



Patrycja Dąca-Roszak, PhD

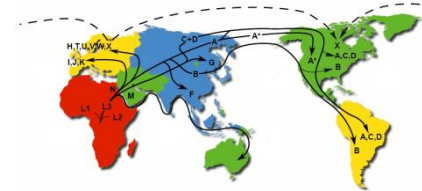
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Who am I?

I live in Poznań (Poland);

I am a Postdoc at the Division of Molecular and Clinical Genetics in the Institute of Human Genetics PAN in Poznań

My research interests: Human population genetics in the context of forensic science



AriaDNAproject

The aim of the study: identification of new genetic markers for Human population identification for forensic science purpose (terrorist attacks, „old samples“, cell mixtures)

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graph TD; A[POPULATION IDENTIFICATION] --> B[GENOME]; A --> C[TRANSCRIPTOME]; A --> D[EPIGENOME];
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POPULATION IDENTIFICATION

GENOME

- SNP;

TRANSCRIPTOME

- Gene expression differences

EPIGENOME

- CpG loci (DNA methylation profiling)

AriaDNAproject

Material:

DNA and RNA isolated from **B-lymphocyte cell lines** from Europeans (CEU) and Chinese (CHB) populations (Coriell Cell Repositories);

Methods:

- highthroughput methods: Illumina microarrays: SNP microarrays, mRNA microarrays and methylome microarrays (data analysed by bioinformatics)
- microarray data validation: TaqMan Array Mico Fluidic Cards (TLDA)- measurement of gene expression; SBE reaction (SNP-population test), pirosequencing and bioinformatic data validation coming from Illumia 450BeadChip.

SNP markers

SNaPshot minisequencing population test

Illumina Human SNP microarray



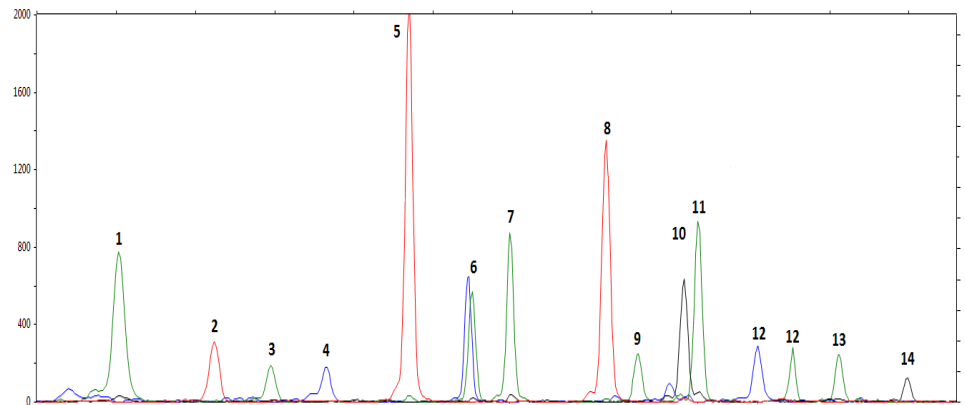
300 SNP classifier



14 the best non-pigmentation SNPs
& gender SNP (amelogenin)



EurEAs_Gplex -SNaPshot assay for
continental population discrimination
and gender identification



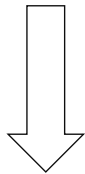
Daca-Roszak P. et al. FSI Genetics 2016

DNA methylation studies

Illumina Human Methylation
450

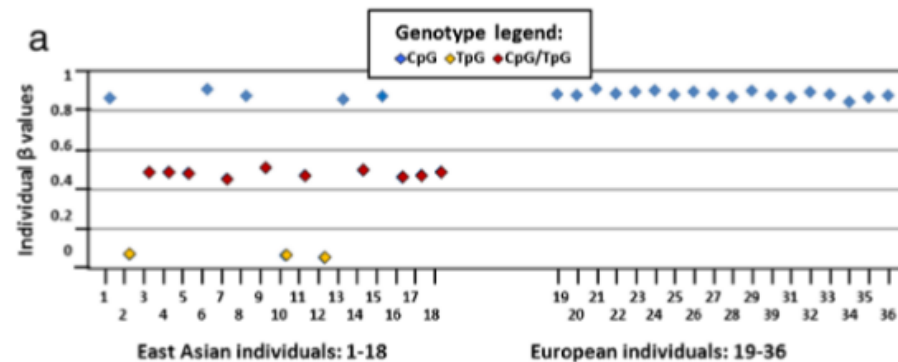
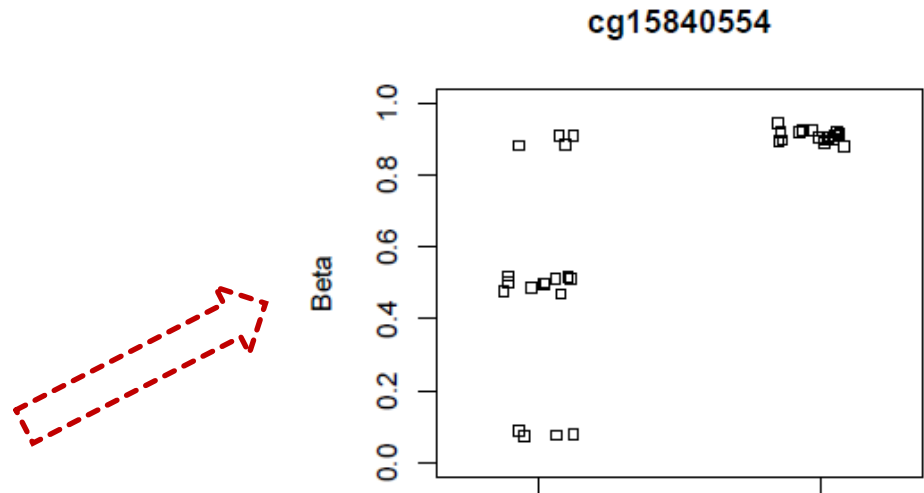


96 CpG pop-diff loci



in silico & laboratory validation

14 CpG pop-specific markers



mRNA markers?

Illumina Human RNA microarray



200 mRNA potential population markers



13 mRNA with statistically significant differences in expression level between CEU/CHB (B-lymphocytes cell-lines)



A subset of 5 transcripts were able to separate a mixture of cell lines according to their ethnic origin