

ASSOCIATION BETWEEN DYSLIPIDAEMIA AND MUTATIONS IN THE GENES *PCSK9*, *LDLR*

Agnese Zarina¹, Linda Piekuse¹, Madara Kreile¹, Dace Juhnevica²,
Karlis Trusinskis², Andrejs Erglis², Astrida Krumina³

¹ Rīga Stradiņš University, Scientific Laboratory of Molecular Genetics

² Pauls Stradiņš Clinical University Hospital, Latvian Cardiology Center

³ Latvian Biomedical Research and Study Centre

Riga, Latvia

For correspondence: zarina.agnese@gmail.com

INTRODUCTION

Coronary heart disease (CHD) is the main cause of death in developed countries. One of the main causes of CHD is atherosclerosis, in which pathogenesis dyslipidemia is a crucial factor. There are several genes involved in cholesterol metabolism, e.g. *PCSK9* and *LDLR*. Mutations and polymorphisms in these genes can be associated with hyper- or hypocholesterolemia, and can cause Familial hypercholesterolemia.

AIM

To determine the association of the polymorphism E670G in the gene *PCSK9* with dyslipidemia and to test patients with dyslipidemia for seven mutations in the gene *LDLR*.

MATERIAL

Group of patients: 38 patients with dyslipidemia (average age – 63.9±10.2 years, 21 males and 17 females).

Control's group: 66 healthy individuals (average age – 22±2.8 years, 10 males and 56 females).

RESULTS

Table 1. Frequency of *PCSK9* gene G allele in patients and control's group.

Gene	Mutation	MAF patients	MAF control group	P value	OR	95% CI
<i>PCSK9</i>	E670G	0.3947	0.1339	3.9 x 10 ⁻⁵	4.217	2.069–8.597

Statistically significant association with dyslipidemia was found with *PCSK9* gene E670G mutation – G allele was more common in patients, than in control's group.

Table 2. Mutation found in the gene *LDLR* in patients with dyslipidemia.

Mutations tested in gene <i>LDLR</i>						
D374Y	P664L	L458P	R329X	E207X	D200G	E80K
–	–	–	–	–	–	*

* – found in 2 patients with dyslipidemia in one allele

Mutation E80K in the gene *LDLR* was found in two individuals with dyslipidemia.

CONCLUSIONS

- Polymorphism E670G in the gene *PCSK9* is one of the genetic risk factors in development of dyslipidemia, but it is not associated with specific biochemical markers;
- Mutation E80K in the *LDLR* gene suggests that two patients have Familial hypercholesterolemia, but to make precise diagnosis, the mutations should be confirmed by other molecular method.

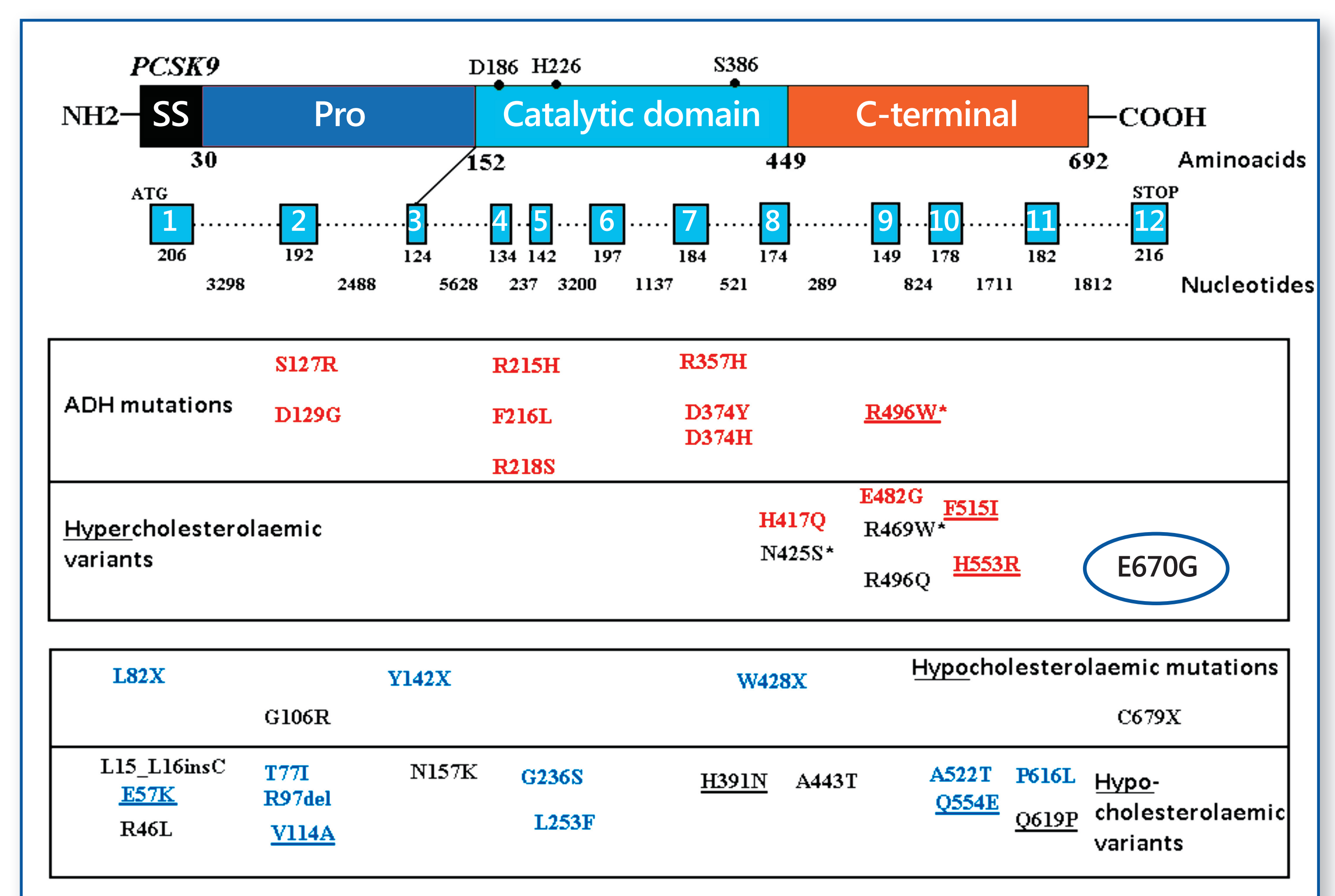


Figure 1. Schematic localisation of the mutations in the gene *PCSK9* (in coding regions) [adapted from Abifadel et al., 2009].

METHODS

Molecular methods:

- DNA extraction
- The E670G polymorphism was detected by RFLP analysis
- The mutations: D374Y, P664L, L458P, R329X, E207X, D200G, E80K in the gene *LDLR* were detected by ELUCIGENE FH20 (Tepnel Molecular Diagnostics).

Statistical analysis: PLINK and SPSS 16.0 were used.

Table 3.

Mutation E670G association with biochemical indices.

Gene	Mutation	Biochemical indices	BETA1	P value
<i>PCSK9</i>	E670G	Total cholesterol	0.7639	0.1246
		HDL	–0.2083	0.1703
		LDL	0.5556	0.1982
		TG	0.5598	0.1489
		APOB	5.457	0.6151
		APOA	5.408	0.6254
		ALAT	0.75	0.9384
		Glucose	–0.1548	0.7538
		ASAT	–1.833	0.6884

HDL – high density lipoprotein; LDL – low density lipoprotein; TG – triglyceride; APOB – apolipoprotein B, APOA – apolipoprotein A; ALAT – alanine transaminase; ASAT – aspartate transaminase.