### Accepted Manuscript

Role of SDF-1 3'A polymorphism in HIV-1 disease progression: A systematic review and meta-analysis

Meide Wei, Chengzhi Rong, Jiangyang Zhao, Xin Liu, Fengxun Yang, Jie Zeng

PII: S0378-1119(18)30837-0

DOI: doi:10.1016/j.gene.2018.07.058

Reference: GENE 43099

To appear in: Gene

Received date: 27 March 2018
Revised date: 3 July 2018
Accepted date: 23 July 2018

Please cite this article as: Meide Wei, Chengzhi Rong, Jiangyang Zhao, Xin Liu, Fengxun Yang, Jie Zeng, Role of SDF-1 3'A polymorphism in HIV-1 disease progression: A systematic review and meta-analysis. Gene (2018), doi:10.1016/j.gene.2018.07.058

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



## ACCEPTED MANUSCRIPT

#### Role of SDF-1 3'A polymorphism in HIV-1 disease progression: a systematic review and meta-analysis

Meide Wei, BSM<sup>1</sup>, Chengzhi Rong, MD<sup>2</sup>, Jiangyang Zhao, MD<sup>2</sup>, Xin Liu, BSM<sup>3</sup>, Fengxun Yang, BSM<sup>3</sup>, Jie Zeng, BSM<sup>3</sup>

<sup>1</sup>Department of Clinical Laboratory, Fourth Affiliated Hospital of Guangxi Medical University, Liuzhou 545000, Guangxi Zhuang Autonomous Region, China

<sup>2</sup>Department of Clinical Laboratory, Children's Hospital, Maternal and Child Health Hospital, Guangxi Zhuang Autonomous Region, Nanning 530021, Guangxi, China

<sup>3</sup>Department of Clinical Laboratory, Liuzhou City People's Hospital, Liuzhou 545000, Guangxi Zhuang Autonomous Region, China Corresponding author:

Jie Zeng:

E-mail: m15077200332@163.com

Tel: +86-0772-2662479

#### Abstract

Background: Chemokine stromal cell-derived factor 1(SDF-1) 3'A polymorphism has been reported to influence HIV-1 disease pathogenesis and progression, but the results remain controversial.

Objectives: A meta-analysis was carried out to evaluate their association.

Methods: Comprehensive literature search of Pubmed, Web of Science and China National Knowledge Infrastructure was conducted. The strength of association between SDF-1 3'A polymorphism and HIV-1 progression was evaluated using the pooled ORs and 95%CIs calculated under different comparison models. Subgroup analyses, heterogeneity, Galbraith plot analyses and test for publication bias were also carried out.

Results: Our result showed that when compared with the typical progressors, the GA+AA and GA genotype of SDF-1 3'A polymorphism was found positively associated with the long-term non-progressors (LTNP) in the Caucasian HIV-1 infectors (GA+AA vs. GG, OR = 1.49, 95%CI: 1.02-2.18, p 0.040; GA vs. GG, OR = 1.58, 95%CI: 1.06-2.35, p = 0.024), while AA genotype was found significantly higher in Asian LTNPs (AA vs. GG+GA, OR = 3.32, 95%CI: 1.25-8.85, p = 0.016).

Conclusions: Our result suggested that HIV-1 infectors with SDF-1 3'A polymorphism have a higher chance of developing late AIDS than infectors with the SDF-1 GG genotype.

**Keywords:** SDF-1, polymorphism, HIV, progression, meta-analysis

#### 1. Introduction

Human immunodeficiency virus-1 (HIV-1), the pathogen of AIDS, is the leading killer among the infectious diseases. According to the global factsheet of 2016, there were still 36.7 million people suffering from HIV-1 infection, with 1.8 million were newly infectors, and 1.0 million died per year for the AIDS-related diseases, indicating that it remains a major challenge for the public health worldwide (http://aidsinfo.unaids.org/). Despite the high-risk behavior and multiple exposures to HIV-1 such as unprotected sex, contaminated blood transfusions and hypodermic needles, some people remain seronegative or uninfected; and there is also a wide range of clinical progression to AIDS after HIV infection, from the symptomatic within 2–3 years (rapid-progressors) to some asymptomatic for more than 10 years without antiretroviral (ART), namely long-term non-progressors (LTNPs)<sup>1,2</sup>, indicating that some individuals have the ability to limit the expansion of the virals.

The factors that lead to the different clinical outcome and disease progression are unknown, but were believed to associate with the differences among viral properties, host genetics and host immune responses<sup>3</sup>. Up to now, much attention has been paid to the host-dependent factors, especially genetic polymorphisms of chemokines and their receptors. Among them, the chemokine receptor CXCR4

### Download English Version:

# https://daneshyari.com/en/article/8644396

Download Persian Version:

https://daneshyari.com/article/8644396

<u>Daneshyari.com</u>