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Original Article

Circulating lncRNA ANRIL level positively correlates with disease risk, severity, inflammation level and poor prognosis of coronary artery disease

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Abstract: The purpose of this study was to investigate the association of long non-coding RNA (lncRNA) ANRIL expression with disease risk, severity, inflammation level and prognosis of coronary artery disease (CAD). A total of 169 patients with unexplained chest pain or CAD-like symptoms underwent coronary angiography and were consecutively recruited, among whom 92 patients were diagnosed with CAD and were included in the CAD group while the other 77 patients were included in the control group. Plasma lncRNA ANRIL level of all patients was detected by quantitative polymerase chain reaction, Gensini score was evaluated via Gensini criterion. In CAD patients, plasma level of inflammatory factors was evaluated by enzyme linked immunosorbent assay, and overall survival (OS) was calculated. Plasma level of lncRNA ANRIL was increased in the CAD group compared to control group ($P < 0.001$) and disclosed a good predictive value for CAD risk (AUC=0.806, 95% CI: 0.741-0.871). In CAD patients, lncRNA ANRIL was positively correlated with Gensini score (r=0.270, P=0.009), high-sensitivity C-reactive protein level (r=0.293, P=0.005), tumor necrosis factor-α level (r=0.271, P=0.009) and interleukin (IL)-6 level (r=0.464, $P < 0.001$) while negatively associated with IL-10 (r=-0.274, P=0.008) level. Additionally, the OS was poorer in CAD patients with high lncRNA ANRIL expression compared to patients with low lncRNA ANRIL expression (P=0.025). In conclusion, Circulating lncRNA ANRIL expression associates with increased disease risk, severity, inflammation level and poor prognosis of CAD.

Keywords: lncRNA ANRIL, plasma, coronary artery disease, disease risk, disease severity

Introduction

Coronary artery disease (CAD) is one of the most common diseases in the world which affects approximately 110 million people and causes 8.9 million deaths every year [1, 2]. Due to unhealthy life style and increased lifespan, CAD is becoming more and more prevalent both in developing countries and developed countries [1-3]. Although great improvement has been achieved in CAD diagnosis and treatment in the past decades, there still lack sensitive and specific biomarkers for early CAD diagnosis and disease monitoring [3-5].

Long non-coding RNA (lncRNA) is a type of RNA which have more than 200 nucleotides but possess little or no open reading frame [6]. According to previous studies, lncRNA is widely distributed in eukaryotic cells and is implicated in various biological activities through epigenetic regulation, transcriptional regulation and post-transcriptional regulation [7-9]. Among the numerous lncRNAs, lncRNA antisense non-coding RNA in the INK4 locus (lncRNA ANRIL) was discovered to be involved in many complicated diseases such as cancers, diabetes and inflammatory diseases [10-12]. More interestingly, there is increasing evidence showing that lncRNA ANRIL plays an important role in cardiovascular diseases [13-15]. For instance, in CAD patients who have received drug-eluting stent (DESs) treatment, lncRNA ANRIL is upregulated in those patients with In-stent restenosis (ISR) compared with patients without ISR [16]. In another study, lncRNA ANRIL expression is also increased in type 2 diabetes mellitus (T2DM) in patients with CAD compared to T2DM patients without CAD [11]. However, the role of lncRNA ANRIL in CAD re-

mains largely unclear. To this end, we conducted the current study to investigate the association of lncRNA ANRIL expression with disease risk, severity and prognosis of CAD.

Materials and methods

Participants

One hundred and sixty-nine adult patients with unexplained chest pain or CAD-like symptoms who were admitted to The Affiliated Hospital of Guizhou Medical University for elective coronary angiography between January 2013 and December 2014 were consecutively included in this study. After coronary angiography, 92 patients with diagnosed with CAD and were included in the CAD group while the other 77 patients were included in the control group. The inclusion criteria of CAD patients were as follows: (1) at least one coronary artery occurred stenosis (≥50%) according to coronary angiography; (2) without surgical history of congenital heart disease, heart valvular disease, vasospastic angina, cardiomyopathy or coronary artery bypass graft. The following patients were excluded: (1) contraindication of coronary angiography; (2) serious heart, lung or kidney dysfunction; (3) history of cancer, malignant blood disease, severe infection or autoimmune diseases; (4) pregnant or lactating women. All patients or their guardians signed informed consents and the study was approved by the Ethics Committee of the Hospital.

Data collection

Clinical data of the patients was collected after enrollment which consisted of (1) baseline characteristics: age, gender, body mass index (BMI), smoking, hypertension, diabetes, and the history of CAD; (2) routine laboratory testing: triglyceride (TG), total cholesterol (TC), high-density lipoprotein cholesterol (HDL-C) and low-density lipoprotein cholesterol (LDL-C).

Coronary artery damage assessment

Gensini score was used to assess the severity of coronary artery damage. First, we gave a basic score to each coronary artery as follows: 1 point for ≤25% narrowing, 2 points for 26 to 50% narrowing, 4 points for 51 to 75% narrowing, 8 points for 76 to 90% narrowing, 16 points for 91 to 99% narrowing, and 32 points for 100%. Second, a multiplier factor was determined according to the importance of the lesion localization in the coronary arterial system as follows: 5 for the left main coronary, 2.5 for the proximal left anterior descending (LAD) and left circumflex (LCX), 1.5 for the mid segment LAD, 1 for the distal segment of LAD and LCX, first diagonal branch, first obtuse marginal branch, right coronary artery, posterior descending artery and intermediate arteries and 0.5 for the second diagonal and second obtuse marginal branches. Finally, the score of each lesion vessel equaled the basic score times the factor of the same location, and the sum of each lesion vessel score was the final Gensini score in this patient.

Sample collection

Blood samples from patients were collected in the anticoagulation tubes and centrifuged at 4°C for 15 min at 1800 g. Then the supernatant was transferred to the EP tube and centrifuged at 4°C for another 10 minutes at 2500 g. Finally, the supernatant was transferred to the cryogenic vials (400~500 μL/vial) and stored at -80°C for further detections.

Measurements of inflammation markers and cytokines

The levels of high-sensitivity C-reactive protein (hs-CRP) and erythrocyte sedimentation rate (ESR) of CAD patients were measured by the PA8800 particular globin analyzer (Perlong Medical, China) and PUC-2068A ESR analyzer (Perlong Medical, China). Human Enzyme-linked immunoassay (ELISA) kits (R&D, USA) were used to determine the concentrations of plasma inflammatory cytokines according to the manufacturer's instructions, including tumor necrosis factor (TNF-α), interleukin-1β (IL-1β), IL-6, IL-8, IL-10 and IL-17.

Measurement of lncRNA ANRIL

All the patients' plasma samples were collected and stored at -80°C after enrollment. Then total RNA extractions were performed using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's recommendations. cDNA was then synthesized using the transcription kit (TOYOBO, Japan), and the relative expression of lncRNA ANRIL was detected by real-time quantitative polymerase chain reaction (RT-qPCR) with the use of SYBR Premix Ex Taq II (Takara, Japan) and Applied Biosystems 7500 HT PCR system (Applied Biosystems, USA). Glyceraldehyde 3-phosphate dehydroge-

Table 1. Characteristics of CAD patients and controls

Characteristics	CAD patients (N=92)	Controls (N=77)	*P* value
Age (years)	60.7 ± 9.3	58.8 ± 8.1	0.149
Gender (male/female)	71/21	58/19	0.778
BMI (kg/m^2)	23.9 ± 3.0	23.6 ± 2.8	0.506
Hypertension (n/%)	81 (88.0)	61 (79.2)	0.119
Diabetes (n/%)	19 (20.7)	14 (18.2)	0.687
Smoke (n/%)	41 (44.6)	40 (51.9)	0.339
Family history of CAD (n/%)	30 (65.2)	22 (28.6)	0.571
TG (mmol/L)	1.79 ± 0.89	1.68 ± 0.81	0.406
TC (mmol/L)	4.72 ± 1.50	4.58 ± 1.61	0.560
HDL-C (mmol/L)	1.08 ± 0.34	1.23 ± 0.38	0.007
LDL-C (mmol/L)	2.85 ± 1.22	2.61 ± 1.09	0.183
Gensini score	45.0 (20.9-69.8)	1.0 (1.0-2.0)	< 0.001

Data were presented as mean value ± standard deviation, median (25th-75th quantiles) or count (percentage). Comparison was determined by t test, Wilcoxon rank sum test or Chi-square test. *P* value < 0.05 was considered significant. CAD: coronary artery disease; BMI: body mass index; TG: triglyceride; TC: total cholesterol; HDL-C: fasting high-density lipoprotein cholesterol; LDL-C: fasting low-density lipoprotein cholesterol.

nase (GAPDH) was utilized as the normalized internal reference and the relative expression of lncRNA ANRIL was calculated using the $2^{-\Delta\Delta Ct}$ method. The primers were as follows: ANRIL: forward: 5'-TGCTCTATCCGCCAATCAGG-3', reverse: 5'-GGGCCTCAGTGGCACATACC-3'; GAPDH: forward: 5'-GAGTCAACGGATTTGGTC-GT-3', reverse: 5'-TTGATTTTGGAGGGATCTCG-3'.

Follow up

Regularly follow up for all CAD patients was performed by telephone until the last follow-up point of March 31, 2018. The median follow-up duration was 43.5 months (range: 5.0-54.0 months). A total of 14 CAD patients were lost in follow up and they were excluded from the overall survival (OS) analysis. OS was defined as the data from enrollment to the data of death from any cause.

Statistical analysis

SPSS 22.0 statistical software (IBM, USA) and Graphpad Prism 6.01 software (GraphPad Software Inc, USA) were used for statistical analysis and chart making process. Data were expressed as mean ± SD, count (percentage) or median (25th-75th quartile). Comparison was determined by Chi-square test, t test or Wilcoxon rank sum test. The diagnostic value of lncRNA ANRIL relative expression for CAD risk was analyzed by receiver operating characteristic (ROC) curve; correlation analysis was performed using Spearman's rank correlation test; the OS difference between lncRNA ANRIL high and low expression patients was determined by Kaplan-Meier method and Log-rank test. *P* value < 0.05 was considered significant.

Results

Characteristics of CAD patients and controls

In the CAD group, there were 71 male patients and 21 female patients, and the mean age was 60.7 ± 9.3 years; in the control group, there were 58 male patients and 19 female patients, and the mean age was 58.8 ± 8.1 years (**Table 1**). No difference of demographic characteristics between the two groups was observed (*P* > 0.05). Meanwhile, HDL-C was 1.08 ± 0.34 mmol/L in the CAD group and was 1.23 ± 0.38 mmol/L in the control group (*P*=0.007), Gensini score was 45.0 (20.9-69.8) in the CAD group and was 1.0 (1.0-2.0) in the control group (*P* < 0.001). Other characteristics were depicted in **Table 1**.

Comparison of lncRNA ANRIL expression between CAD patients and controls and the ROC curve

Plasma level of lncRNA ANRIL in the CAD group was increased compared with control group (*P* < 0.001, **Figure 1A**). ROC curve showed that it well distinguished CAD patients from controls with an AUC of 0.806 (95% CI: 0.741-0.871), and the sensitivity and the specificity at the best cut-off point (lncRNA ANRIL expression: 0.733) was 90.2% and 59.7%, respectively (**Figure 1B**). The best cut-off point was defined as the point that the value of sensitivity plus specificity was the largest. These data indicated that lncRNA ANRIL might served as a biomarker for predicting CAD risk.

Association of lncRNA ANRIL expression with disease severity and inflammation level in CAD patients

Plasma lncRNA ANRIL expression was positively associated with Gensini score (r=0.270,

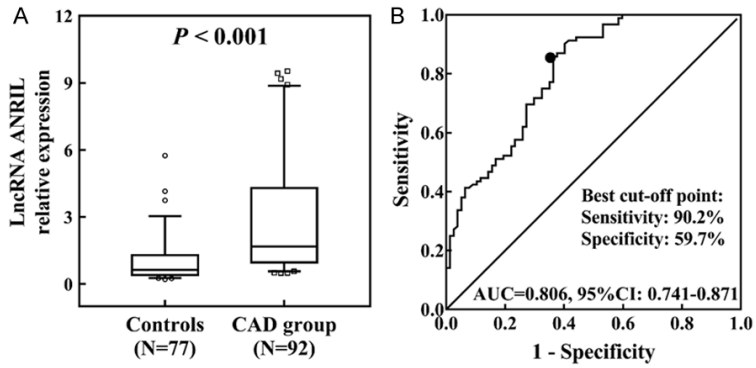

Figure 1. LncRNA ANRIL levels in two groups and the ROC curve. LncRNA ANRIL expression was increased in CAD group compared with control group (A). ROC curve disclosed that it well discriminated CAD patients from controls with an AUC of 0.806 (95% CI: 0.741-0.871), and the sensitivity and the specificity at the best cut-off point was 90.2% and 59.7%, respectively (B). Comparison between two groups was determined by Chi-square test. ROC curve was utilized to evaluate the diagnostic value of lncRNA ANRIL expression for CAD risk. *P* value < 0.05 was considered significant. lncRNA, long non-coding RNA; ANRIL, antisense non-coding RNA in the INK4 locus; CAD coronary artery disease; ROC, receiver operating characteristic curve; AUC, area under the curve.

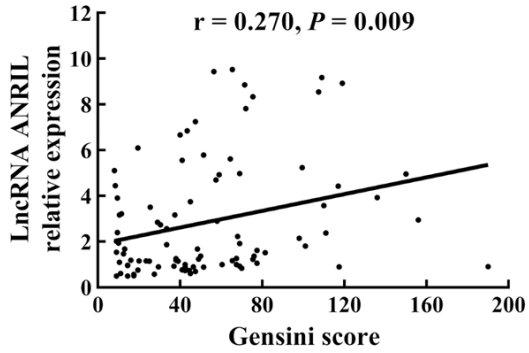

Figure 2. Correlation of lncRNA ANRIL expression with disease severity in CAD patients. LncRNA ANRIL level was positively correlated with Gensini score. Correlation analysis was performed using Spearman's rank correlation test. *P* value < 0.05 was considered significant. lncRNA, long non-coding RNA; ANRIL, antisense non-coding RNA in the INK4 locus; CAD coronary artery disease.

P=0.009), suggesting that lncRNA ANRIL expression was associated with increased severity of CAD (**Figure 2**). Besides, lncRNA ANRIL was also positively correlated with hs-CRP (r=0.293, *P*=0.005), TNF-α (r=0.271, *P*=0.009) and IL-6 (r=0.464, *P* < 0.001) while negatively associated with IL-10 (r=-0.274, *P*=0.008), implying that it was also correlated with elevated inflammation level of CAD (**Table 2**). As for ESR (r=0.198, *P*=0.059), IL-1β (r=0.099, *P*=0.346), IL-8 (r=0.185, *P*=0.078) or IL-17 (r=0.098, *P*=0.351), no correlation of lncRNA ANRIL level was observed with them.

Association of lncRNA ANRIL expression with OS of CAD patients

Among the 92 CAD patients, 14 patients were lost to follow up, hence a total of 78 CAD patients were recruited to survival analysis. Then the 78 CAD patients were divided into lncRNA ANRIL high expression group (n=39) and lncRNA ANRIL low expression group (n=39) based on the median level of lncRNA ANRIL (1.675). The median OS was 46.6 months (95% CI: 42.0-52.2 months) in lncRNA ANRIL high expression group, which was lower than that of 51.8 months (95% CI: 50.1-53.4 months) in lncRNA ANRIL low expression group (*P*=0.025), indicating that lncRNA ANRIL was associated with worse OS of CAD patients (**Figure 3**).

Discussion

In the current study we discovered that (1) lncRNA ANRIL expression was increased in CAD patients compared with controls and it well discriminated CAD patients from controls. (2) lncRNA ANRIL level was associated with increased disease severity and inflammation level as well as worse OS of CAD patients.

LncRNA ANRIL locates within the p15/CDKN2B-p16/CDKN2A-p14/ARF gene cluster, it can bind to polycomb repressive complex (PRC) 1 and PRC2, and then exert its epigenetic regulations [17, 18]. In a recent study, lncRNA ANRIL is overexpressed in atherosclerotic systemic lupus erythematosus (SLE) patients compared with non-atherosclerotic patients and it presents with good predicting value for atherosclerosis in SLE patients [19]. In another study, lncRNA ANRIL was also found to be upregulated in T2DM patients with CAD compared to T2DM patients without CAD [18]. ROC curve discloses that it might served as a novel biomarker for predicting CAD in T2DM patients [11]. In addition, CAD patients who have receiv-

Table 2. Correlation of LncRNA ANRIL relative expression with systematic inflammation markers and inflammatory cytokines

Items	LncRNA ANRIL relative expression	
	Correlation coefficient (r)	*P* value
hs-CRP	0.293	0.005
ESR	0.198	0.059
TNF-α	0.271	0.009
IL-1β	0.099	0.346
IL-6	0.464	< 0.001
IL-8	0.185	0.078
IL-10	-0.274	0.008
IL-17	0.098	0.351

Correlation was determined by spearman correlation analysis. *P* value < 0.05 was considered significant. hs-CRP: hypersensitive C-reactive protein; ESR: erythrocyte sedimentation rate; TNF: tumor necrosis factor; IL: interleukin.

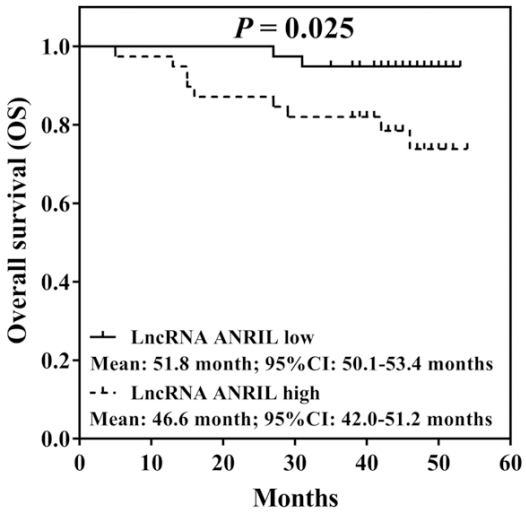

Figure 3. Correlation of lncRNA ANRIL level with OS of CAD patients. The median OS was 46.6 months (95% CI: 42.0-52.2 months) in lncRNA ANRIL high expression group, which was lower than that of 51.8 months (95% CI: 50.1-53.4 months) in lncRNA ANRIL low expression group. OS analysis was determined by Kaplan–Meier method and Log-rank test. *P* value < 0.05 was considered significant. lncRNA, long non-coding RNA; ANRIL, antisense non-coding RNA in the INK4 locus; CAD coronary artery disease; OS, overall survival.

ed DESs treatment are more likely to occur ISR in lncRNA ANRIL high expression patients than that in lncRNA ANRIL low expression patients, and lncRNA ANRIL high expression could be a risk factor for ISR [16]. These studies illustrate that lncRNA ANRIL might be involved in cardiovascular diseases especially CAD. However, whether lncRNA ANRIL expression associates with CAD risk is not known. In the present study, we discovered that lncRNA ANRIL expression was higher in CAD patients than in controls, and it clearly distinguished CAD patients from controls, suggesting that lncRNA ANRIL was correlated with increased CAD risk. Possible reasons for our results might be that: (1) lncRNA ANRIL binds to PRC1 and PRC2, then promotes myocardial infarction and increases CAD risk through epigenetic regulations [17, 18]. (2) lncRNA ANRIL might also upregulate inflammatory cytokine levels via sponging microRNAs (miRNAs) and then elevate myocardial infarction and inflammation injury, which further cause CAD [20].

Accumulating data have suggested that lncRNA ANRIL is correlated with increased disease severity and inflammation level of many diseases [15, 19, 20]. In atherosclerotic SLE patients, lncRNA ANRIL is positively associated with SLE duration, complement 3 level, SLE disease activity index and systemic lupus international collaborating clinics (SLICC) index, indicating that lncRNA ANRIL is correlated with increased disease severity and inflammation level of atherosclerotic SLE [19]. In patients with atherosclerosis, lncRNA ANRIL expression is positively associated with disease severity [15]. LncRNA ANRIL is also observed to be highly expressed in human coronary endothelial cells (HCAECs) and CAD mice models, more than that in human umbilical vein endothelial cells and control mice, respectively [20]. Besides, upregulating lncRNA ANRIL levels in HCAECs enhances IL-6, IL-8, TNF-α, inducible nitric oxide synthase, intercellular cell adhesion molecule 1, vascular cell adhesion molecule 1, vascular endothelial growth factor and heat shock protein 70 expressions [20]. More importantly, elevated lncRNA ANRIL expression in CAD patients associates with higher blood pressure, cholesterol, triacylglycerol and homocysteine levels [20]. Partly in accordance to these studies, our study showed that lncRNA ANRIL expression was positively correlated with Gensini score, hs-CRP, TNF-α, IL-6 and IL-10 levels as well as shorter OS, indicating that lncRNA ANRIL level was associated with increased severity, inflammation level and poorer prognosis. The possible explanation might be due to that: lncRNA ANRIL binds to PRC1 and PRC2 and then modulates inflammatory cytokine levels,

which further contribute to elevated inflammatory injury, disease severity and poorer OS [17, 18]. (2) lncRNA ANRIL might also act as a miRNA sponge (such as miR-181) thereby increasing inflammatory cytokine levels and disease severity, and causing a poor prognosis [20].

There were some limitations in this study. To begin with, some characteristics between CAD group and control group were different, including HDL-C level and Gensini score, which might cause selection bias. However, it was justified that HDL-C level was lower whereas Gensini score was higher in CAD group than that in control group. Secondly, the underlying roles of lncRNA ANRIL in CAD pathogenesis have not been explored in this study. Lastly, this was a small-sample study with only 92 CAD patients enrolled, thus future studies with larger sample size needed to be conducted.

In conclusion, circulating lncRNA ANRIL expression associates with increased disease risk, severity, inflammation level and poorer prognosis of CAD.

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Disclosure of conflict of interest

None.

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References

[1] GBD 2015 Mortality and Causes of Death Collaborators. Global, regional, and national life expectancy, all-cause mortality, and cause-specific mortality for 249 causes of death, 1980-2015: a systematic analysis for the global burden of disease study 2015. Lancet 2016; 388: 1459-1544.

[2] GBD 2015 Disease and Injury Incidence and Prevalence Collaborators. Global, regional, and national incidence, prevalence, and years lived with disability for 310 diseases and injuries, 1990-2015: a systematic analysis for the Global Burden of Disease Study 2015. Lancet 2016; 388: 1545-1602.

[3] Hanson MA, Fareed MT, Argenio SL, Agunwamba AO and Hanson TR. Coronary artery disease. Prim Care 2013; 40: 1-16.

[4] Roberts R. Genetics of coronary artery disease. Circ Res 2014; 114: 1890-1903.

[5] Roger VL, Go AS, Lloyd-Jones DM, Benjamin EJ, Berry JD, Borden WB, Bravata DM, Dai S, Ford ES, Fox CS, Fullerton HJ, Gillespie C, Hailpern SM, Heit JA, Howard VJ, Kissela BM, Kittner SJ, Lackland DT, Lichtman JH, Lisabeth LD, Makuc DM, Marcus GM, Marelli A, Matchar DB, Moy CS, Mozaffarian D, Mussolino ME, Nichol G, Paynter NP, Soliman EZ, Sorlie PD, Sotoodehnia N, Turan TN, Virani SS, Wong ND, Woo D, Turner MB; American Heart Association Statistics Committee and Stroke Statistics Subcommittee. Executive summary: heart disease and stroke statistics--2012 update: a report from the American heart association. Circulation 2012; 125: 188-197.

[6] Carninci P, Kasukawa T, Katayama S, Gough J, Frith MC, Maeda N, Oyama R, Ravasi T, Lenhard B, Wells C, Kodzius R, Shimokawa K, Bajic VB, Brenner SE, Batalov S, Forrest AR, Zavolan M, Davis MJ, Wilming LG, Aidinis V, Allen JE, Ambesi-Impiombato A, Apweiler R, Aturaliya RN, Bailey TL, Bansal M, Baxter L, Beisel KW, Bersano T, Bono H, Chalk AM, Chiu KP, Choudhary V, Christoffels A, Clutterbuck DR, Crowe ML, Dalla E, Dalrymple BP, de Bono B, Della Gatta G, di Bernardo D, Down T, Engstrom P, Fagiolini M, Faulkner G, Fletcher CF, Fukushima T, Furuno M, Futaki S, Gariboldi M, Georgii-Hemming P, Gingeras TR, Gojobori T, Green RE, Gustincich S, Harbers M, Hayashi Y, Hensch TK, Hirokawa N, Hill D, Huminiecki L, Iacono M, Ikeo K, Iwama A, Ishikawa T, Jakt M, Kanapin A, Katoh M, Kawasawa Y, Kelso J, Kitamura H, Kitano H, Kollias G, Krishnan SP, Kruger A, Kummerfeld SK, Kurochkin IV, Lareau LF, Lazarevic D, Lipovich L, Liu J, Liuni S, McWilliam S, Madan Babu M, Madera M, Marchionni L, Matsuda H, Matsuzawa S, Miki H, Mignone F, Miyake S, Morris K, Mottagui-Tabar S, Mulder N, Nakano N, Nakauchi H, Ng P, Nilsson R, Nishiguchi S, Nishikawa S, Nori F, Ohara O, Okazaki Y, Orlando V, Pang KC, Pavan WJ, Pavesi G, Pesole G, Petrovsky N, Piazza S, Reed J, Reid JF, Ring BZ, Ringwald M, Rost B, Ruan Y, Salzberg SL, Sandelin A, Schneider C, Schönbach C, Sekiguchi K, Semple CA, Seno S, Sessa L, Sheng Y, Shibata Y, Shimada H, Shimada K, Silva D, Sinclair B, Sperling S, Stupka E, Sugiura K, Sultana R, Takenaka Y, Taki K, Tammoja

K, Tan SL, Tang S, Taylor MS, Tegner J, Teichmann SA, Ueda HR, van Nimwegen E, Verardo R, Wei CL, Yagi K, Yamanishi H, Zabarovsky E, Zhu S, Zimmer A, Hide W, Bult C, Grimmond SM, Teasdale RD, Liu ET, Brusic V, Quackenbush J, Wahlestedt C, Mattick JS, Hume DA, Kai C, Sasaki D, Tomaru Y, Fukuda S, Kanamori-Katayama M, Suzuki M, Aoki J, Arakawa T, Iida J, Imamura K, Itoh M, Kato T, Kawaji H, Kawagashira N, Kawashima T, Kojima M, Kondo S, Konno H, Nakano K, Ninomiya N, Nishio T, Okada M, Plessy C, Shibata K, Shiraki T, Suzuki S, Tagami M, Waki K, Watahiki A, Okamura-Oho Y, Suzuki H, Kawai J, Hayashizaki Y; FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). The transcriptional landscape of the mammalian genome. Science 2005; 309: 1559-1563.

[7] Qian X, Zhao J, Yeung PY, Zhang QC and Kwok CK. Revealing lncRNA structures and interactions by sequencing-based approaches. Trends Biochem Sci 2019; 44: 33-52.

[8] Dhanoa JK, Sethi RS, Verma R, Arora JS and Mukhopadhyay CS. Long non-coding RNA: its evolutionary relics and biological implications in mammals: a review. J Anim Sci Technol 2018; 60: 25.

[9] Zampetaki A, Albrecht A and Steinhofel K. Long non-coding RNA structure and function: is there a link? Front Physiol 2018; 9: 1201.

[10] Zhang JJ, Wang DD, Du CX and Wang Y. Long noncoding RNA ANRIL promotes cervical cancer development by acting as a sponge of miR-186. Oncol Res 2018; 26: 345-352.

[11] Rahimi E, Ahmadi A, Boroumand MA, Mohammad Soltani B and Behmanesh M. Association of ANRIL expression with coronary artery disease in type 2 diabetic patients. Cell J 2018; 20: 41-45.

[12] Aarabi G, Zeller T, Heydecke G, Munz M, Schafer A and Seedorf U. Roles of the Chr.9p21.3 ANRIL locus in regulating inflammation and implications for anti-inflammatory drug target identification. Front Cardiovasc Med 2018; 5: 47.

[13] Holdt LM and Teupser D. From genotype to phenotype in human atherosclerosis--recent findings. Curr Opin Lipidol 2013; 24: 410-418.

[14] McPherson R, Pertsemlidis A, Kavaslar N, Stewart A, Roberts R, Cox DR, Hinds DA, Pennacchio LA, Tybjaerg-Hansen A, Folsom AR, Boerwinkle E, Hobbs HH and Cohen JC. A common allele on chromosome 9 associated with coronary heart disease. Science 2007; 316: 1488-1491.

[15] Holdt LM, Beutner F, Scholz M, Gielen S, Gabel G, Bergert H, Schuler G, Thiery J and Teupser D. ANRIL expression is associated with atherosclerosis risk at chromosome 9p21. Arterioscler Thromb Vasc Biol 2010; 30: 620-627.

[16] Wang F, Su X, Liu C, Wu M and Li B. Prognostic value of plasma long noncoding RNA ANRIL for in-stent restenosis. Med Sci Monit 2017; 23: 4733-4739.

[17] Yap KL, Li S, Muñoz-Cabello AM, Raguz S, Zeng L, Mujtaba S, Gil J, Walsh MJ, Zhou MM. Molecular interplay of the noncoding RNA ANRIL and methylated histone H3 lysine 27 by polycomb CBX7 in transcriptional silencing of INK4a. Mol Cell 2010; 38: 662-674.

[18] Kotake Y, Nakagawa T, Kitagawa K, Suzuki S, Liu N, Kitagawa M and Xiong Y. Long non-coding RNA ANRIL is required for the PRC2 recruitment to and silencing of p15(INK4B) tumor suppressor gene. Oncogene 2011; 30: 1956-1962.

[19] Abd-Elmawla MA, Fawzy MW, Rizk SM and Shaheen AA. Role of long non-coding RNAs expression (ANRIL, NOS3-AS, and APOA1-AS) in development of atherosclerosis in Egyptian systemic lupus erythematosus patients. Clin Rheumatol 2018; 37: 3319-3328.

[20] Guo F, Tang C, Li Y, Liu Y, Lv P, Wang W and Mu Y. The interplay of LncRNA ANRIL and miR-181b on the inflammation-relevant coronary artery disease through mediating NF-kappaB signalling pathway. J Cell Mol Med 2018; 22: 5062-5075.