# Exogenous shock, genetic diversity and social change:
# The case of alcohol and European colonization

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# *Introduction*

- Broad theoretical framework: Non-social factors and social change

- Natural disasters, geography and climate, genes

- Not 'primordialism', but additive effect to social factors

- May genetic diversity affect social change?

# *Theoretical framework*

- Biological and cultural/social evolution
- These processes are not mutually exclusive; there is interdependence between these cycles (Dobzhansky, 1973).
- Genes affect individual level
- How genetic diversity affects societal level?
- Relations between genetic diversity and social change are complicated. It is not one-direction effect: it is mutual co-evolutionary cycle

# Exogenous shock, genes and social change

- Although some studies associate certain genes with prosocial behavior, it is hardly to say that any genetic polymorphisms are responsible for social change, at least directly. There are no 'democracy' or 'authoritarianism' genes, as well as 'capitalism' genes.
- Is it possible to find link between genetic diversity and social change?
- The proposed mechanism is an **exogenous shock**
- Exogenous shock may increase the significance of genotype differences among populations, and genetic diversity may become an important factor of social and political change

# *Exogenous shock, genes and social change*

Fig.1. Exogenous shock, genes and social change
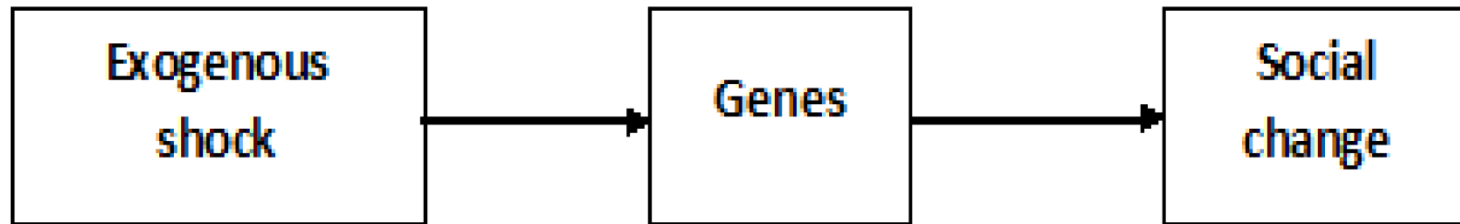
# *Exogenous shock, genes and social change*

- Shocks bring new challenges and threats to populations. These challenges may require biological and cultural adaption as a response to new conditions. Biological and genetic change is very slow. Inability of genotype to adapt too fast may lead to social change. The gap between biological and social adaptation may cause social change.

- Koenen et al. (2009) : genetic factors – 5-HTTLPR serotonin transporter – were among important predictors of posttraumatic stress disorder (PTSD) after the 2004 Florida hurricane. **NB!** Low-risk environments (low crime rates and low unemployment rates) decreased risk of PSTD, but high-risk environments increased risk of PSTD.

# Exogenous shock, genes and social change

- The lack of immunity among Native Americans to germs brought by Europeans, was a crucial factor of the colonization success (Diamond, 1997). Native Americans could not adapt so fast – and lost their lives, lands and sovereignty.

- **The 'slavery hypothesis'**. The higher rates of hypertension among African Americans might be explained by conditions on slavery ships which transported slaves through the Atlantics. High mortality rates – due to salt and water deprivation, diarrhea, dehydrating seasickness and sweating - led to selection of individuals with an enhanced genetic-based ability to conserve salt. It became a distinct survival advantage over others (Wilson and Grim, 1991). The more efficient use of salt caused problems for their descendants in the future under conditions of salt-rich diet.

# Alcohol dependence and European colonization

- Case-study - the use of strong alcohol as factor of European colonization in America, Africa and Eurasia
- The start of European colonization can be dated at the end of the 15th century
- Re-invention of distillation and mass spread of strong alcohol beverages in Europe may be dated by the 14-15th century. It coincides with the start of European colonization
- Numerous historical evidences from America, Asia, and Africa indicate that native populations suffered not only from 'guns, steel and germs' (Diamond, 1997), but liquor as well.
- Alcohol abuse and alcohol dependence among native populations in America, Africa and Eurasia
- Loss of lands and independence by many native populations
- Alcohol was surely not the only factor of European colonization – as well as technological superiority, more advanced social organization, immunity to infectious deceases etc., but we argue that it was among significant factors
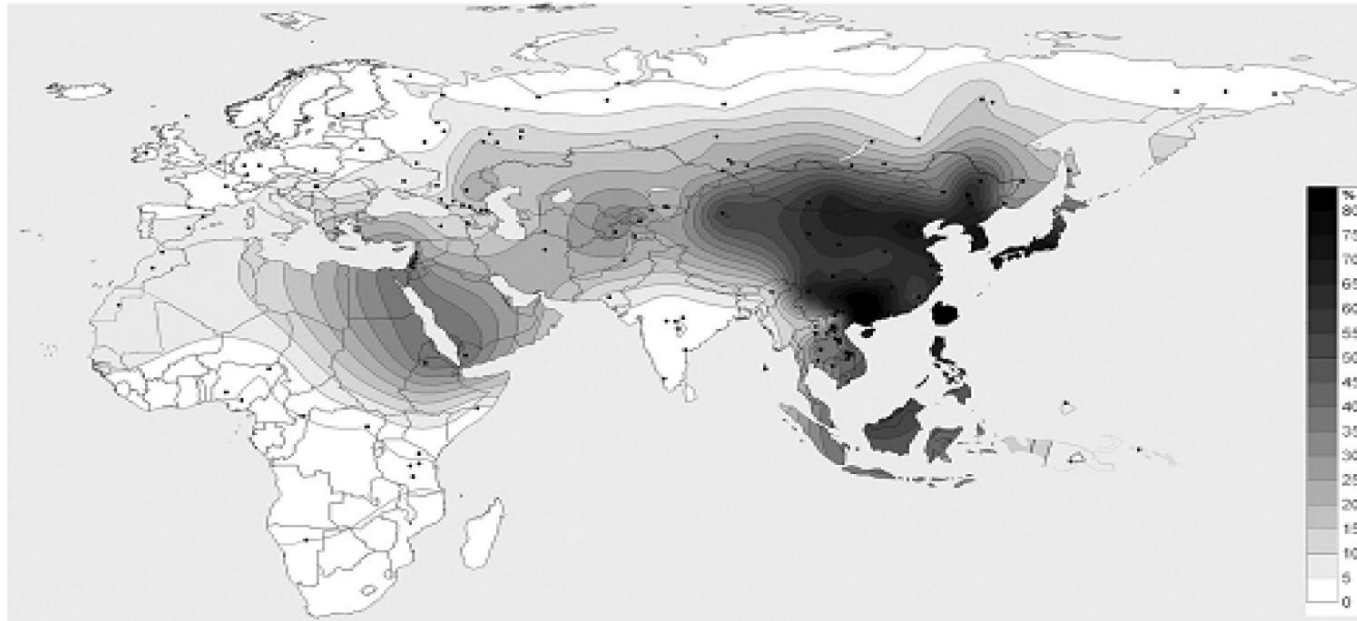
# Alcohol dependence and European colonization

- If invention of distillation is a product of social evolution, alcohol consumption is an outcome of biological evolution.

- The process of alcohol metabolism is associated with certain genetic polymorphisms.

- Alcohol is first oxidized by alcohol dehydrogenase (ADH) to acetaldehyde, which is then oxidized to acetate by acetaldehyde dehydroganase (ALDH). Enzymes encoded by two gene families, alcohol dehydrogenase (ADH) and aldehyde dehydrogenase (ALDH), mediate alcohol metabolism in humans.

- Allelic variants have been identified that alter metabolic rates and influence risk for alcoholism.

- Specifically, **ADH1B*48His** and ALDH2-2 have been shown to confer protection against alcoholism, presumably through accumulation of acetaldehyde in the blood, what results *"flushing syndrome"* – elevated blood flow, dizziness, accelerated heart rate, sweating and nausea

- This allele is significantly frequent among some Asian and Jewish populations.

# Table1. Some ADH1B*Arg48Hys frequencies from the ALFRED database

| Population | ADH1B*Arg48Hys frequency |
|---|---|
| Moroccans (Africa) | 0,080 |
| Abkhaz (Europe) | 0,190 |
| Russians (Europe) | 0,059 |
| Uzbek (Asia) | 0,286 |
| Ewenki (Asia) | 0,090 |
| Han (Asia) | 0,775 |
| Japanese (Asia) | 0,780 |
| Koreans (Asia) | 0,777 |
| Maori (Oceania) | 0,450 |
| Papuan New Guinea (Oceania) | 0,069 |
| Chukchi (Asia) | 0,020 |
| Cheyenne (N.America) | 0 |
| Otomi (N.America) | 0,068 |
| Southwestern Amerindians (N.America) | 0 |
| Maya, Yucatan (N.America) | 0,060 |

# ADH1B*Arg48Hys allele frequency map
## (Source: Borinskaya et al., 2009)

# Alcohol dependence and European colonization

- Relatively low frequencies are detected among European, North African, and some Middle Eastern populations (Mulligan et al., 2003; Borinskaya et al., 2009; Borinskaya et al., 2011).

- Among African populations relatively frequent is allele **ADH1B*370Cys** with similar effect (Borinskaya et al., 2011).

- The higher frequency – the more protective effect (people consume less alcohol)
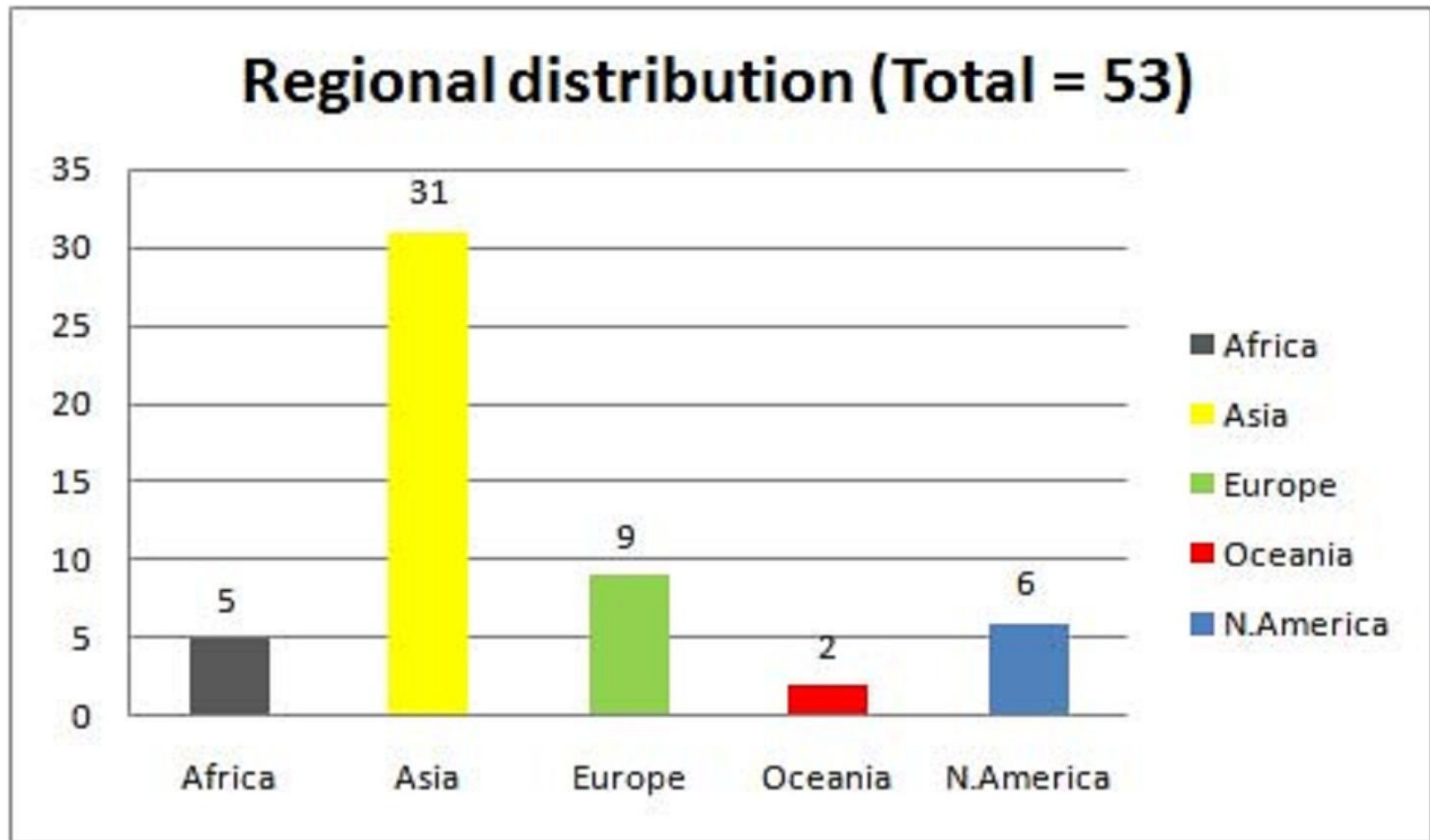
# *Hypothesis*

- We argue that there is a correlation between probability of being colonized by Europeans and allele frequencies responsible for metabolism of alcohol.

- *Hypothesis*: the risk of colonization by European powers is higher for indigenous populations which had genotype with lower allele frequencies that could 'protect' them against alcohol abuse.

- *Social organization hypothesis*. Alcoholism was a major social issue in many European countries.  However, the advanced level of social organization is the response: European populations had states, which were ruled by governments (=policies). Europeans had an instrument for social adaptation, but non-European populations with only tribal social organization did not.

- **Alcohol + social organization = alcoholism**
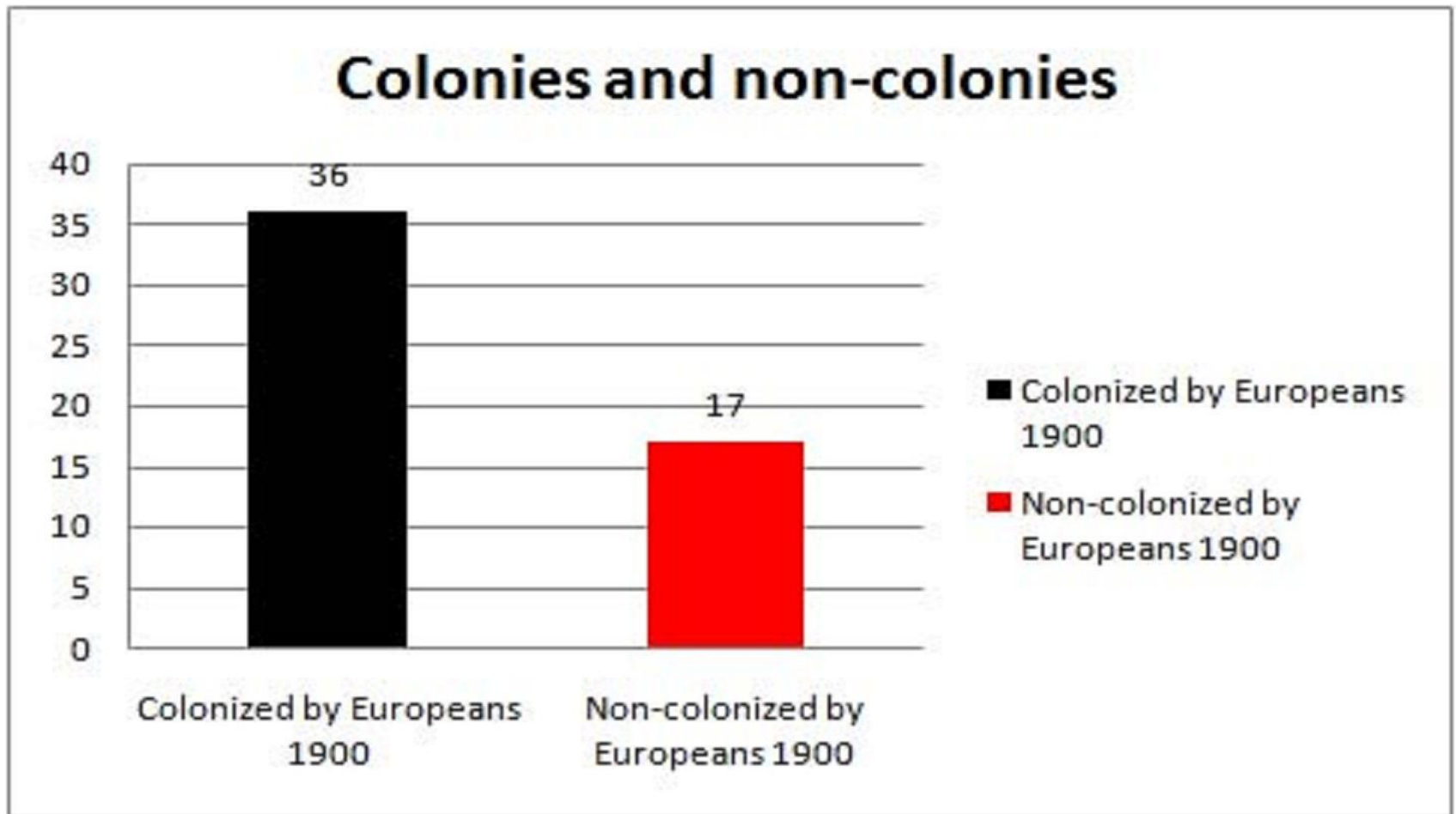
- It is a gene-environment effect

# Variables

- Dependent variable is **colonization1900** (by Europeans since the 16th century to the year 1900).

- The unit of analysis is *population*. The list of populations coincides with list of frequencies of ADH1B*Arg48Hys polymorphism, mostly from the ALFRED database.

- "1" – is for colonization by Europeans," 0" – for independence or non-European colonization

- The areas covered are Europe, Asia, Africa, Americas and Australia.

- 53 cases in our sample

# DV – "Colonization 1900"



## Regional distribution (Total = 53)

| Region | Value |
|--------|-------|
| Africa | 5 |
| Asia | 31 |
| Europe | 9 |
| Oceania | 2 |
| N.America | 6 |

# DV - "Colonization 1900"

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## Colonies by great powers

| | Russia | Great Britain | Spain | Others |
|---|---|---|---|---|
| Value | 19 | 8 | 6 | 20 |

Legend:
- Russia
- Great Britain
- Spain
- Others
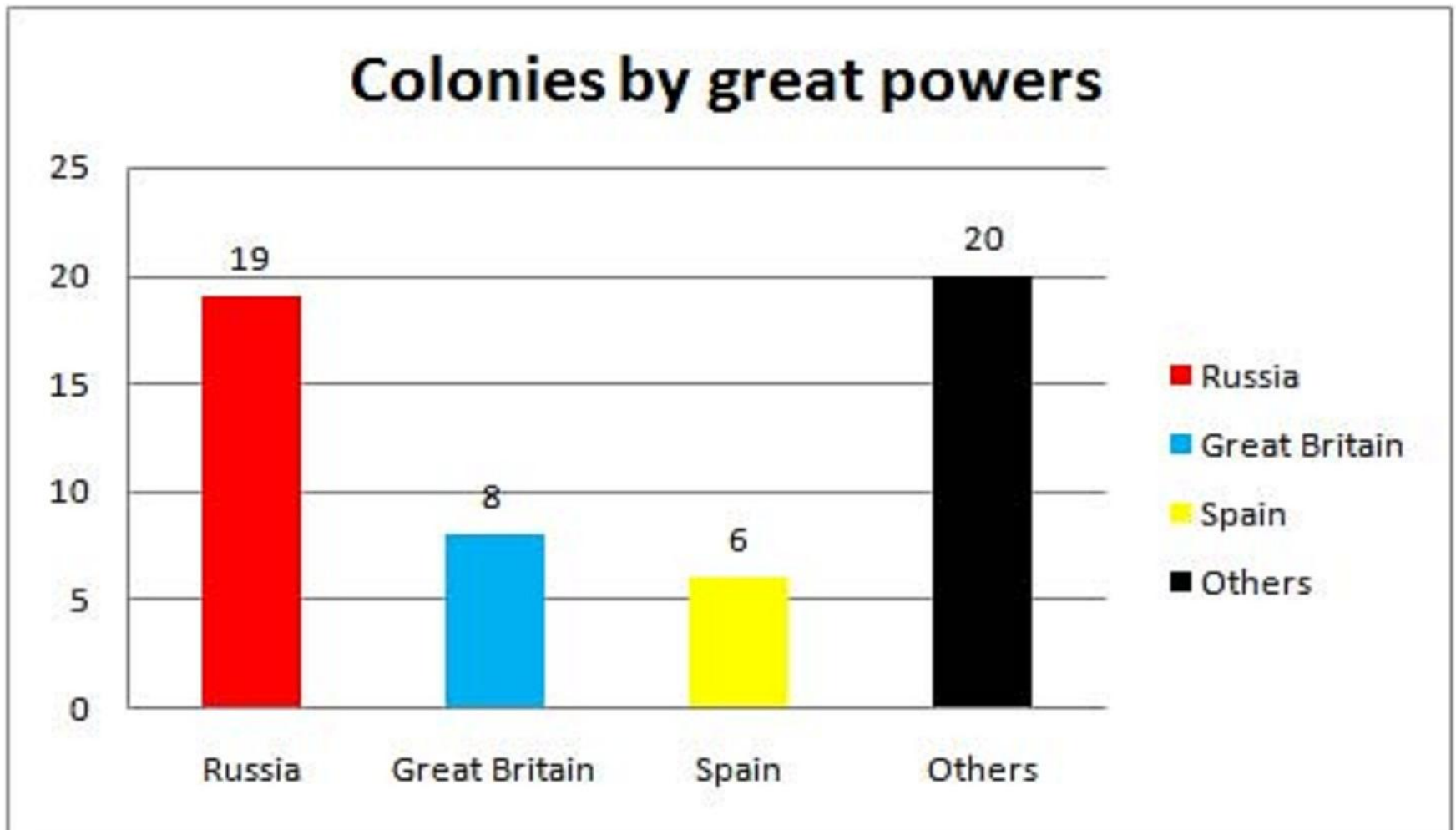
# Variables

- ***Independent variable*** – allele frequencies of ADH1B*Arg48Hys polymorphism (the ALFRED Database)

*Control variables:*

- **Index of technologic development**: We measure technology development as mean value of 3 indicators («0»/ «1»): *existing writing* before colonization , *existence of firearms* (even purchased/ imported), *existence of metals* before colonization («0»/ «1»). Populations with lower index of technology development are more likely to be colonized by European powers.

- **Economy type**: «1» - sedentary agriculture, «0,5» - nomads; «0» - hunters-gatherers. We expect that economically developed populations may have better chances to resist the European colonization.

# Control variables

- **Pathogen history** – index of historic pathogen prevalence, for 7 diseases (leishmaniasis, schistosomes, trypanosomes, malaria, filaria, dengue, typhus), from D.Murray&M.Schaller (2010). We expect that the higher index of historic pathogen prevalence the lower is probability of European colonization. *NB! This data is country-based, but not population-based*.

- **Population density** – rough estimations of population density in 1900. We take estimates for population in 1900 (country-based) and refer them to contemporary country areas. We expect that smaller populations have fewer chances to resist European colonization.

- **Colonization 1800** - (fact of colonization of that population by *Europeans* before 1800: «1» - yes, «0» - no; no colonization or non-European colonization = "0"). Data are checked with the State Antiquity database.
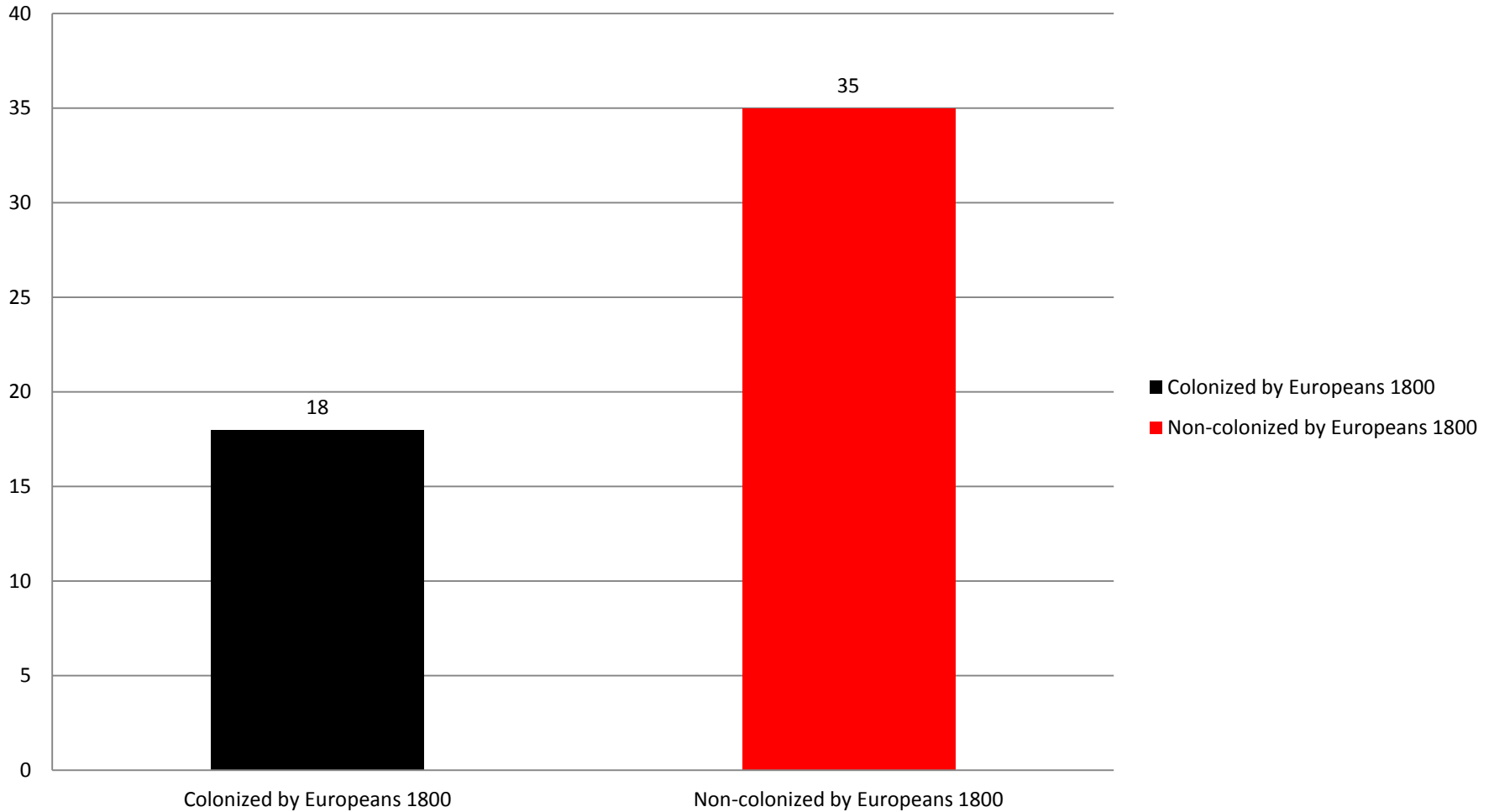
# Correlation matrix

| | Colonization by 1900 | Colonization by 1800 | Frequency of allele Arg48His | history of statehood | type of economy | pathogen history | technology devel-t index | population density |
|---|---|---|---|---|---|---|---|---|
| **Colonization by 1900** | 1 | **,493**[**] | **-,578**[**] | -,225 | -,234 | **-,471**[**] | **-,499**[**] | **-,487**[**] |
| **Colonization by 1800** | **,493**[**] | 1 | **-,280**[*] | -,111 | -,149 | **-,347**[*] | **-,341**[*] | **-,367**[**] |
| **Frequency of allele Arg48His** | **-,578**[**] | **-,280**[*] | 1 | **,324**[*] | **,322**[*] | **,337**[*] | **,414**[**] | **,493**[**] |
| **history of statehood** | -,225 | -,111 | **,324**[*] | 1 | ,210 | ,186 | **,607**[**] | ,068 |
| **type of economy** | -,234 | -,149 | **,322**[*] | ,210 | 1 | ,167 | ,230 | -,027 |
| **pathogen history** | -,471 | **-,347**[*] | **,337**[*] | ,186 | ,167 | 1 | ,135 | **,468**[**] |
| **technology devel-t index** | **-,499**[**] | **-,341**[*] | **,414**[**] | **,607**[**] | ,230 | ,135 | 1 | ,171 |
| **population density** | **-,487**[**] | **-,367**[**] | **,493**[**] | ,068 | -,027 | **,468**[**] | ,171 | 1 |

# Factors of colonization (1)

| | Standardized Beta – coefficients | | |
|---|---|---|---|
| | *Model 1 (DV – Colonization 1900)* | *Model 2 (DV – Colonization 1900)* | *Model 3 (DV –Colonization 1800)* |
| **Technology development index** | **- 0,532\*\*** | **-0,435\*\*** | **-0,300\*** |
| **Type of economy** | -0,131 | - | - |
| **History of statehood** | 0,177 | - | - |
| **Population density** | **-0,412\*\*** | **-0,286\*** | - |
| **Pathogen history** | - | **-0,271\*** | **-0,306\*** |
| *R-square* | *0,470* | *0,494* | *0,209* |
| *Adjusted R-square* | *0,425* | *0,463* | *0,177* |
| *Observations* | *51* | *51* | *51* |

# Factors of colonization (2)

| | Standardized Beta − coefficients | | |
|---|---|---|---|
| | Model 4 (DV – Colonization 1900) | Model 5 (DV – Colonization 1900 China, Japan, Korea excluded) | Model 6 (DV –Colonization 1900) |
| Technology development index | -0,315** | -0,317** | -0,252* |
| Frequency of allele Arg48His | -0,342** | -0,273* | -0,326** |
| Colonization 1800 | - | - | 0,230* |
| Pathogen history | -0,313** | -0,346** | -0,247* |
| R-square | 0,502 | 0,437 | 0,544 |
| Adjusted R-square | 0,472 | 0,401 | 0,506 |
| Observations | 52 | 49 | 52 |

# Factors of colonization (3)

| | Standardized Beta – coefficients | |
|---|---|---|
| | **Model 7 (DV – Colonization 1900)** | **Model 8 (DV – Colonization 1900 China, Japan, Korea excluded)** |
| **Technology development index** | **-0,440\*\*** | **-0,456\*\*** |
| **Frequency of allele Arg48His** | **-0,355\*\*** | **-0,266\*** |
| **Pathogen history** | **-0,333\*\*** | **-0,373\*\*** |
| **History of statehood** | 0,219 | 0,246 |
| *R-square* | *0,532* | *0,478* |
| *Adjusted R-square* | *0,493* | *0,431* |
| *Observations* | *52* | *49* |

# Results

- Models show that frequency of Arg48His allele is significant with sign as predicted. We suggest that it provides an evidence of importance of genetic diversity (alcohol metabolism) as one of potential factors of European colonization.

- Why? How one may explain this correlation? Genetic mutations? Infections?

# Next steps:

- Extending sample (to get data beyond the ALFRED database)

- Including genetic controls (like SNP - Single Nucleotide Polimorphisms) to control for neutral genetic drift

- Logistic regressions

# THANK YOU FOR YOUR ATTENTION!