Laboratory for Comparative Social Research

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
- 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).
- 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

Social change

Alcohol dependence and European colonization

- 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.
- The alcohol trade significantly influenced the growth of the world economic system in the early modern world.
- The Atlantic Trade. The ‘Golden Triangle’: slaves from Africa – sugarcane in the West Indies - rum in America.
- Alcohol became so important to the slave trade that by the late 18th century Western Africa was purchasing almost 3 mln liters of alcohol per year, and by the mid-19th century almost 24 million liters per year. In the overall Atlantic slave trade in its 300 year history, perhaps 5-10% of all slaves were purchased with European alcohol. The Portuguese especially relied on their trade for slaves in Angola. Records indicate that 25% of the almost 1.2 mln slaves sold out of Angola in the 18th century were bought with Brazilian cachasa (Hames, 2012: 49).

Alcohol dependence and European colonization

- In the late 19th century, alcohol became a currency in some African states: Nigeria (Diduk, 1993: 2), South Africa (Hames, 2012: 84).
- In North America alcohol was one of the major trade items with Native Americans. As a result of Native American enthusiasm for alcohol the Europeans traded it to them in exchange for their land and other goods as furs, and sometimes even sexual access to their wives. The biggest profits for traders came for trading alcohol, sometimes as much as 400%-900%.
- Although native populations often consumed alcohol in the pre-colonial periods, it was available mostly during festivals and rituals. With the advent of Europeans alcohol became available all the time; local populations introduced European habits to drink daily.
- 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

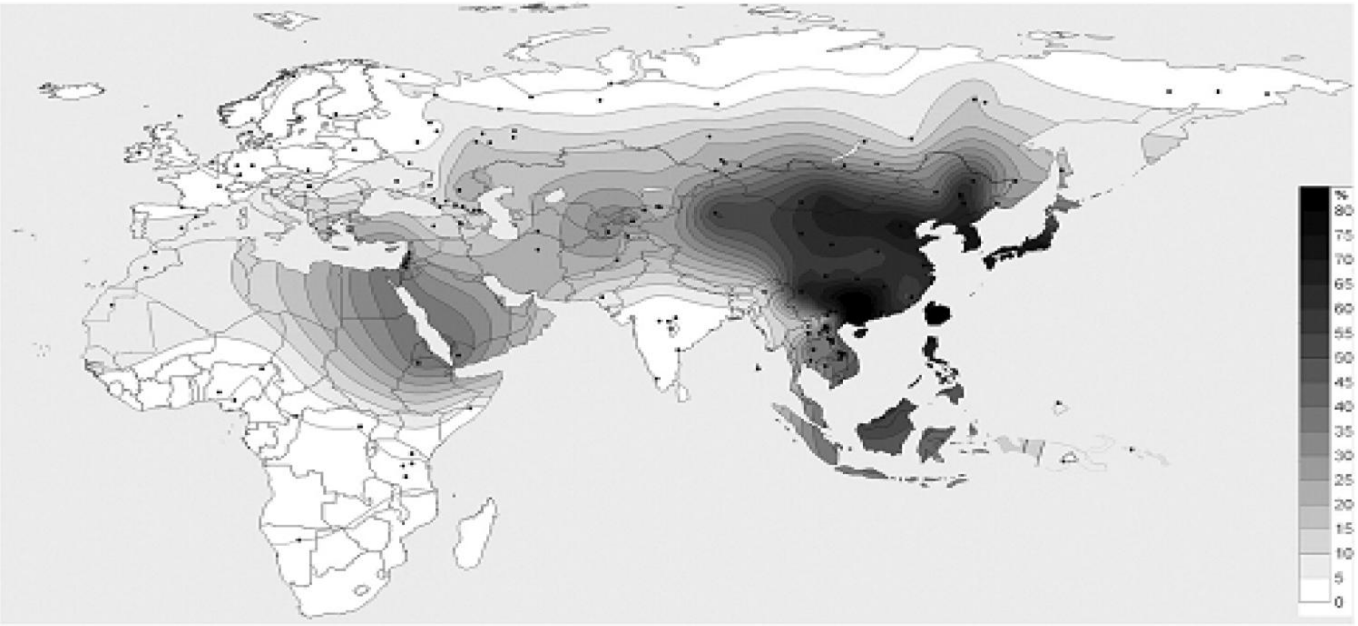
- If invention of distillation is a product of social evolution, alcohol consumption is an outcome of biological evolution.
- The process of alcohol metabolism is associated with certain genetic polymorphisms.
- Alcohol is first oxidized by alcohol dehydrogenase (ADH) to acetaldehyde, which is then oxidized 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

- We tested correlation between Arg48His(Arg370Cys) allele frequency and modern alcohol consumption for 64 populations, based on the WHO data (WHO 2011). The correlation is **-0,318** (p=0.010); if Koreans excluded - **-0,43** (p=0.00). That means that higher allele frequency is associated with some less consumption of alcohol.
- Relatively low frequencies are detected among European, North African, and American 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)

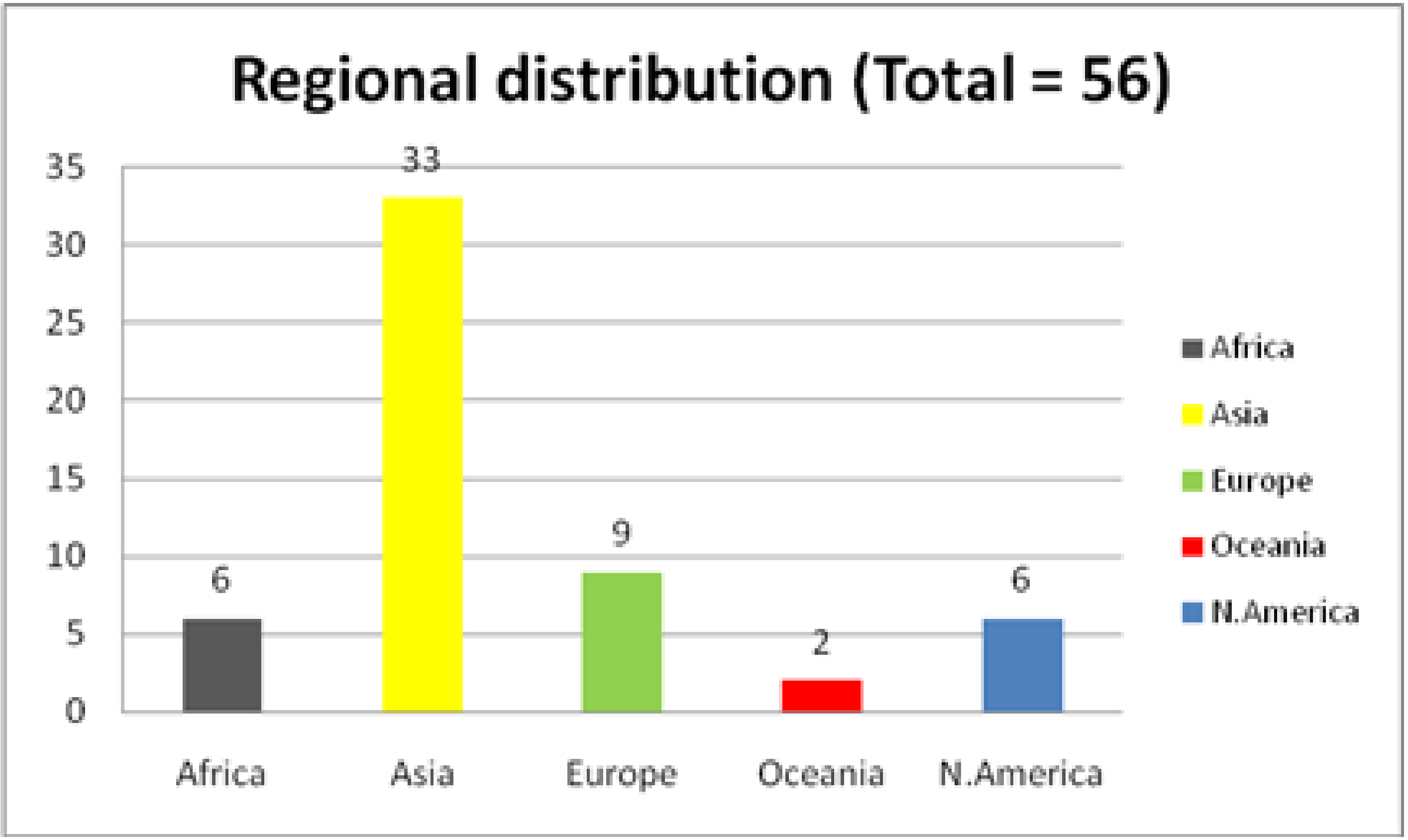
Hypothesis

- 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* <u>is rejected</u>
- *Unequal trade hypothesis.* Alcohol was one of the major items in trade with indigenous populations. European merchants benefited from the increased demand, earning sometimes from 400% to 900% profits. Such unequal exchange, given the increasing demand for spirits from non-Europeans was likely to lead to economic dependence of native populations in Africa, America and Asia. Economic dependence has led to political dependence and colonization.
- No empirical testing

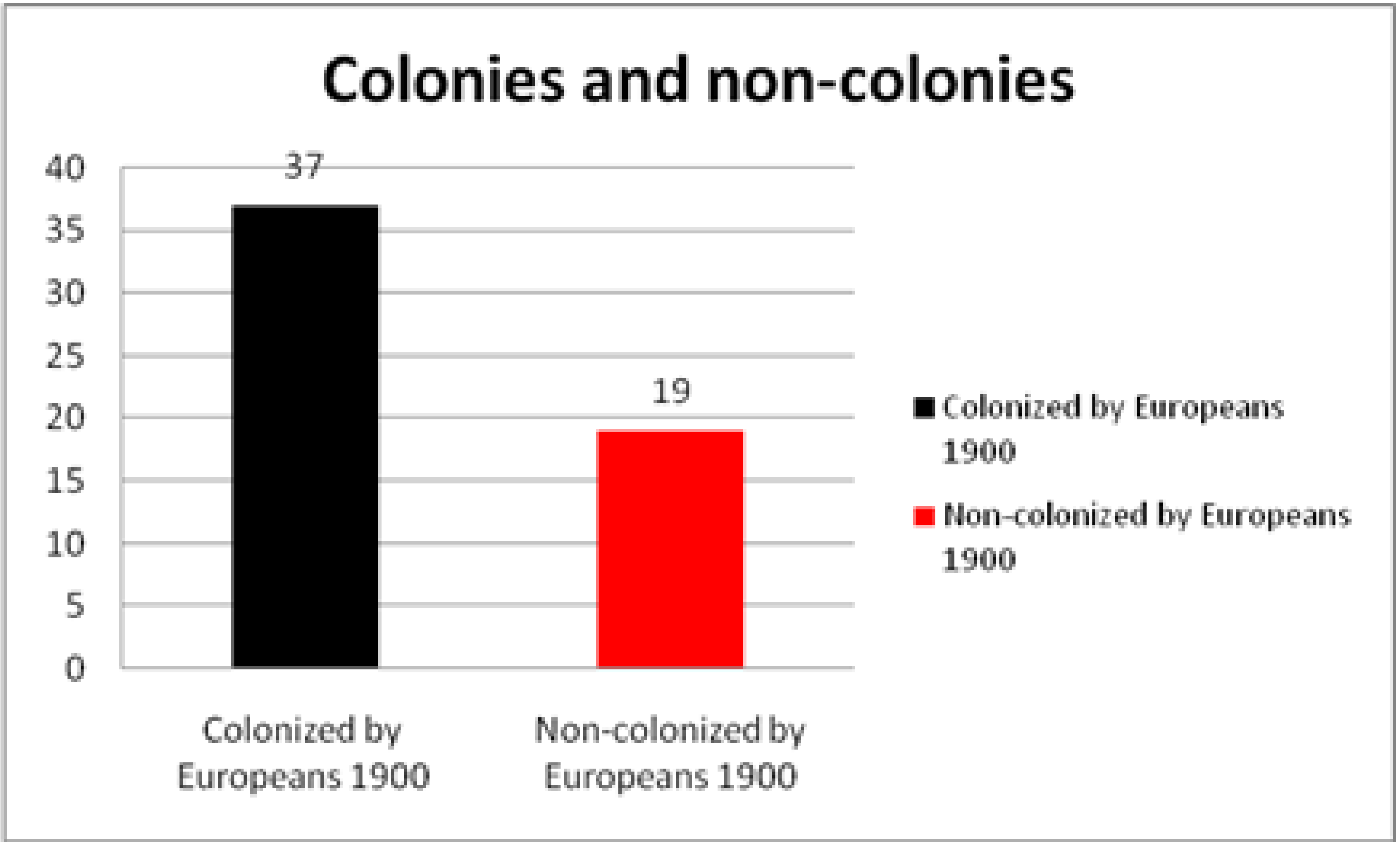
Variables

- Dependent variable is ***colonization 1900*** (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.
- 56 cases in our sample

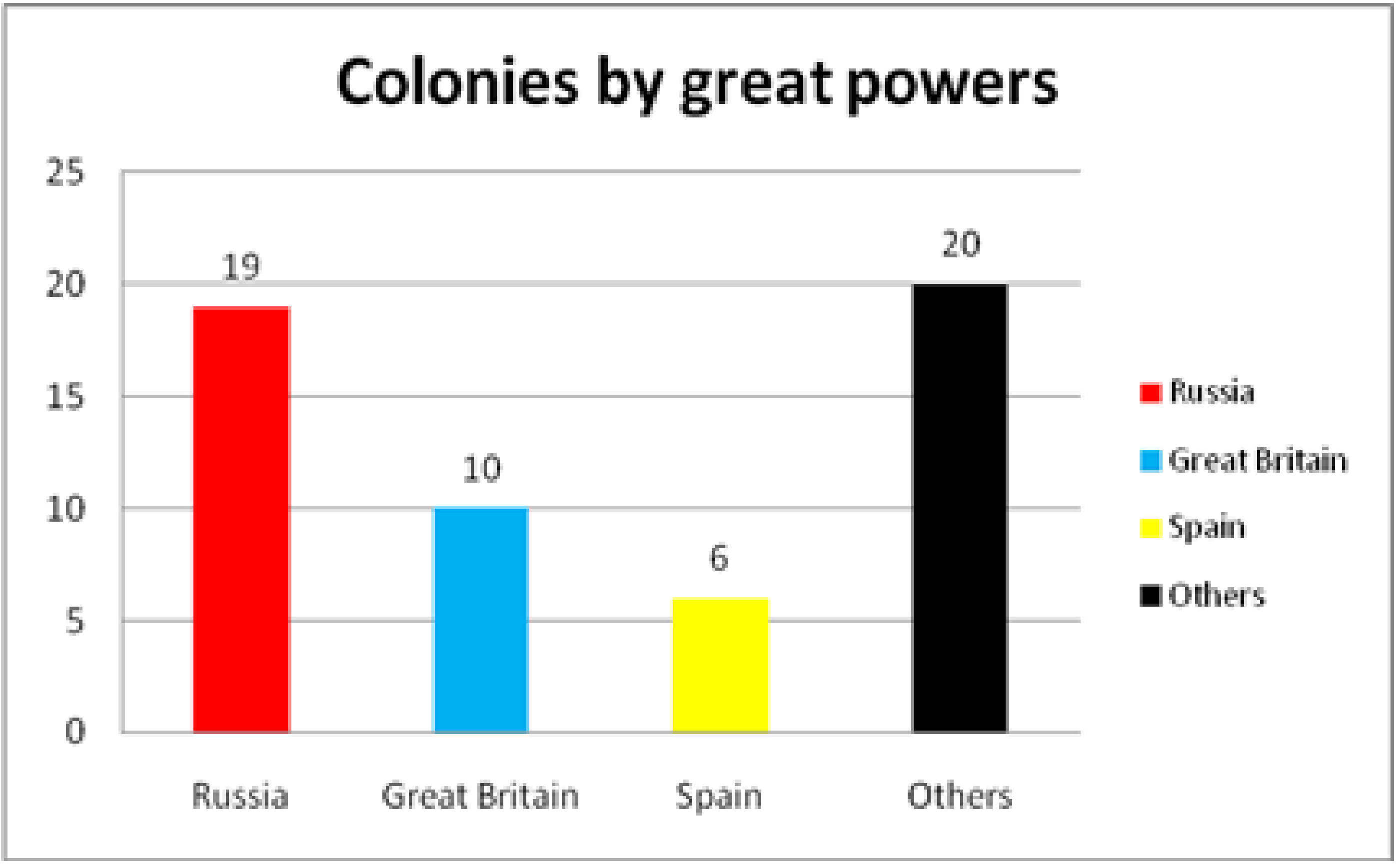
DV – “Colonization 1900”



DV - “Colonization 1900”



DV - “Colonization 1900”



Variables

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

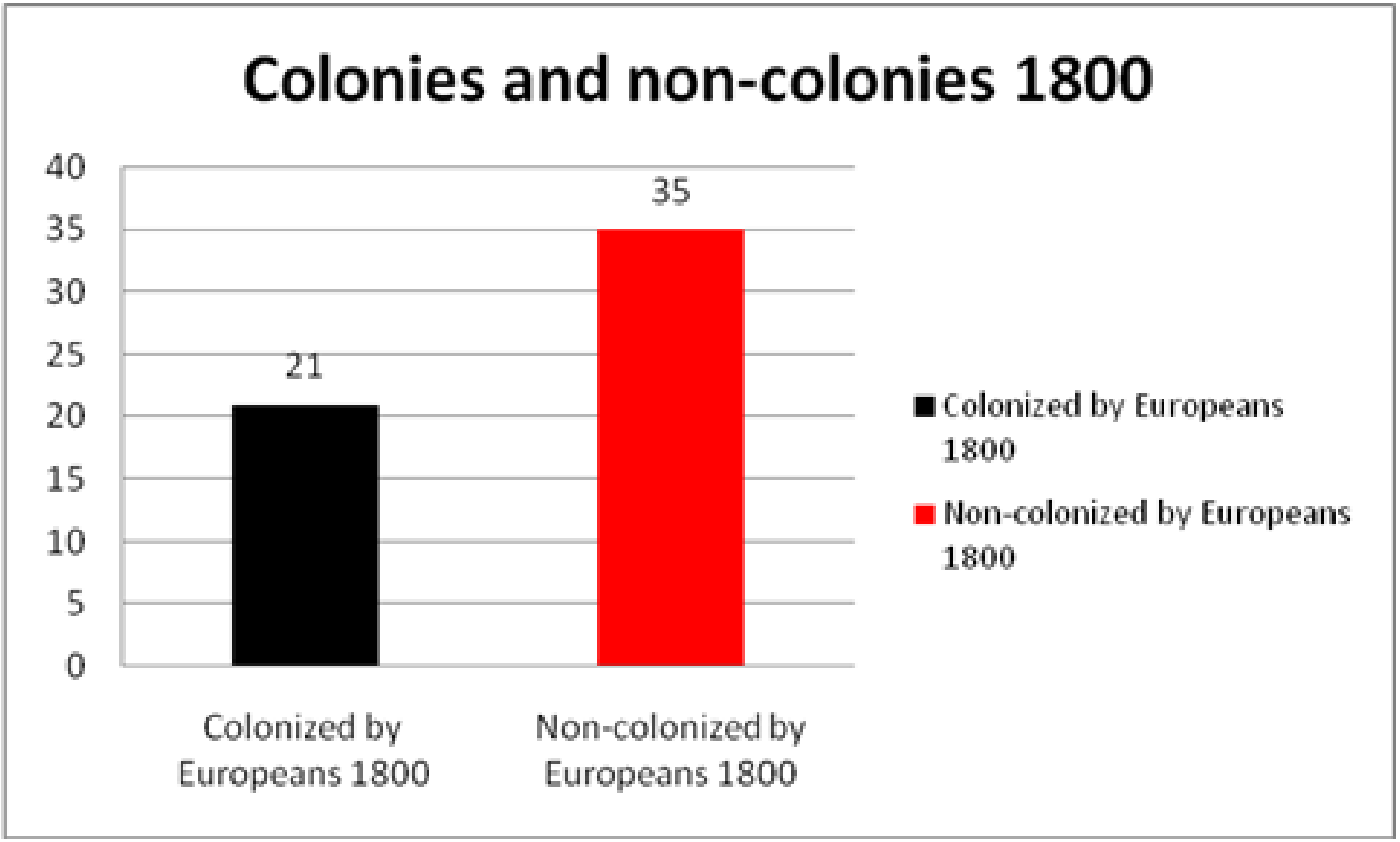
Control variables:

- **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.

Colonization 1800



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	,514**	-,552**	-,255	-,246	-,472**	-,495**	-,438**
Colonization by 1800	,514**	1	-,283*	-,104	-,144	-,319*	-,336*	-,291*
Frequency of allele Arg48His	-,552**	-,283*	1	,289*	,306*	,314*	,365**	,469**
history of statehood	-,255	-,104	,289*	1	,241	,250	,626**	,111
type of economy	-,246	-,144	,306*	,241	1	,198	,270*	-,020
pathogen history	-,472**	-,319*	,314*	,250	,198	1	,195	,490**
technology devel-t index	-,495**	-,336*	,365**	,626**	,270*	,195	1	,199
population density	-,438**	-,291*	,469**	,111	-,020	,490**	,199	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	**-0,517** (0,204)**	**-0,417** (0,147)**	**-0,284* (0,172)**
Type of economy	-0,110 (0,188)	-	-
History of statehood	0,156 (0,144)	-	-
Population density	**0,350** (0,002)**	-0,220 (0,002)	-
Pathogen history	-	**-0,275* (0,084)**	**-0,264* (0,088)**
R-square	*0,408*	*0,441*	*0,180*
Adjusted R-square	*0,361*	*0,408*	*0,149*
Observations	*54*	*54*	*54*

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	**-0,311** (0,146)**	**-0,312** (0,150)**	**0,245* (0,143)**
Frequency of allele Arg48His	**-0,343** (0,218)**	**-0,278* (0,257)**	**0,311** (0,209)**
Colonization 1800	**-**	**-**	**0,266* (0,105)**
Pathogen history	**0,304** (0,073)**	**0,332** (0,076)**	**-0,242* (0,071)**
R-square	*0,486*	*0,429*	*0,544*
Adjusted R-square	*0,457*	*0,394*	*0,508*
Observations	*55*	*52*	*55*

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?

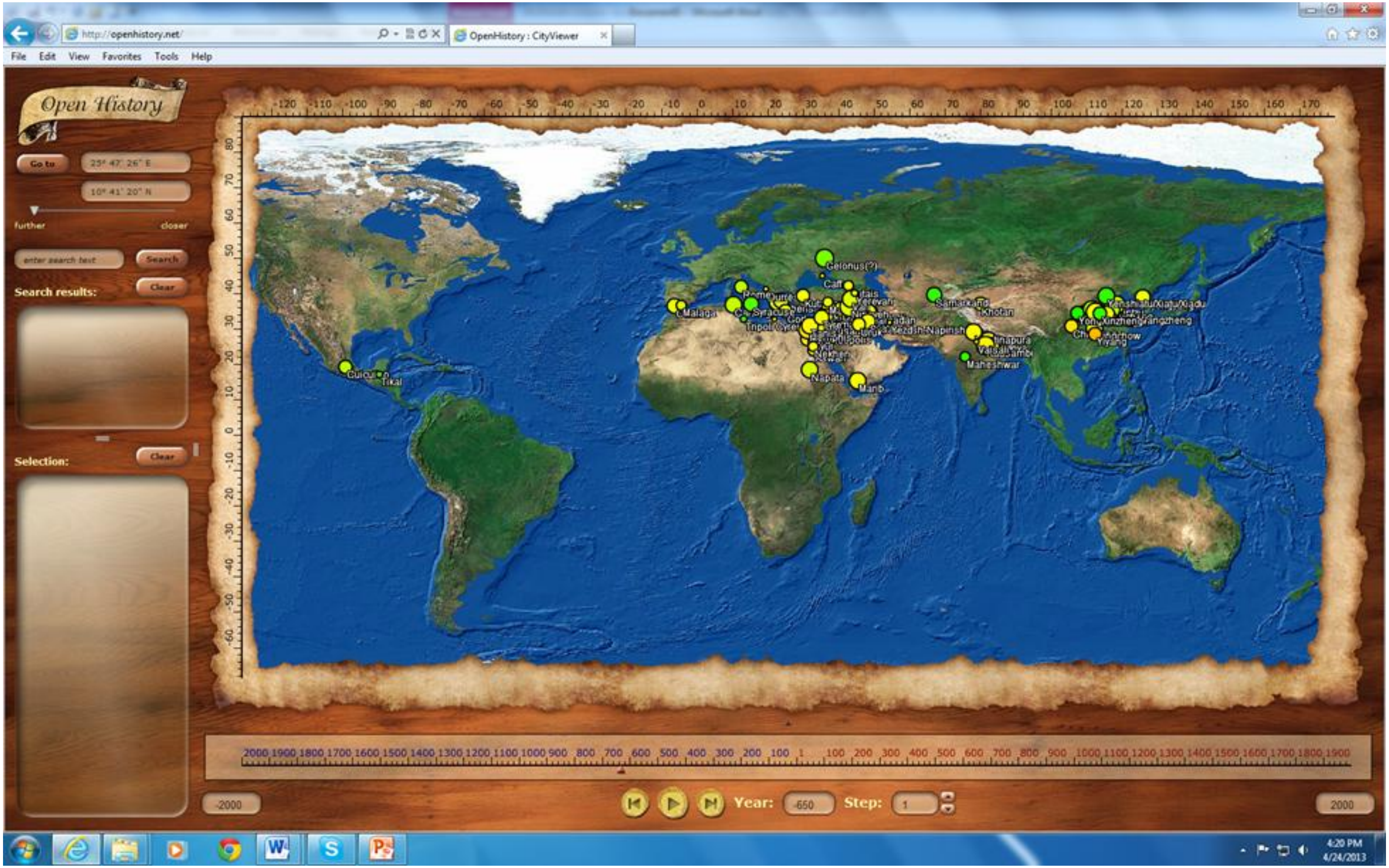
Discussion

- How can one explain distribution of Arg48His/ Arg370Cys alleles?
- Ancient urbanization, statehood, population density
- Statehood is strongly associated with increased population density and urbanization. Increased population density – via emergence of urban settlements - may lead to growth in infectious diseases
- Ancient urbanization is reported to be connected with the frequency of an allele (SLC11A1 1729 + 55del4) associated with natural resistance to intracellular pathogens such as tuberculosis and leprosy (Barnes et al., 2010).

Discussion

- We collected data on ancient urbanization at 650 BCE and correlated it on the Murray’s and Schaller’s index of historic pathogen prevalence (Murray and Schaller, 2010), both 7 and 9 items.
- We take data for ancient urbanization from the OpenHistory Project
- For 650 BC there are records of urban settlements for 20 geopolitical areas in Africa, Asia, Europe and America.

Ancient urbanization 650 BC



http://openhistory.net/

25° 47' 26" E

10° 41' 20" N

Year: -650

Step: 1

Discussion

	N of cities to 650 BC	*Urban population estimate*	*Pathogen history 7 items*	*Pathogen history 9 items*
N of cities to 650 BC	1	**,887****	,383	,408
Urban population estimate	**,887****	1	,358	**,469***
Pathogen history 7 items	,383	,358	1	**,924****
Pathogen history 9 items	,408	**,469***	**,924****	1
N=20				

Discussion

	N of cities to 650 BC	***Urban population estimate***	***Pathogen history 7 items***	***Pathogen history 9 items***
N of cities to 650 BC	1	**,893****	**,563***	**,594***
Urban population estimate	**,893****	1	,480	**,588***
Pathogen history 7 items	**,563***	,480	1	**,929****
Pathogen history 9 items	**,594***	**,588***	**,929****	1

N=17 (*Yemen, Sudan and Mexico excluded)*

Discussion

- We assume that ancient urbanization is an important factor in understanding change in allele frequency for some genes at least, including the case of Arg48His. Distribution of this allele might be explained by increased population density – and increase in infectious disease load - in the areas where first ancient states and cities emerged.

‘Mutual social biological cycle’

Social change	**Biological change**	**Social change**
States / Population density *Ancient urbanization*	Pathogens/ Genetic mutations/ *Change in Arg48His allele frequency*	*Probability of European colonization*

Next steps:

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

THANK YOU FOR YOUR ATTENTION!