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學術文獻回顧與分析程序

訂主題



下關鍵字



整理編輯



篩選文獻



瀏覽全文



Association of high body lead store with severe intracranial carotid atherosclerosis

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ABSTRACT

Objective: Lead is involved in the pathogenesis of atherosclerosis and hypertensive disease and may be related to cerebrovascular disease. We studied the association of body lead level with stroke subtypes and severity of cerebral atherosclerosis in order to identify the significance of lead exposure to cerebrovascular disease.

Methods: From April, 2002 to March, 2005, we studied the lead level in all patients receiving digital subtraction angiography. Diameter stenosis at extracranial carotid, intracranial carotid and vertebro-basilar system was calculated according to the NASCET criteria. A blood sample and a mobilization test of 72-h urine sample were collected for lead measurement.

Results: In a total of 213 subjects, 19 were free of stroke (blood lead level = 4.62 ± 2.41 $\mu\text{g/dL}$, body lead store = 39.04 ± 20.91 μg) and 194 were stroke patients (4.89 ± 2.75 $\mu\text{g/dL}$, 45.13 ± 29.8 μg ; all stroke vs. non-stroke, $P > 0.05$). In the 153 subjects with atherosclerotic origin, body lead store but not blood lead level in the intracranial carotid system was significantly higher in $\geq 50\%$ group than $< 50\%$ group (blood lead: 5.61 ± 3.02 $\mu\text{g/dL}$ vs. 4.80 ± 2.50 $\mu\text{g/dL}$, Student's t -test, $P = 0.129$; body lead store: 51.7 ± 27.0 μg vs. 41.9 ± 23.5 μg , Student's t -test, $P = 0.038$, multivariate logistic regression, odds ratio = 1.02, 95% CI: 1.00–1.03, $P = 0.043$). However, there was no significant association between lead level and stenotic severity in extracranial and vertebrobasilar systems ($P > 0.05$).

Conclusion: Our study demonstrated that long-term lead exposure as measured by body lead store might carry a potential risk of intracranial carotid atherosclerosis.

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1. Introduction

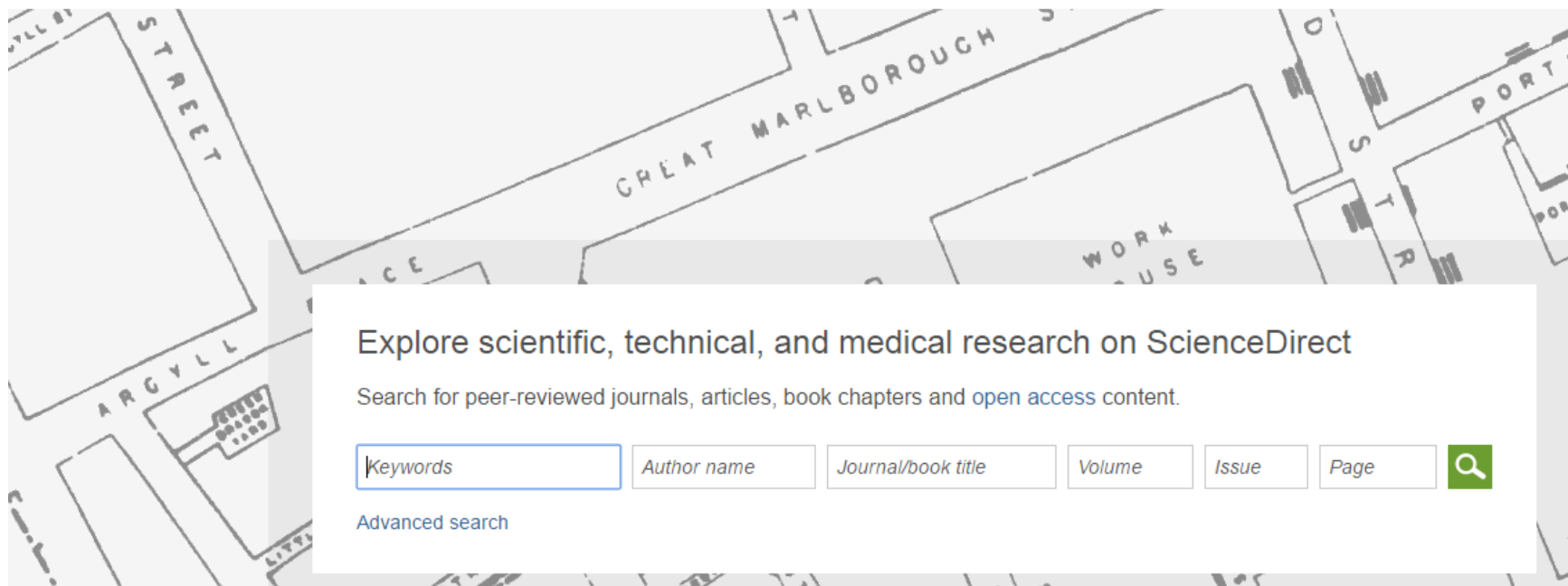
Previous studies indicated that lead has specific toxicities in the proliferation, fibrinolysis, and extracellular matrix formation of vascular endothelial and smooth muscle cells, resulting in vascular disorders such as atherosclerosis in experimental animals (Kaji, 2004). Lead may induce aortic atherosclerosis in pigeons (Revis et al., 1981) and stimulate the proliferation of cultured rabbit aortic smooth muscle cells in varying degrees (Lu et al., 1990). Lead can also stimulate the proliferation of the vascular smooth muscle cells and fibroblasts (Fujiwara et al., 1995) and inhibit the repair process of damaged endothelial cell layer (Fujiwara et al., 1997) in in vitro studies. Animal study showed that lead may cause severe injury to endothelium of brain vasculature (Bradbury and Deane, 1988;

Linnamagi and Kaasik, 1995) and induces cerebral microvascular dysfunction with following changes in cerebral blood flow (Linnamagi and Kaasik, 1995). Hence, it is likely that lead is involved in the pathogenesis of cerebral atherosclerosis and may be related to cerebrovascular disease.

Cerebrovascular disease or stroke has been one of the first three leading causes of death in the past four decades in Taiwan (Jeng and Su, 2007) and is more common in Taiwanese than in Whites (Hu et al., 1992; Goldstein et al., 2006). The distribution of cerebral atherosclerosis in stroke patients is different between races, and atherosclerosis of the larger extracranial arteries is more prevalent in Whites, while occlusive disease of the intracranial arteries is more often seen in patients of Black or oriental origin (Feldmann et al., 1990; Leung et al., 1993; Liu et al., 1996; Jeng and Su, 2007). Regarding stroke subtype, small vessel occlusion and large artery

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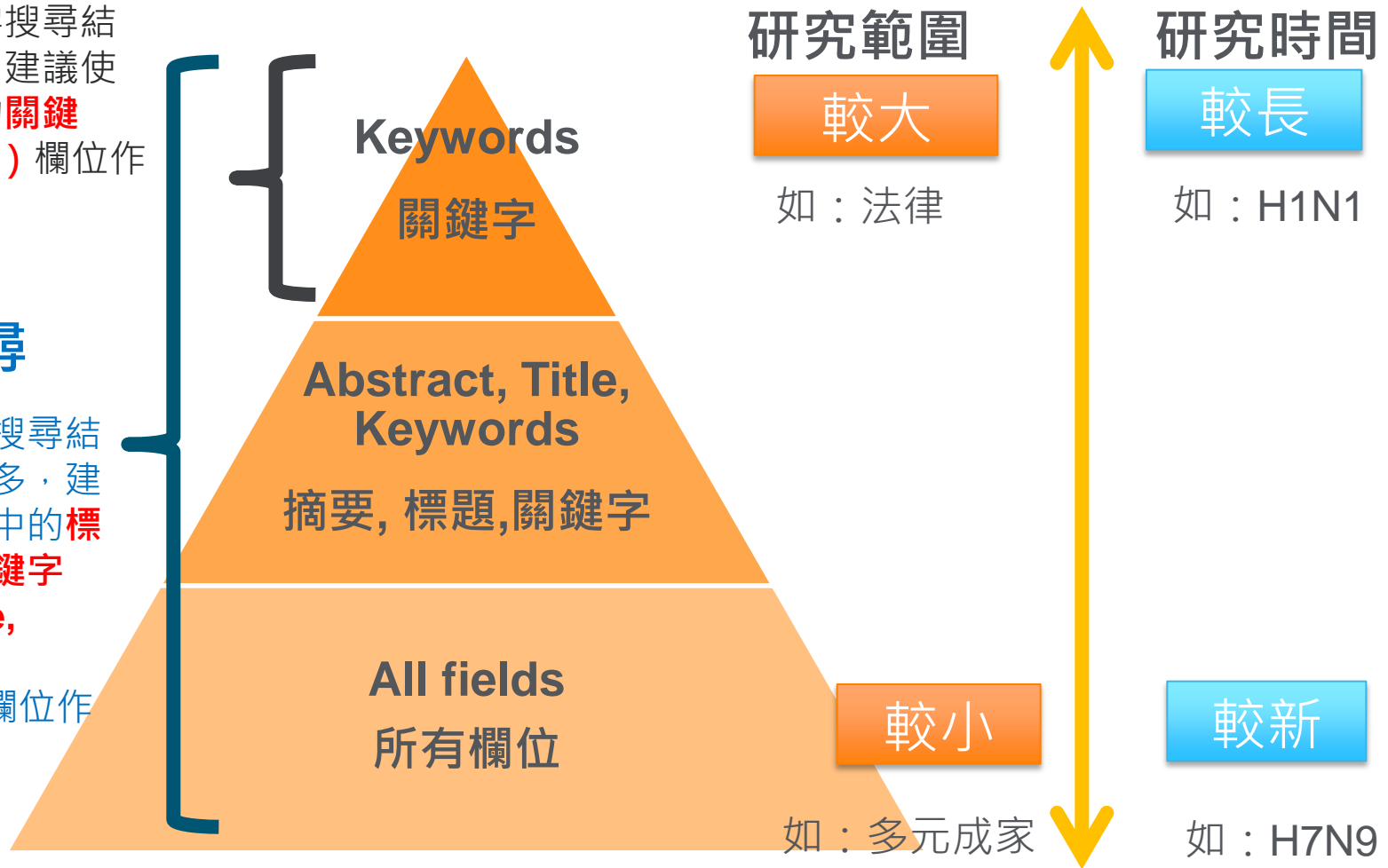
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快速檢索-文獻

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The screenshot shows the ScienceDirect search interface. At the top, a search bar contains the keyword 'zika'. Below the search bar, there are fields for 'Author name', 'Journal or book title', 'Volume', and 'Issue'. The search results show 2,855 results found. On the left, there are 'Refine filters' for 'Year', 'Publication title', and 'Topic'. The main results list includes articles like 'Initial experience with imported Zika virus infection in Spain' and 'Epidemiology of Zika Virus'. Annotations with arrows point to various elements: the search bar, the search filters, the article titles, and the PDF download links.

- All fields欄位輸入任意關鍵字 (兩個單字, 請輸入" ")
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big data [All Sources(- All Sciences -)]		Delete
"big data" or computation [All Sources(- All Sciences -)]		Delete
zika [All Sources(- All Sciences -)]		Delete
ACE or "Angiotensin-Converting Enzyme" or ACTN3 or "alpha actinin 3" [All Sources(- All Sciences -)]	241,594 articles	Edit Delete
ACE or "Angiotensin-Converting Enzyme" or ACTN3 or "alpha actinin 3" AND LIMIT-TO(contenttype, "JL,BS","Journal") [All Sources(- All Sciences -)]	227,658 articles	Edit Delete
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Search results: 1,683 results found for KEYWORDS("food safety").

Refine filters

Year

- 2015 (4)
- 2014 (212)
- 2013 (250)
- 2012 (195)
- 2011 (148)
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Publication title

- Food Control (350)
- International Journal of Food Microbiology (144)
- Food and Chemical Toxicology (136)
- Journal of Food Composition and Analysis (129)
- Food Policy (58)
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Topic

- food safety (329)
- coli o157 (53)
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- Journal (1,683)

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Journals

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Search results: 2,855 results found. [See image results](#)

Refine filters

Year

- 2017 (21)
- 2016 (1,043)
- 2015 (100)
- 2014 (77)
- 2013 (56)
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Publication title

- Marine Chemistry (195)
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Journal of Clinical Anesthesia, Volume 35, December 2016, Pages 136-144
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Epidemiology of Zika Virus Review Article

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1. 先勾選要
匯出的文章

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The screenshot shows the ScienceDirect search results page for 'zika'. The search results list several articles related to Zika virus. The 'Download PDFs' button is highlighted. A callout box explains the steps: '1. 請先勾選要下載的文獻' and '2. 再點選Download multiple PDFs'. Another callout box describes the automatic naming function: '自動命名功能，文獻可設定依照作者名、出版年份、文章標題、期刊名稱等組合命名。'. The 'Download Options' section shows a dropdown menu for 'Select PDF file naming:' with the selected option '(Publication Year)_(Document Title)_(Publication Name).pdf'. A 'Create my own' button is also visible. Below this, a 'Create My Document Naming Convention' window is shown, where users can select file naming bits from a list (e.g., First Author, Volume, Issue, First Page, Last Page, ISSN/ISBN) and a 'Selected File Naming Bits' list (e.g., Publication Year, Publication Name, Document Title). A 'Prefix' field is set to 'food_safety_'. A 'File Name Preview' shows the resulting filename: 'food_safety_2015_Food-Control_Evaluation-of-ready-to-eat-sashimi-in-northern-Portugal-restaurants.pdf'. A callout box explains the naming convention: '客製化檔名關鍵字：您可輸入方便您管理文獻的縮寫，還可以指定縮寫在檔名的位置，Prefix：縮寫放在最前面；Suffix：縮寫放在最後面。'. Another callout box points to the 'Create My Document Naming Convention' window, labeled '客製化檔名選單'. A final callout box points to the 'File Name Preview' section, labeled '預覽檔名'.

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預覽檔名

Article outline Show full outline

- Summary
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- Introduction
- Results
- Discussion
- Experimental Procedures
- Acknowledgments
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文章架構

Figures and tables



Table 1



Table 1



圖表縮圖

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Volume 141, Issue 7, June 2010, Pages 1110-1112

Article

LINE-1 Retrotransposons

Christine R. Beck¹, Pamela Collier⁴, Catriona Macfarlane⁴, Maika Malign⁵, Jeffrey M. Kidd⁵, Evan E. Eichler^{5,6}, Richard M. Badge⁴, John V. Moran^{1,2,3}

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<http://dx.doi.org/10.1016/j.cell.2010.05.014>

Referred to by James R. L...
Retrotransposition and Structural Variation in the Human Genome
Cell, Volume 141, Issue 7, 25 June 2010, Pages 1110-1112
 PDF (412 K)

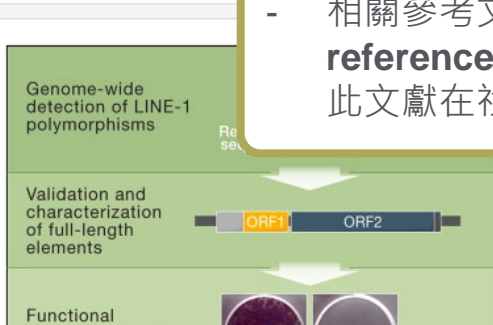
文章本文

Summary

Highly active (i.e., "hot") long interspersed element-1 (LINE-1) retrotransposition activity in the human genome remains largely unexplored. Here, we identify 68 full-length L1s that are differentially abundant in reference sequence. The majority of these elements are located in the Genotyping 26 elements revealed that 10% of the H952 subset of the Human Genome Reference Consortium is abundant in the human population. This continues to be a major source of interindividual genetic variation.

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Graphical Abstract



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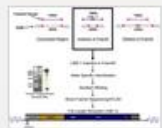
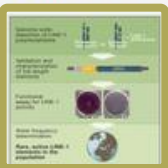
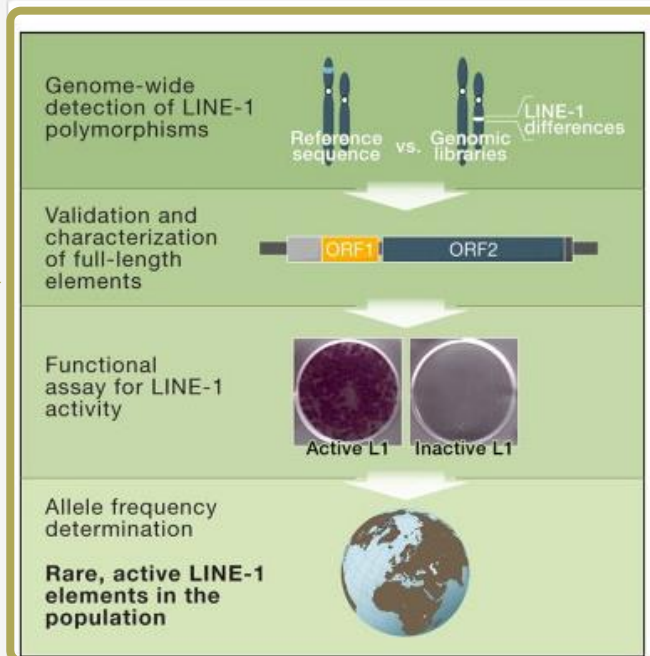


Table 1

Gene	Accession	Length (bp)	GC Content (%)
LINE-1	U000000000	282	41.5
ORF1	U000000000	100	41.5
ORF2	U000000000	182	41.5

Graphical Abstract



Highlights

- The human population contains more active LINE-1s than pre

在圖片右下角的Figure options:

1. **View workspace:** 可在右側 workspace(工作區)瀏覽
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Figure options ▲

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文章內表格儲存編輯

The screenshot shows a research article interface. On the left, there is a sidebar with a 'Table 1' icon and a list of thumbnails. A yellow arrow points from the 'Table 1' icon to a large table in the main content area. The table contains text from a scientific paper, including a list of items (a, b, c) and a 'Table options' dropdown menu. The dropdown menu has two options: 'View in workspace' and 'Download as CSV'. A yellow box highlights the 'Table options' dropdown and its options. Another yellow box highlights the 'Table options' dropdown and its options, with an arrow pointing to a list of instructions.

Table 1

點選左側縮圖後，表格便會放大至中間

2006). Column 9: the number of elements from column 7 that were active in retrotransposition assays. Column 10: elements from column 9 that retrotransposed at levels > 10% of L1.3, a known active element. Column 11: the number of the HGR hot elements that were present in each individual (Brouha et al., 2003).

- Daughters of Hap Map trios.
- Differs from Kidd et al. (2008).
- One element recurred in ABC11 & 12- #4-1 and #5-77. Neither allele is active, and the element is in dbRIP.

Fosmids fulfilling the above mapping criterion were subjected to a sequence-specific oligonucleotide hybridization using probes directed against diagnostic sequences in the L1Hs 5' UTR identified insertion fosmids that contained putative dimorphic L1Hs elements (Boissinot et al., 2000 and Tuzun et al., 2005). Sequence L19088 enabled the identification of L1Hs elements (Dombroski et al., 1993 and Saito et al., 2003) and/or direct repeats (Badge et al., 2003) and/or direct repeats (length) L1Hs element in the fosmid library. The identified L1Hs elements were used to identify L1Hs elements in the fosmid library (command = start) (Kent, 2002).

Flanking sequences also were used to determine whether any of the L1Hs elements were present in a database of known polymorphic retrotransposon insertions (dbRIP; <http://dbrip.brocku.ca/>) (Wang et al., 2006). Two additional L1Hs elements were identified through direct sequencing of the fosmids (#1-(2-1) and 3-(2-1)).

Table options ▲

- View in workspace
- Download as CSV

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