Selectin E

**Alternative Names**
- SELE
- E-Selectin
- Endothelial Leukocyte Adhesion Molecule
- ELAM1
- ELAM

**Record Category**
- Gene locus

**WHO-ICD**
- N.B.: Classification not applicable to gene loci.

**Incidences per 100,000 Live Births**
- N/A to gene loci

**OMIM Number**
- 131210

**Mode of Inheritance**
- N/A

**Gene Map Locus**
- 1q24.2

**Description**
Selectin E is a surface glycoprotein expressed on endothelial cells upon activation by cytokines. This protein supports the rolling of leukocytes on activated endothelial cells, which is an important step for the successful recruitment of leukocytes and circulating monocytes into tissues. Like other members of the selectin family, Selectin E plays an important role in inflammation and in the adhesion of metastatic cancer cells to the endothelium. Double-knockout mouse experiments suggest that E-selectin plays an essential role in both early and advanced stages of atherosclerotic lesion development and that mutations in this gene may act as a genetic risk factor for coronary atherosclerosis.

**Molecular Genetics**
The SELE gene is located on the long arm of chromosome 1, at 1q22-q25, where it spans a length of close to 17 Kb with its 14 exons and 13 introns. The selectin proteins are transmembrane proteins having three extracellular domains; an amino-terminal lectin domain, an epidermal growth factor domain, and short consensus repeat units that contain six conserved cysteine residues.

Several polymorphisms have been discovered in the SELE, the most important being the A561C (rs5361) and the G98T (rs1805193) polymorphisms. The former is a single base A to C transition polymorphism in exon 4, which results in an amino acid substitution serine to arginine at position 128 (p.S128R) of the EGF-domain of the SELE protein. This polymorphism is associated with an increase in the ligand-binding function of the protein, while at the same time leading to a loss in ligand specificity, thereby increasing leukocyte recruitment. The second polymorphism is a G to T transition in the untranslated region of the gene and has been speculated to influence the expression of SELE.

In a study aimed at the investigation of the association of endothelial cell adhesion molecule Selectin E polymorphisms and their role in the pathogenesis of atherosclerosis, Motawi et al. (2012) studied 285 individuals, classified into four groups: 63 cerebrovascular atherosclerotic patients, 75 cardiovascular patients, 72 peripheral atherosclerotic patients and 75 normal healthy individuals. The frequency of the mutant AC genotype of Selectin E in peripheral, cerebral and cardiovascular atherosclerotic patients and 75 normal healthy individuals. The frequency of the mutant AC genotype of Selectin E in peripheral, cerebral and cardiovascular atherosclerotic patients was significantly higher than in control subjects (29%, 29% and 28% vs. 8%, respectively). However, no significant difference was observed in the frequency of mutant CC allele between all atherosclerotic patients and control groups.

Similarly, Issac et al. (2014) investigated the possible association between SELE rs5355C>T gene polymorphism and the presence of carotid atherosclerosis in ESRD patients. They recruited 70 subjects into this study: 40 ESRD patients [age
(mean ± SD) 43.42 ± 13.94 years] and 30 age- and
gender-matched healthy individuals assigned to the
control group. Issac et al. (2014) found no
significant relationship between the SELE
rs5355C>T gene polymorphism and the incidence
of ESRD. Serum PAPP-A showed a statistically
significant increase in SELE rs5355TT versus CC
in both patients and controls. There was no
association on comparing right intima-media
thickness (IMT), left IMT, right cross-sectional area
(CSA) and left CSA with the CC, CT and TT
genotypes of SELE rs5355C>T. There was a
statistically significant increase in DBP in TT
genotype carriers when compared with CC
genotype carriers (p = 0.009). There was a
statistically significant decrease in high-density
lipoprotein cholesterol (HDL-C) in TT genotype
carriers when compared with CT genotype carriers
in the whole study group (p = 0.003). Issac et al.
(2014) reasoned that the lack of a direct association
between SELE rs5355C>T gene polymorphism,
serum PAPP-A level and IMT suggests that their
hypothesized association with carotid
atherosclerosis might reflect an indirect mechanism
of SELE rs5355C>T gene polymorphism and serum
PAPP-A with cardiovascular risk factors such as
blood pressure and HDL-C rather than a direct
effect on the vasculature.

Saudi Arabia
Abu-Amero et al. (2007) studied the possible
interactive effect of the E-selectin p.S128R
polymorphism and Type 2 Diabetes Mellitus
(DM2) as a risk for acquiring Coronary Artery
Disease (CAD) in the Saudi population. The study
population consisted of 1112 Saudi patients (767
males, 345 females) with CAD and 427 Saudi
individuals (238 males, 189 females) with valvular
disease or chest pain, but without any significant
coronary stenosis. PCR-RFLP using PstI was used to
determine the presence of the SELE p.S128R
polymorphism. The results showed that in the
absence of DM2, the presence of the R allele did
not have a significant effect on the development of
CAD. However, the likelihood of acquiring CAD
was significant in the presence of DM2 and the S
allele. Additionally, the odds of CAD increased
from 5.44 to 6.11 in the presence of the R allele and
DM2, pointing to an augmentation of the effect of
DM2 by the presence of the R allele on the
individual’s susceptibility to CAD. Multiple
logistic regression analysis with other confounding
variables such as cholesterol, triglyceride, gender,
age, hypertension, family history and smoking gave
very similar results to the univariate analysis. Abu-
Amero et al. (2007) concluded that although the
mutant p.S128R polymorphism alone is not
associated with CAD, its presence significantly
contributes to the potency of DM2 as a risk factor
for acquiring the disease.

References
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Related CTGA Records
N/A

External Links
http://bme.virginia.edu/ley/e-selectin.html

Contributors
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