.876. In multivariate analysis, there was an increased risk of IS associated with MBL levels $\geq 1050 \mu\text{g/L}$ (OR: 4.76, 95% CI: 1.59–15.13) after adjusting for possible confounding factors. **Conclusion:** MBL discovery and replication studies presented here show MBL to be a risk marker for IS in the Chinese population, which appears to be a novel finding.

KEYWORDS: mannose-binding lectin; acute ischemic stroke; risk factor

Introduction

China has 2.5 million new stroke cases every year. In addition, approximately 1.6 million people in China will die and 7.5 million stroke survivors every year (15%–30% of survivors will be permanently disabled), which has exceeded heart disease as the second leading cause of death and disability [1]. Stroke places a tremendous burden on health resources in China. Early and accurate prediction of outcome in stroke is important and influences risk-optimized therapeutic strategies [2]. Revascularization is possible if the stroke patient is brought to a well-equipped stroke unit in a particular window of time. However, it is difficult for

patients to reach such a center within this window, even in developed countries. With increased interest in clinical proteomics, the use of comparative investigations of differential protein expression is more common than ever before for diagnostic and prognostic assessments of disease states.

Blood protein markers provide a source for novel disease risk markers and have potential to enhance the understanding of disease pathogenesis [3]. The discovery of novel candidate protein biomarkers from serum using high-throughput proteomic technologies has attracted enthusiasm in the biomedical research community. Liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) is an alternative approach that couples protein fractionation with mass spectrometry to generate a comprehensive catalog of the proteome of analyzed fluid samples [4]. One of the greatest strengths of tandem mass spectrometry for protein identification is the inherent ability to sequence peptides directly from mixtures [5]. Protein-peptide quantification using labeling strategies usually requires labeling of the cysteinyl or amino groups of all peptides with isotope-coded

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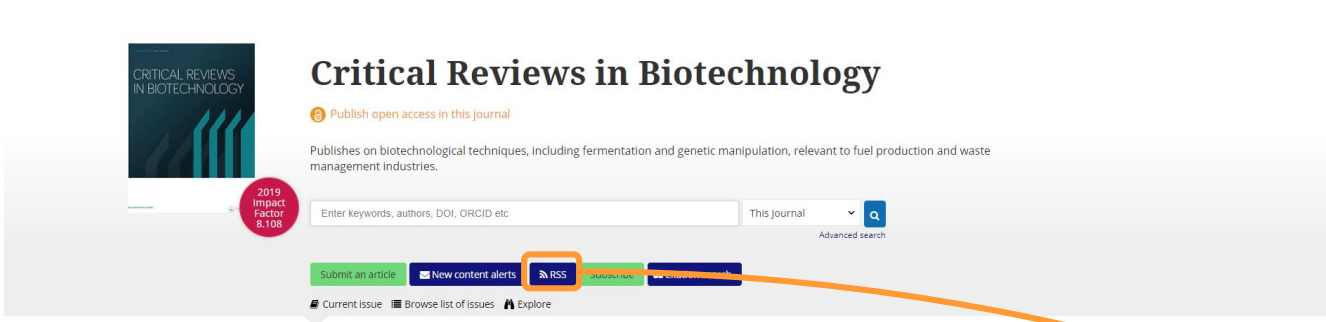
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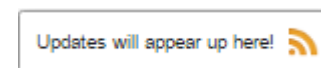




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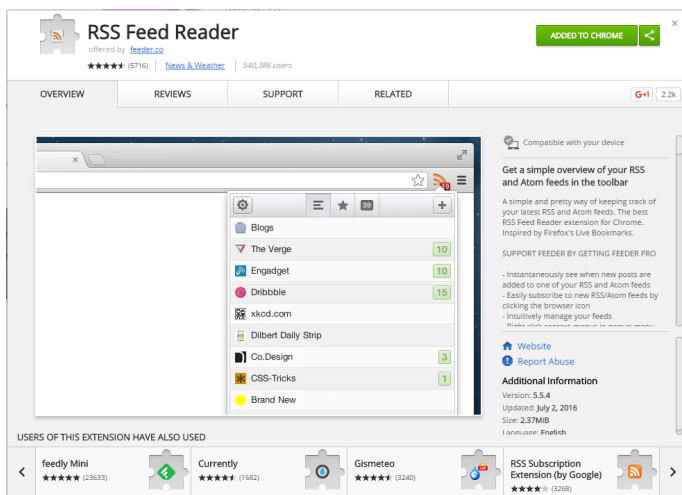


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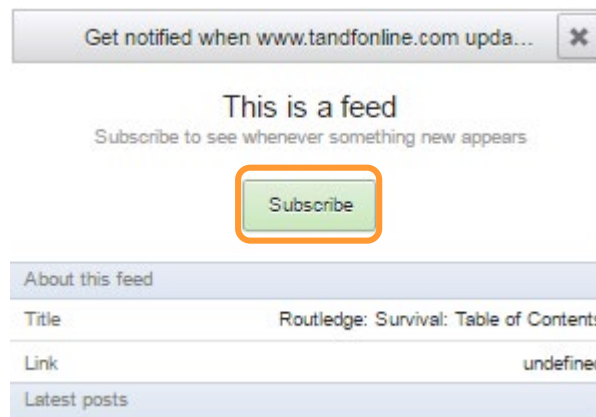
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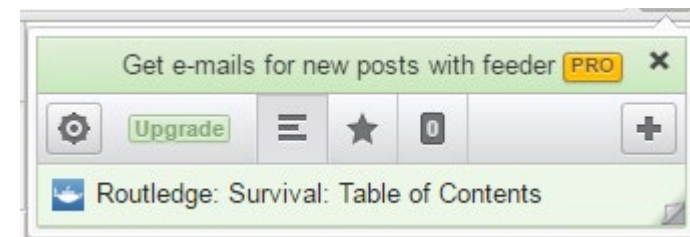
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