

# Meta-Analyses of Epigenetics Risk Factors for Heart Disease Prevention: **NOS3 HUMAN GENE VARIATIONS ACROSS DIFFERENT RACE-ETHNICITY GROUPS**

Nien-Tzu Chang, PhD, RN, National Taiwan University

Pamela Shiao, PhD, RN, FAAN, Azusa Pacific University

F. DelaCruz, MSN, DNP Student, Azusa Pacific University



## 25th International Nursing Research Congress Faculty Disclosure

<i>Faculty Name</i>	Nien-Tzu Chang, PhD, RN
<i>Conflicts of interest:</i>	None
<i>Employer:</i>	National Taiwan University
<i>Sponsorship / Commercial support</i>	None

<i>Faculty Name</i>	Pamela Shiao, PhD, RN, FAAN
<i>Conflicts of interest:</i>	None
<i>Employer:</i>	Azusa Pacific University
<i>Sponsorship / Commercial support</i>	None

<i>Faculty Name</i>	F. Delacruz, MSN, DNP Student
<i>Conflicts of interest:</i>	None
<i>Employer:</i>	Azusa Pacific University
<i>Sponsorship / Commercial support</i>	None

# Introduction



- Ischemic heart disease (IHD) is the major leading cause of death worldwide.
- Endothelial NOS3 gene mutation variations increase risks of IHD in various populations.
- NOS3 affects metabolism cycle, critical for preventing systematic inflammation as an epigenetics risk factor for heart health.

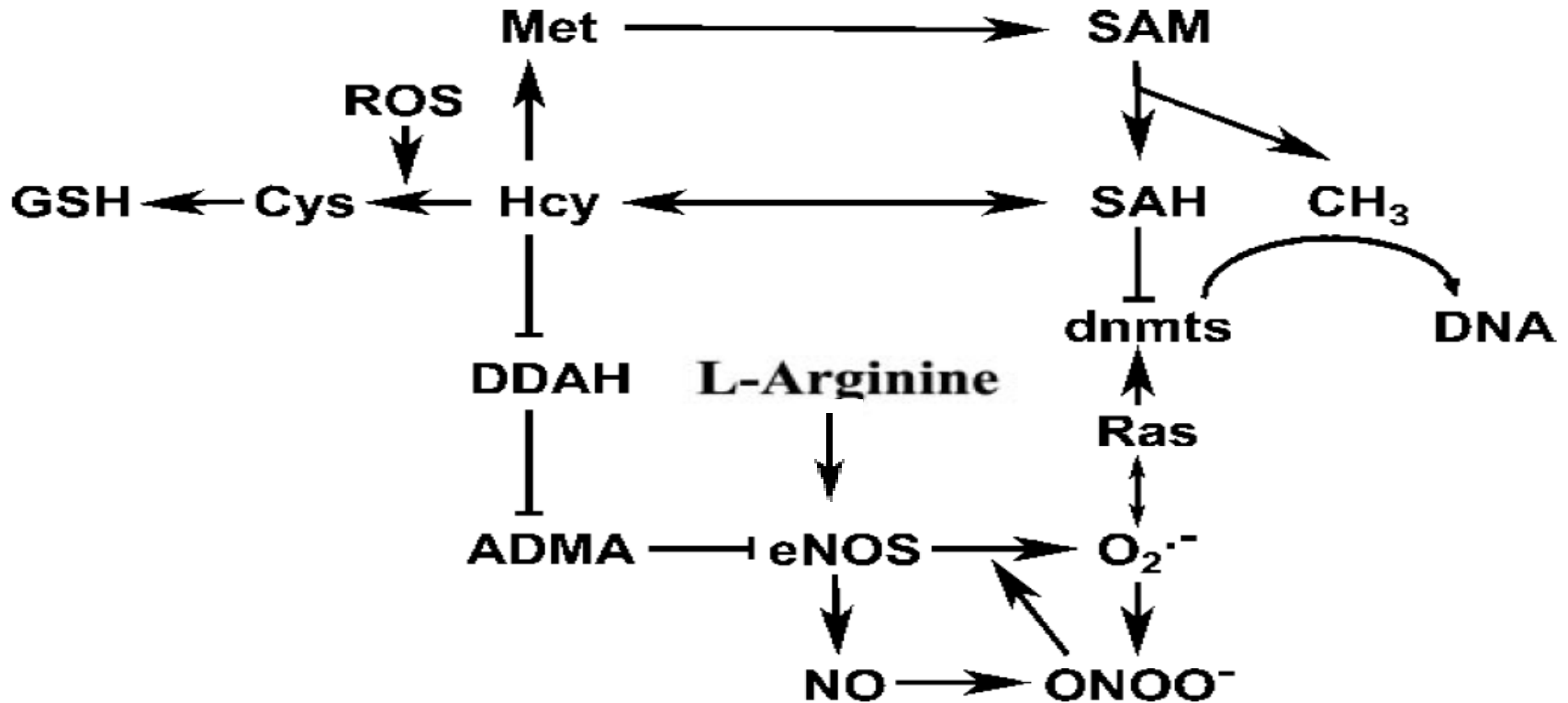
# Purpose

- The purpose of this meta-analysis is:
  - ▣ To identify the association of **NOS3 894G>T** **gene** variations with IHD in various populations
  - ▣ To identify the related lifestyle risk factors for IHD prevention.

# NOS3

- Nitric oxide: endothelium adhesion, platelet aggregation and vascular smooth muscle cell proliferation.
- Nitric oxide synthases: neuronal NOS1, inducible NOS2 and endothelial NOS3 (eNOS).
- G894T SNP in the promoter region of the NOS3: endothelial dysfunction, early event in IHD.

# DNA methylation pathway, NOS



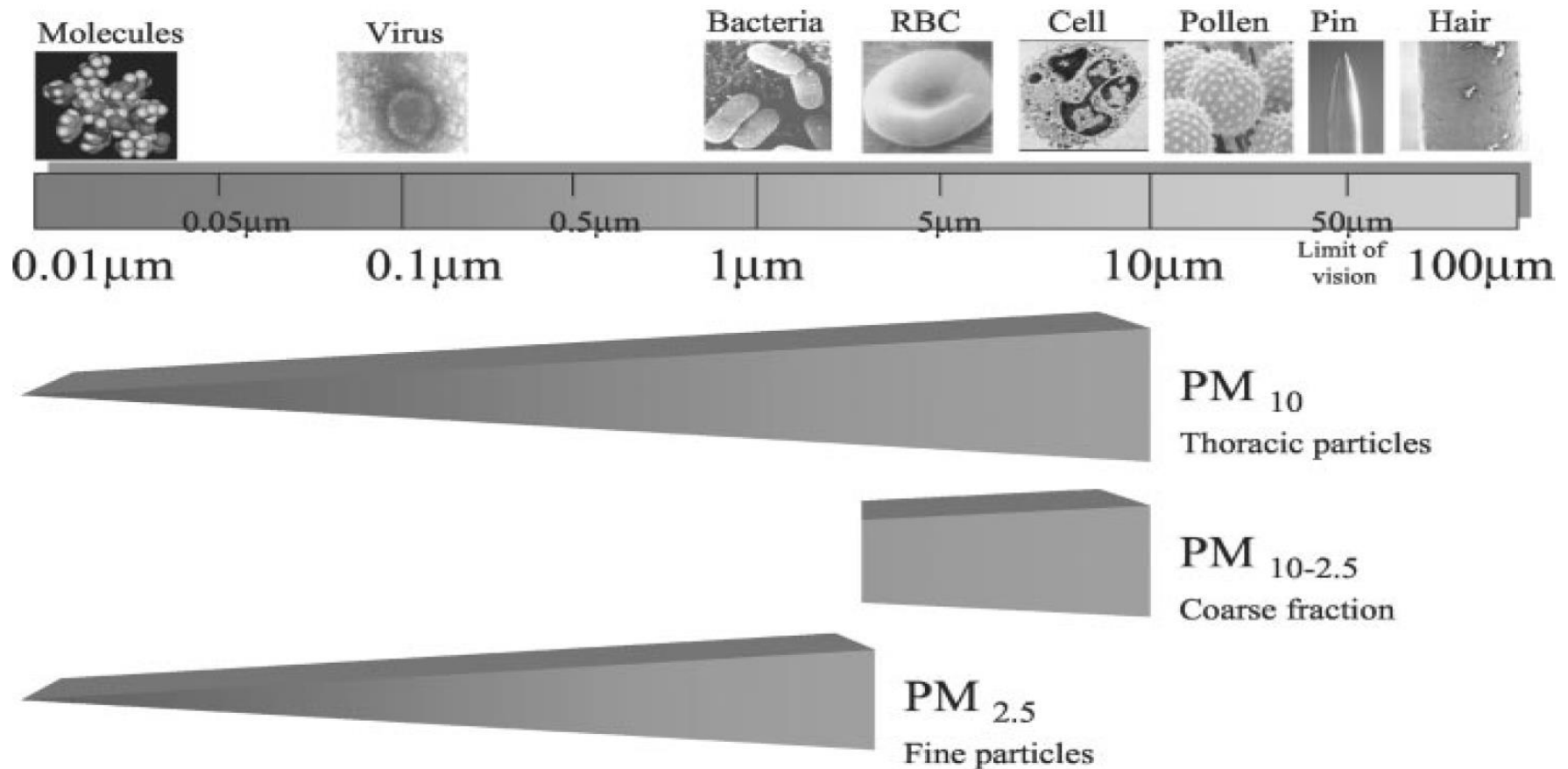
Adapted from Campos et al. [2007]

*Neoplasia* 2007;9:1118

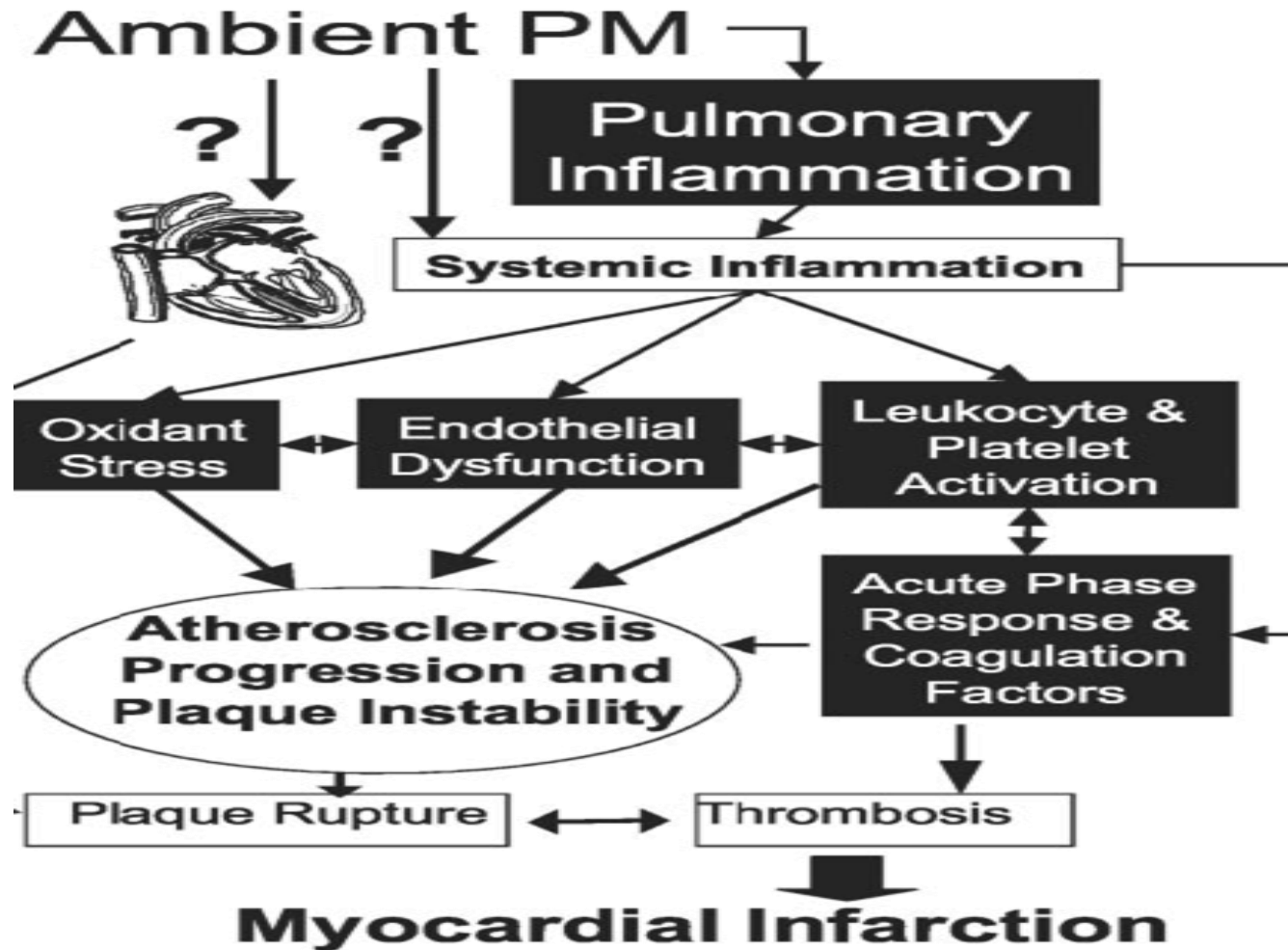
*Circulation* 2004;109:1813

<http://www.heartfixer.com/AMRI-Nutrigenomics.htm>

# Environment, Particulate matter, & IHD



# Biological mechanisms linking PMx & IHD



Adapted from Brook et al. [2004]



# NOS3, IHD, and Lifestyle

- In humans, variations of the NOS3 gene have been found to be increasing the risk of IHD across country groups and subsequently.
- Life style risk factors: smoking, air pollution, nutritional intake were associated with increased risks for IHD.

# Publication search and inclusion criteria

- Key words: NOS3, G894T, CAD, IHD, case control, meta-analysis = 229 articles
- Studies Excluded for
  - ▣ not case-control (n=11)
  - ▣ not IHD (n=106)
  - ▣ no NOS3 894G>T gene count (n=34).
  - ▣ Duplicate (n=29)
- Studies Included = 49

# Preliminary Analyses

- 49 studies, 13,830 cases and 10,595 controls.
- Gene mutation variations (GT and TT subtypes) - Caucasians (47.5-64.8%), Africans (42.9-55.9%), Eurasians (33.9-45.1%), and Asians (13.5-30.7%) for control and case groups.
- Inter-rater evaluations- search progression, quality scores, data coding were completed to ensure data accuracy for pooled meta-analyses.

# Relative risk: NOS G894T (49 studies)

NOS3 G894T	IHD Cases (%)	Controls (%)	RR (95% CI)	p-value
GG	7260 (52.5)	6288 (59.3)	0.92 (0.89-0.96)	p<0.001
GT	5135 (37.1)	3390 (32.0)	1.11 (1.04-1.18)	p=0.002
TT	1435 (10.4)	892 (8.4)	1.32 (1.13-1.56)	p<0.001

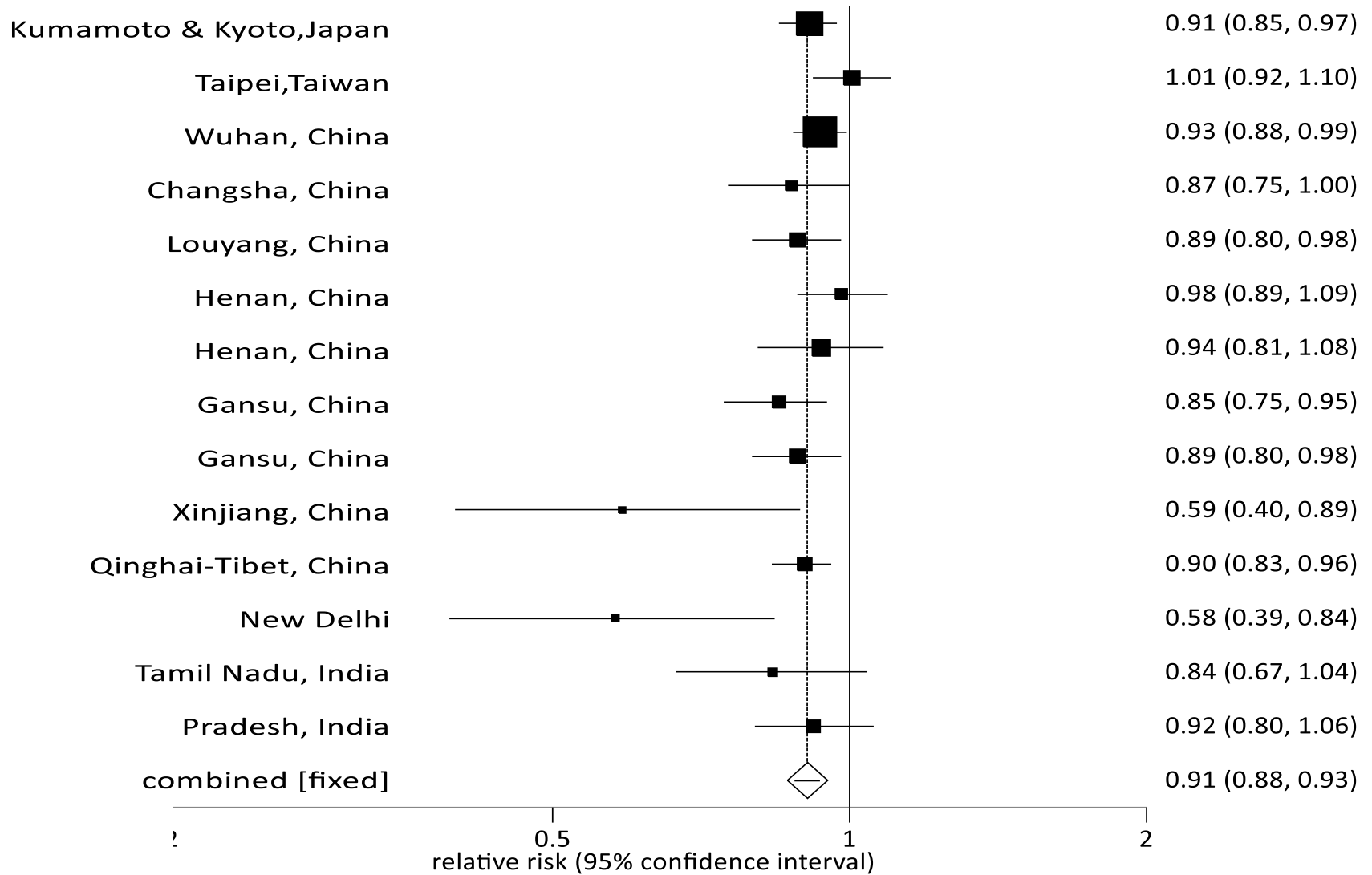
# Relative risk: Eurasian population (9 studies)

NOS3 G894T	IHD Cases n (%)	Controls n (%)	RR (95% CI)	p-value
GG	860 (49.5)	805 (56.7)	0.85 (0.76-0.96)	p=0.068
GT	668 (38.5)	513 (36.2)	1.07 (0.97-1.17)	p=0.155
TT	208 (12.0)	101 (7.1)	1.82 (1.18-2.80)	p=0.007

# Relative risk - Asian & Caucasian population

G894T (n, studies)	IHD Cases n (%)	Controls n (%)	RR (95% CI) * P < 0.05
GG Caucasian (16)	3268 (44.0)	1842 (43.5)	<b>0.97</b> (0.93-1.014)
<b>GG Asian</b> (22)	2626 (88.7)	3277 (83.6)	<b>0.91*</b> (0.88-0.93)
GT Caucasian (16)	3160 (32.3)	1785 (42.2)	<b>0.97</b> (0.92-1.01)
<b>GT Asian</b> (22)	818 (27.6)	603 (15.4)	<b>1.39**</b> (1.26-1.52)
TT Caucasian (16)	997 (13.4)	607 (14.3)	<b>1.18</b> (0.96-1.45)
<b>TT Asian</b> (22)	102 ( 3.4)	42 (1.1)	<b>1.82**</b> (0.38-0.98)

# NOS3 GG Asian

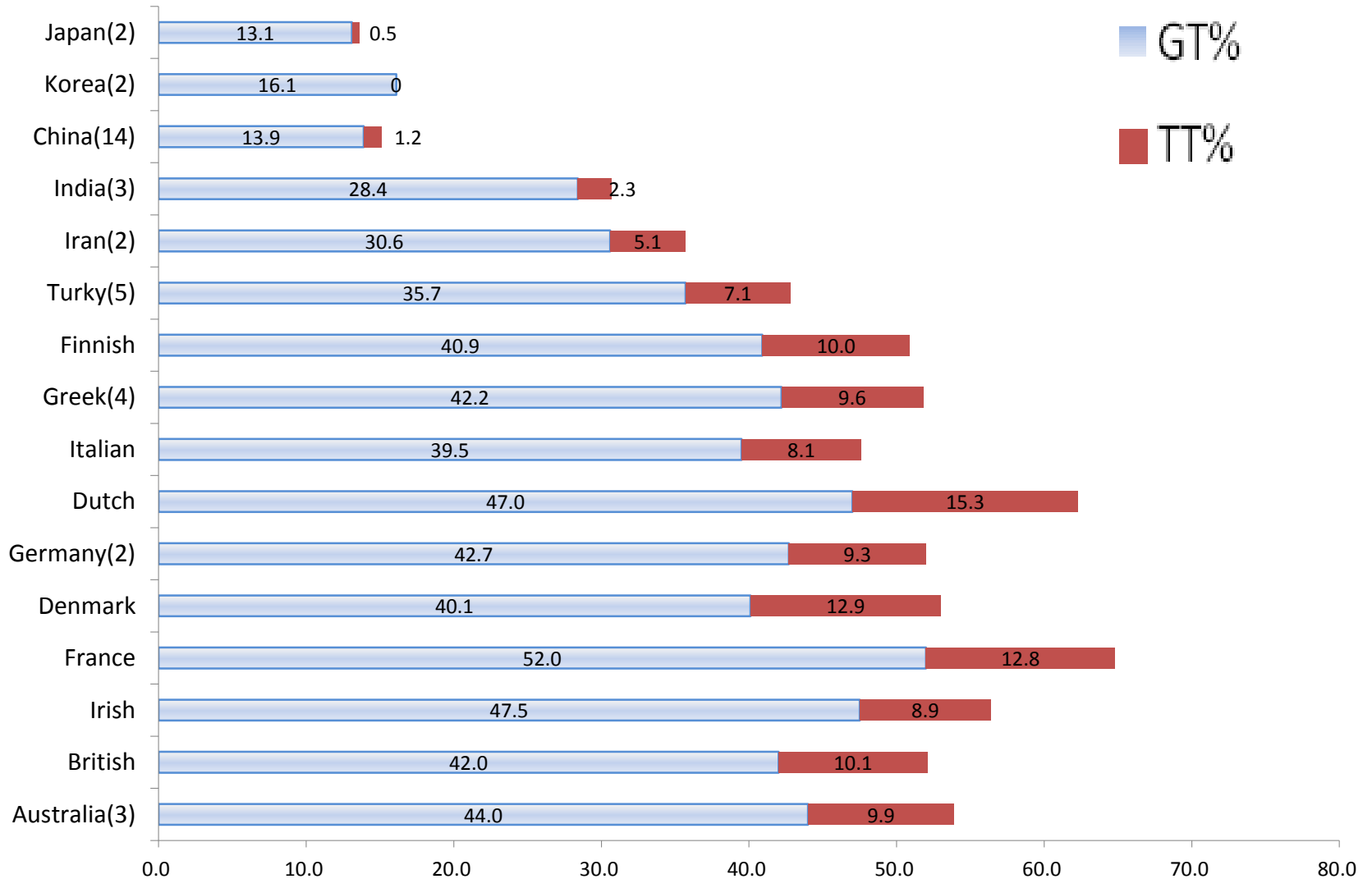


# Lifestyle Analyses

Lifestyle	Cases	Control	RR (95% CI)	P-value
Smoking (24)	4118 (59.8)	3212 (56.5)	1.68 (1.39 to 2.04)	p<0.0001
DM (19)	1706 (24.2)	414 ( 8.9)	3.16 (2.40 to 4.17)	p<0.0001
Hyper- lipidemia (8)	1551 (51.3)	505 (21.9)	2.92 (1.97 to 4.33)	p<0.0001



# Gene mutation (GT+TT) variations, control group





Human (GRCh37) ▾

Location: 7:150,695,611-150,696,611

Variation: rs1799983

- Variation displays**
- └ Explore this variation
  - └ Genomic context
    - └ Genes and regulation (5)
    - └ Flanking sequence
  - Population genetics**
  - └ Individual genotypes (1785)
  - └ Linkage disequilibrium
  - └ Phenotype Data (7)
  - └ Phylogenetic Context (6)
  - └ Citations (145)
  - └ External Data
    - └ LOVD

⚙ Configure this page

📄 Add your data

📄 Export data

🔖 Bookmark this page

🔗 Share this page

📄 Download view as CSV

## rs1799983 SNP

**Original source**

Variants (including SNPs and indels) imported from dbSNP (release 138) | [View in dbSNP](#)

**Alleles**

T/G | Ambiguity code: **K** | MAF: **0.20** (T)

**Location**

Chromosome **7:150696111** (forward strand) | [View in location tab](#)

**Co-located**

with **HGMD-PUBLIC** [CM981388](#)

**Most severe consequence**

**Missense variant** | [See all predicted consequences \[Genes and regulation\]](#)

**Evidence status** ⓘ



**Clinical significance** ⓘ



**Synonyms** ⊕

This variation has **10** synonyms - click the plus to show

**HGVS names** ⊕

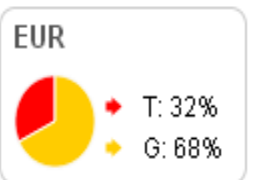
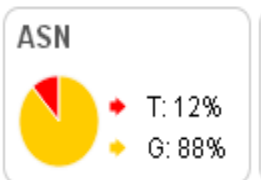
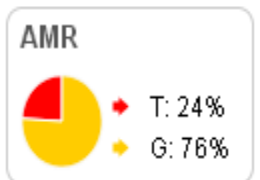
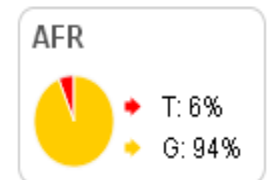
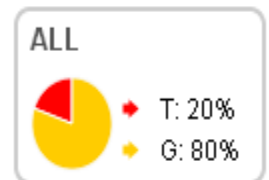
This variation has **9** HGVS names - click the plus to show

**Genotyping chips** ⊕

This variation has assays on **4** chips - click the plus to show

## Population genetics ⓘ

### 1000 Genomes allele frequencies



Sub-populations ⊕ Sub-populations ⊕ Sub-populations ⊕ Sub-populations ⊕

1000 Genomes (19) ⊕

## AMR sub-populations

CLM



MXL



PUR



## ASN sub-populations

CHB



CHS



JPT



## EUR sub-populations

CEU



FIN



GBR



IBS



# Conclusion and Discussion

- NOS3 GG (wild type) is protective from IHD; GT and TT gene variations are associated with increased IHD risk; Subgroups: Eurasian and Asians significant.
- Smoking, DM and hyperlipidemia increased IHD risk.
- Future studies: epigenetic factors for population health, gene variations in the prevention of IHD.

***THANK YOU FOR YOUR ATTENTION***