GENES AND TECHNOLOGY DIFFUSION

by

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Abstract

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This paper endeavors to shed light on one of the most puzzling questions in modern economics literature: why different countries enjoy different levels of technological development. The main hypothesis is that certain alleles of DRD4 gene may affect individual novelty-seeking behavior, and, consequently, the frequency of the alleles in population may shape the aggregate outcomes. Genetic backgrounds of different propensity towards novelty-seeking are explained, theoretical model is built to link individual behavior with aggregate outcomes. Theoretical predictions are tested empirically on different measures of aggregate level of technology and innovations in the country. The influence of frequency of C allele on the measures of level of technologies and innovations was found to be positive, significant, while the evidence on the influence of 7R is less reliable.

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GLOSSARY

Allele. One of several forms of a gene.

Axon. A part of a neuron, which channels signals from the body of a neural cell to other neural cells or parts of the body

Dopamine. A neurotransmitter, responsible for reward-driven learning.

Dopamine receptors. Proteins in the brain, which receive and react to signals sent with the means of neurotransmitter dopamine.

Gene. A unit of heredity of the organism, which contains information necessary to form the parts of the organism. The information encoded in genes is passed from parents to their off-springs

Gene expression. The process of building a functional unit from a gene.

Neuron. A building cell of a neural system

Neurotransmitter. A chemical that transports signals from neurons to target cells.

Polymorhism. A part of the gene, which may have 2 or more variations, which lead to different gene expression.

Promoter. A part of the gene that facilitates the process of transcription.

Striatum. A part of the brain, in which dopamine receptors are predominantly concentrated.

Synapse. A structure through which a neuron passes a signal to other cells, either electrical or chemical.

Transcription. A process of creating RNA molecules from DNA sequence, the first stage of gene expression.

Chapter 1

INTRODUCTION

Why countries have vastly different levels of development is a key question in economics. These differences are also highly persistent which is highly puzzling given that countries can imitate the success of other countries by adopting their technologies and institutions. Several theories of technology adoption have been popular in economics and other sciences. According to Diamond (1997) the pace of human economic and technological growth as well as the spread of technologies was determined by climatic and geographical factors and biodiversity of the living environment. On the back of his reasoning, Europe and Asia offered some vital conditions for human economic development if contrasted with the rest of the continents: firstly, Eurasia is a home for the majority domesticated plants and animals, which granted resources for expanded reproduction; secondly, relatively lower geographical and ecological barriers in Eurasia slowed the diffusion of innovations much less than in mountainous, forest-clad and northerly southward stretched continent of America or Africa.

The first neoclassical models considered technology an exogenous variable, determination of which was independent of action of economic agents (Solow, 1957). Although the seminal models of economic growth looked at rather how the level of technology, imposed by force outside of the model, influenced the economy, the formulation of a growth model with Cobb-Douglas production function enables the researcher to estimate the so called "Solow residual", which is sometimes referred to as total factor productivity (Romer, 2000). A huge body of literature studies the factors that influence TFP. Issakson (2007) concludes that population health and education, quality of institutions, trade openness and the

size of imports, financial development and the level of competition are the most significant determinants of TFP.

The more recent neoclassical growth literature (see Romer (1990) for example) provides an endogenous justification of economic growth and technological level. Simply put, the increase in the level of economic growth provides resources, which may be invested into innovations to increase technological level, which, in its turn, facilitates economic growth. Among the implications of the Romer's model is that economy with larger capital stock may enjoy faster growth rates and more developed technology level, in addition, trade openness may be beneficial as well. However, Jones (1995) questions the validity of predictions of some endogenous growth models by pointing at the fact that though the number of scientists and researchers expanded dramatically during the postwar era, the economic growth remained roughly constant.

This paper offers an alternative determinant of technology level in the country. In particular, it examines whether the differences among people's genotype can explain different levels of technology diffusion among countries, in particular, whether specific genes may influence technology adoption level directly. This research paper tackles the questions that have rarely been under exploration before. The literature concerning the effect of genes on the adoption of technologies is comprised of Spolaore and Wacziarg (2011).

The main hypothesis of the paper is that the societies characterized by higher frequencies of certain alleles of DRD4 gene polymorphisms are more technologically advanced. The idea behind this presupposition is that genes may in fact influence the human temperament. People with different genotypes may have different attitude to the rewarding experience (such as the consumption of food or drugs or novelty seeking). Dopamine is the chemical that is responsible

for reward-seeking behavior (according to Arrias-Corrion and Poppel, 2007), hence variation in genes that encode the dopamine receptor may lead to different attitude towards novelty seeking which may particularly but not exclusively influence the willingness to adopt new technologies, desire to innovate.

Recently, a new research frontier emerged that lies on the conjunction of economics and genetics. Benjamin (2007) identifies three cases where economics and genetics can interwork and contribute to the development of knowledge base. Firstly, economics may provide the framework under which the genetic influence may be modified by market forces, secondly, some causal relationships may be found between genetic and economic data, finally, economics may assist in developing policy responses to genetic facts. The so-called candidate studies look at how specific genes may influence economic (or behavioral) outcomes. Knafo et al. (2008) were among the first who documented how genes can contribute to the process of decision making in scope of the simple economic game. The AVPR1a RS3 repeat was found to be associated with altruism. A number of studies were devoted to association between genes and risk-taking behavior. Kuhnen and Chiao (2009) conclude that genes, which regulate seratonine and dopamine transmission, in particular, DRD4 and SLC6A4 genes may account for individual differences in financial risk seeking. Dreber et al. (2009) found similar results concerning the DRD4 gene, however, in the restricted sample of male population.

Besides exploring behavioral expressions of genes, several studies endeavor to find a causal relationship between human genotype and cultural profile. Chiao and Blizinsky (2010) documented that some part of variation individualistic and collectivistic dimensions of culture can be attributed to 5-HTTLPR polymorphism of SLC6A4 gene. Way and Lieberman go further and argue that MAOA-uVNTR and OPRM1 A118G genes are associated with cultural

differences. It should be noted, that latter studies, unlike those previously cited, look at the frequencies of specific alleles at the national, rather than individual level of study. They show how the higher proportion of certain alleles in the population acting together with social and ecological level may have an influence on psycho-cultural differences thus supplying proofs? for the aggregate influence of population's genotype. A more common approach to estimate the influence of genetics on the aggregate level is to use the measure of genetic distance. Spolaore and Wacziarg (2006) find correlation between differences in income per capita and genetic distance, even when a large set of controls is accounted for. In economic literature genetic data is sometimes used as an instrumental variable. Guiso et al. (2009) instrument the variable of trust for the genetic distance between European countries and find that the increase in genetic distance reduces the trust dramatically which in turn depresses bilateral trade. Gorodnichenko and Roland (2011) use genetic distance to the USA and population frequencies of the short allele of 5-HTTLPR polymorphism as an instrument for cultural dimension of individualism. They find that the more genealogically related the country is to the USA (the less if genetic distance) the higher is the individualism score and the greater is output per worker in the country.

Although the interplay between economics and genetics offers new opportunities in expanding the comprehension of human behavior, genoeconomic studies are marked by some challenges. One of them is low statistical power, the consequence of a relatively small sample size, which, coupled with the low true value of genetic effect, yields insignificant estimates. For example, Beauchamp et al. (2011) studied the influence of genome on the number of .years of education using two samples, one, from Framingham Heart Study, another – from Rotterdam study, and failed to reproduced the results obtained from the former sample using the data from the latter.

In addition to the fact that this paper is one of the first in its field, it also deals with the issue of technology adoption, which is important for modern economic theory per se. Differences in technology adoption may be responsible for the differences in countries TFP and income per capita and are an important determinant of the wealth of nations. Comin and Hobijn (2010) find that the economic advancement of Singapore and Japan is largely due to the diminishing of technology adoption lags. Moreover, variation in technology adoption level accounts for a quarter of per capita income incongruence. According to Comin, Hobijn and Rovito (2008) different levels of technology usage principally explain the disparities in countries' total factor productivity. Thus, the factors that determine the speed of technology adoption may also shed light on the puzzle why some nations are richer than others.

In the empirical literature on behavioral genetics a number of papers were dedicated to the influence of VNTR and 521 C/T polymorphisms of DRD4 gene on the personal novelty-seeking behavior. The scope of this paper is to study the influence of country-level frequency of certain alleles on the aggregate level of technology adoption and innovations.

The rest of the paper is organized in such a manner: Chapter 2 contains literature review, in Chapter 3 a theoretical model is developed, methodology is explained in Chapter 4, Chapter 5 contains data description, Chapter 6 contains the results, their analysis and discussion, Chapter 7 concludes.

Chapter 2

LITERATURE REVIEW

The section of literature review consists of two parts: the first describe the determinants of technology diffusion, the second explains how genetics can explain the novelty-seeking and innovative behavior.

2.1 Determinants of diffusion of technologies

One of the first and most influential papers on technology diffusion was written by Zvi Griliches (1957), in which he analyzed the use of hybrid corn seeds in different states and the factors that determined its expansion. It was concluded that the diffusion of a technology follows an S-shaped curve, which is characterized by a limited number of parameters – its slope, origin and ceiling. A number of attempts have been made to reveal the factors that influence the dissimilarities in the speed of the diffusion of technology across countries. Comin and Hobijn (2010) focused on the technology diffusion lags – the period between the invention and adoption of a certain technology. They develop a growth model with technology diffusion and find that lag length can be explained by the productivity of the underlying capital. Barro and Sala-i-Martin (1997) develop an alternative endogenous growth model in which the source of growth in the long-run is driven by innovations in foremost economies, the followers, on the other hand, copy ideas with increasing costs as the pool of new ideas shrinks. Among the most significant factors that determine the leadership of the country in R&D activity are infrastructure, taxation and enforcement of property rights. Another definition of technology usage was introduced by Comin, Hobijn and Rovito (2008). They outline diffusion lags for a certain country and technology as the time, which has passed since the level of technology in the USA was the same as

in the country of interest nowadays. Among the findings of this research is the correlation among diffusion lags of different technologies and with income per capita. Comin and Hobijn (2009) analyzed how lobbies influenced technological diffusion. They found that in the countries with poor institutions new technologies which have comparable predecessors are more likely to be adopted with a considerable delay, due to the barriers erected by the incumbents using preceding technology. Irmen (2008) argues that the openness of the country, its investment rate and size of subsidies to innovations may also influence levels of technology adoption. Benhabib and Spiegel (2009) found evidence in support of hypothesis that the stock of human capital plays an important role for technology diffusion process, even if controlled for geo-political determinants. Nunn and Puga (2012) found significant effect of geography on economic development. They argued that terrain ruggedness may have hindered productive activities. Acemoglu and Robinson (2012) provide a number of examples which prove that claim that one of the most important factors for the adoption of technologies and economic development is the quality of institutions. Extractive economic institutions discourage incentives to innovate and slow down entrepreneurial activity. On the other hand, inclusive political and economic institutions favor technological and economic development.

The literature that relates technology diffusion with genetic characteristics of nations is scarce. The innovative explanation of different levels of technology among countries was given by Spolaore and Wacziarg (2011) who found the relationship between the genetic relatedness among nations and their distance to technological frontier (i. e. the distance in years from technological frontiers). Their main conclusion stated that genetic distance between nations can be a substantial obstacle to technology diffusion across countries. However, the authors didn't establish the mechanism through which genetic distance affects

technology adoption (culture, institutions or human capital are mentioned as possible candidates).

2.2. Biological foundations of novelty seeking

This paper argues that certain genes may influence human behavior in such a way that would facilitate the technological development. Some genes may impact human temperament in such a way that may motivate novelty seeking activities, which may induce the adoption of new technologies. The assumption of genetic inheritance of temperament traits was developed by Cloninger (1987) and Cloninger (1993). Several numerical measures were developed to take the gage of human personality traits and temperament. Cloninger, Przybeck and Svrakic (1991) developed a so-called Tridimensional Personality Questionnaire which recognized the existence of three personality measures (novelty seeking, harm avoidance and reward dependence). Cloninger et al. (1994) developed a multidimensional Temperament and Character Inventory (TCI) measure of human temperament and personal traits, according to which the four types of temperament were identified: novelty seeking, harm avoidance, reward dependence and persistence. Several twin studies tested the abovementioned hypothesis of inheritable nature of temperament. Heath et al. (1994) analyzed 2680 twin pairs from Australia and found that genetic variation accounted for 54%-61% of the variation in TPQ traits. The genetic difference in this study was captured by the zygosity of the twins. Monozygotic twins (identical twins) develop from a single zygote (fertilized egg-cell) and they are almost identical from the genetic point of view, while dizygotic twins are born form several fertilized egg-cells, as a consequence, their genotypes differ. Thus, although the differences in genotype were proved to be substantial determinants of novelty seeking behavior, the particular genes which were responsible for the differences in genetic scores were not uncovered. In the empirical literature on behavioral

genetics several genes were tested for their association with novelty seeking. The most widespread objects of analysis are the polymorphisms (specific mutations) of the DRD4 gene (which encodes the dopamine receptor D4).

Human brain goes for novelty seeking. As early as in the 19th century, Wilhelm Wundt noticed that people are more stimulated by a complicated experience. According to Arrias-Carrion and Poppel (2007) dopamine is responsible for the hedonic pleasure the organism feels as a reaction to some experience (for example, food, drugs). Berns (2005) comprehensively describes the mechanism through which novelty seeking is highly praised by human brain. A part of human brain called striatum receives signals from other parts of the brain regarding the actions than can potentially be put to action. To understand how human brain sends signals to striatum, one needs to understand, how neurons may send signals to each other. The neutron has a part called axon that releases either chemical or electrical signals to other neurons or parts of the body. The dendrite is a part of neuron that reacts to signals, sent by other neurons. Neurons may send chemical signals by releasing special substances – neurotransmitters, which bind to specific receptors on the dendrite of a neuron receiving a signal. The structure through which chemical signal is transmitted between neurons is called synapse (the scheme of a synapse is illustrated in Figure 1).

Striatum is characterized by a vast presence of dopamine receptors, which are activated by a neurotransmitter dopamine. According to Berns (2005) dopamine is released when a person is going to do something novel. This means that neurons, that are responsible for certain actions, may release dopamine. When a dopamine reaches a dopamine receptor in striatum, it acts as a kind of a reward stimulating this part of the brain. As a consequence, striatum sends signals to basal ganglia system, which controls action selection.

Dopamine is released when the action assumes some novelty to the brain, it is a kind of reward for novel behavior. To put it simple, if one has a lot of alternatives of how to act in a specific moment, all possible actions are sent as signals to striatum. If action leads to novelty – it is accompanied by dopamine emission, which grants that striatum will react and this action will be executed. To understand this one can consider a counterexample – a person with suppressed dopamine system, which means that she can't produce "reward" associated with specific action, she can't manage her movement and decide what she wants – that can occur during Parkinson's disease which is caused by the death of dopamine-producing cells. Thus, if the action is novel, it is more likely to be conducted due to the effect of dopamine on striatum.

2.2.1 DRD4 gene: exon III VNTR

What makes different people have different inclination toward novelty seeking is the difference in dopamine receptors that react on dopamine emission. There are different types of dopamine receptors in human brain, called D1, D2, D3, D4. A closer look at dopamine receptor D4 (DRD4) may shed light on the differences in novelty-seeking among people. It is established that what determines how this receptor acts is a gene (a unit of heredity – part of a chromosome), called DRD4. One of the parts is called a. There exist several mutations (polymorphisms) of DRD4. One of them occurs at the so-called "48 base pair VNTR in exon III". VNTR means that this part of the gene consists of a sequence of nucleotides (building blocks of genes and DNA) that repeats for several times (if we call possible blocks as A, T, C, G, then the sequence A-C-G-G-A-C-G-G-A-C-G-G is the three times repeat). In this case the number of repeats can be from 2 to 10. Thus different variants (alleles) of the DRD4 which encode D4 dopamine receptor may lead to different reaction on a rewarding experience (for example, novelty-seeking behavior). Under certain circumstances, the action of dopamine receptors is blocked by dopamine antagonists. One of such substances is

clozapine[1], which is highly affine to dopamine receptor D4 (this drug is used to suppress the dopamine system during schizophrenia) – see Figure 2 for illustration.

Dopamine receptors are no longer available to react to dopamine stimuli when clozapine binds to them. There is some evidence in Ebstein (1996) that suggests that the dopamine receptors, encoded by the 7R allele are less likely to fall under the adverse influence of clozapine, thus, the work of dopamine receptor will not be violated, and the presence of 7R allele in the genotype of a person may make her more inclined to novelty-seeking behavior.

2.2.2 DRD4 gene: 521C-T promoter

The promoter of DRD4 gene can be represented by one of the two alleles: C or T. The promoter region is responsible for the transcription of the gene (a kind of archived copy of information) into RNA, which will eventually lead to gene expression in the form of the dopamine receptor D4. Okuyama et al. (2000) indicate that T allele is associated with 40% less transcriptional activity which may hamper gene expression and, eventually, the efficiency of the dopamine receptor.

Based on the information described above, one can suspect that people with 7R dominant allele of VNTR and dominant C allele in C521-T promoter region can lead to better efficiency of dopamine receptors and thus favor novelty-seeking which is associated with dopamine emission. The hypothesis of this paper is that if there is a plenty of abovementioned alleles in the population, the population if general will be more inclined to invent new things and improve technological level of the society. It is also possible that societies with a lot of 7R allele but with low C allele may not benefit from "clozapine-resisting" allele since the gene will

[1] See International Union od Basic and Clinical Pharmacology Database for a list of dopamine antagonists at: http://www.iuphar-db.org/DATABASE/ObjectDisplayForward?objectId=217

not be able to express itself (transcribe) efficiently and vice versa – the effect of the presence of large amount of allele that improves transcription efficiency may be devastated by the absence of receptors which may resist clozapine.

A number of studies were devoted to the test of the hypotheses that the 7R allele of the VNTR polymorphism of the DRD4 gene and the C allele of the 521 C/T polymorphism are associated with novelty seeking. Ebstein et al. (1996) were among the first who documented the empirical connection between the presence of 7R allele and novelty-seeking trait. Dreber et al (2009) found a relationship between the presence of 7R allele and risk taking among men. However, the meta-analysis of 36 published papers on the issue documented no effect of the 7R allele of VNTR polymorphism on the novelty-seeking behavior. Although, the same observed that some variation in novelty-seeking behavior may be attributed to 521 C/T polymorphism. Anyway, the mechanism of genetic influence on human temperament is rather complex and novelty-seeking behavior may be moderated by several genes simultaneously.

Chapter 4

THEORETICAL MODEL

In the previous section a link between genetic factors and personal propensity to novelty seeking was established. Section presents a simple model that explores whether individual results influence the aggregate level outcomes.

The economy consists of three sectors: production of final good, variety of intermediate goods and a research sector. The production function in the economy reminds that of Dixit and Stiglitz (1977) and Romer (1990):

$$Y_t = L_t^{1-a} \int_{i\epsilon\Omega} (F_{it} x_{it})^a \, di \tag{2}$$

where L_t is the total amount of labor devoted to the production of final good, $L_t = \int_{i\epsilon\Omega} L_{it} \, di$, x_{it} - is the amount of a certain intermediate good, F_{it} is its quality, *t* – a time index, *i* – index of individual intermediate good.

Final good is treated as numeraire, in final good sector the profit of the firms consists of revenues (2) exclusive of payroll and purchases of intermediate good:

$$\Pi_t = L_t^{1-a} \int_{i\epsilon\Omega} (F_{it} x_{it})^a \, di - \, w_t L_t - \int_{i\epsilon\Omega} p_{it} x_{it} \, di \tag{3}$$

where w_t is the wage in the economy at period *t*, p_{it} is the price of individual intermediate good *i*. Taking first-order conditions of (3):

$$\frac{\partial \Pi_t}{\partial L_t} = (1-a)\frac{Y_t}{L_t} - w_t = 0 \tag{4}$$

$$\frac{\partial \Pi_t}{\partial x_{it}} = a L_t^{1-a} {F_{it}}^a {x_{it}}^{a-1} - p_{it} = 0 \tag{5}$$

where (4) determines the wage in the economy, (5) – price for the intermediate good.

Economy consists of a mass of households, which produce intermediate goods, devote part of their labor L_{it} to the manufacturing of final good and the rest $(1 - L_{it})$ – to research activities, the labor endowment is equal to unity for each household. Each household i maximizes its lifetime utility given by:

$$U \equiv \sum_{t=0}^{\infty} \beta^t (u(c_{it}) + v(\frac{F_{it}}{F_t}, \phi)) \quad (6)$$

where $u(c_{it})$ is a standard utility function from consumption of a final good and $v(\frac{F_{it}}{F_t}, \phi)$ is a utility[2] from innovative activity (which is reflected by the individual level of quality of intermediate good in comparison with the aggregate technological level $F_t \equiv \int_{i \epsilon \Omega} F_{it}\, di$). The term ϕ reflects genetic characteristics of the individual, the presence or absence of alleles, favorable to novelty seeking: $\phi \epsilon \{0,1\}$ and $v\left(\frac{F_{it}}{F_t}, 1\right) > v\left(\frac{F_{it}}{F_t}, 0\right)$ which corresponds to the fact that in the presence of novelty-enhancing allele human brain is more is more willing to accept novel actions (since, as was argued before, in presence of C allele or 7R allele, novel actions are more probable to activate a dopamine system in the brain, increasing the "reward" the brain gets for performing a novel action). Population consists of agents which either have or doesn't have the abovementioned alleles. The function v is assumed to have constant elasticity in $\frac{F_{it}}{F_t}$: $v'\left(\frac{F_{it}}{F_t}, \phi\right) \frac{\frac{F_{it}}{F_t}}{v(\frac{F_{it}}{F_t}, \phi)} = \sigma$. Without the loss of generality it can be assumed that $v > 0$. Households maximize their utility subject to the budget constraint:

$$c_{it} + A_{it+1} = (1 + r_t)A_t + \pi_{it} + w_t L_t \quad (7)$$

[2] This utility function is built upon a resembling utility function from Gorodnichenko and Roland (2010). In their case, the utility was derived from social status reward due to innovative activity, it was monotonically increasing in innovative activity (quality of intermediate good). This function is increasing in the level of quality of intermediate goods. This is consistent with the argument from the previous section that human brain likes novel actions, as they activate its dopamine system. Activation of dopamine system is synonymous to satisfaction (for example, it is well-established that such drugs as cocaine and metamphetamine act directly on the dopamine system).

where $\pi_{it} = (p_{it} - 1)x_{it}$ is the profit from the production if intermediate good (the cost of production is equal to 1). By plugging (5) in (7) one can rewrite the budget constraint as

$$c_{it} + A_{it+1} = (1 + r_t)A_t + (aL_t^{1-a}{F_{it}}^a{x_{it}}^{a-1} - 1)x_{it} + w_t L_t \quad (8)$$

Another constraint that households face is the production function of technological level (quality) of intermediate products:

$$F_{it} = F_{it-1}^{\gamma}(1 - L_{it})^{1-\gamma} \quad (9)$$

The Lagrangian to the household problem is thus

$$J = \sum_{t=0}^{\infty} \beta^t (u(c_{it}) + v(\frac{F_{it}}{F_t}, \phi)) -$$

$$-\beta^t \lambda_{it}\big(c_{it} + A_{it+1} - (1 + r_t)A_t + \big(aL_t^{1-a}{F_{it}}^a{x_{it}}^{a-1} - 1\big)x_{it} + w_t L_t\big) -$$

$$-\beta^t \mu_{it}(F_{it} - F_{it-1}^{\gamma}(1 - L_{it})^{1-\gamma}) \quad (10)$$

The choice variables are $c_{it},\ A_{it+1},\ L_{it},\ F_{it},\ x_{it}$ and the first order conditions are the following:

$$\frac{\partial J}{\partial c_{it}} = \beta^t u'(c_{it}) - \beta^t \lambda_{it} = 0, \quad u'(c_{it}) = \lambda_{it} \quad (11)$$

$$\frac{\partial J}{\partial A_{it+1}} = -\beta^t \lambda_{it} + \beta^{t+1}(1 + r_t)\lambda_{it+1=0}, \quad \lambda_{it} = \beta(1 + r_t)\lambda_{it+1} \quad (12)$$

$$\frac{\partial J}{\partial L_{it}} = \beta^t \lambda_{it} w_t - \beta^t \mu_{it} F_{it-1}^{\gamma}(1 - L_{it})^{-\gamma}(1 - \gamma) = 0,$$

$$\lambda_{it} w_t = \mu_{it} F_{it-1}^{\gamma}(1 - L_{it})^{-\gamma}(1 - \gamma) \quad (13)$$

$$\frac{\partial J}{\partial F_{it}} = \frac{\beta^t v'\left(\frac{F_{it}}{F_t}, \phi\right)}{F_t} + \beta^t \lambda_{it} a^2 L_t^{1-a}{F_{it}}^{a-1}{x_{it}}^a - \beta^t \mu_{it} +$$

$$+\beta^{t+1}\mu_{it+1}\gamma F_{it}^{\gamma-1}(1 - L_{it})^{1-\gamma} = 0 \quad (14)$$

$$\mu_{it} = \frac{v'\left(\frac{F_{it}}{F_t}, \phi\right)}{F_t} + \lambda_{it} a^2 L_t^{1-a}{F_{it}}^{a-1}{x_{it}}^a + \beta\mu_{it+1}\gamma F_{it}^{\gamma-1}(1 - L_{it})^{1-\gamma} \quad (15)$$

$$\frac{\partial J}{\partial x_{it}} = \lambda_{it}\beta^t(a^2 L_t^{1-a}{F_{it}}^a{x_{it}}^{a-1} - 1) = 0, \quad a^2 L_t^{1-a}{F_{it}}^a{x_{it}}^{a-1} = 1 \quad (16)$$

Marginal utility is equal to shadow price of wealth, according to equation (11), equation (12) reflects the inter-temporal choice between consumption today and tomorrow, equation (13) states that utility gains from working in the final good sector (marginal wage multiplied by marginal utility of wealth) equal to utility gains from working in the research sector (marginal utility from increase in quality multiplied by marginal increase in quality). Marginal value of quality consists of gains of utility, marginal profit from increased demand on intermediate good of higher quality and gains from better future technology, according to equation (16).

From (4), (11) and (12)

$$\mu_{it} = \frac{u'(c_{it})Y_t}{F_{it-1}^{\gamma}(1-L_{it})^{-\gamma}(1-\gamma)} \tag{17}$$

Plug (17) into (15) to get

$$\frac{u'(c_{it})Y_t(1-a)}{F_{it-1}^{\gamma}(1-L_{it})^{-\gamma}(1-\gamma)L_t} = \frac{v'\left(\frac{F_{it}}{F_t},\phi\right)}{F_t} + u'(c_{it})a^2 L_t^{1-a} {F_{it}}^{a-1} {x_{it}}^{a} + \\ + \beta \frac{u'(c_{it+1})Y_{t+1}(1-a)}{F_{it}^{\gamma}(1-L_{it+1})^{-\gamma}(1-\gamma)L_{t+1}} \tag{18}$$

Using (9)

$$\frac{u'(c_{it})Y_t(1-a)(1-L_{it})}{F_{it}(1-\gamma)L_t} = \frac{v'\left(\frac{F_{it}}{F_t},\phi\right)}{F_t} + \frac{u'(c_{it})a^2 L_t^{1-a} {F_{it}}^{a} {x_{it}}^{a}}{F_{it}} + \\ + \beta \frac{u'(c_{it+1})Y_{t+1}(1-a)(1-L_{it+1})}{F_{it+1}(1-\gamma)L_{t+1}} \tag{19}$$

In the steady state $L_{it} = L_{it+1} = L_i$ and thus $L_t = L_{t+1} = L$. Since L_i is constant, from (9) it can be inferred that F_{it} is constant as well ($F_{it} = F_{it+1} = F_i = 1 - L_i,\ F = 1 - L$). From (16) it is obvious that x_{it} is constant as well, thus, the aggregate production level will be constant over time. If one multiplies both sides of (19) by F_{it} and remember the constant elasticity property of function *v*:

$$\frac{u'(c_{it})Y(1-a)(1-L_i)}{(1-\gamma)L} = \sigma v\left(\frac{F_i}{F_t},\phi\right) + u'(c_{it})a^2 L_t^{1-a} {F_i}^{a} {x_i}^{a} +$$

$$+\beta \frac{u'(c_{it+1})Y(1-a)(1-L_i)}{(1-\gamma)L} \quad (20)$$

The market clearing condition that consumption of final good is equal to the production of the final good $\int_{i\epsilon\Omega} c_{it}\, di = Y$. From (11) and (12) and assuming a usual form of utility function $(c_{it}) = \log c_{it},\ c_{it+1} = \beta(1+r_t)c_{it},\quad \frac{c_{it+1}}{c_{it}} = \beta(1+r_t)$, which means that consumption of every agent grows at a constant rate, equal to all agents. Since aggregate output in the steady state is constant, consumption grows at zero rate, thus, one can rewrite (20) as follows:

$$Y(1-a)(1-L_i) = [\sigma v\left(\frac{F_i}{F_t}, \phi\right) + a^2 L_t^{1-a} {F_i}^a {x_i}^a]\,(1-\gamma)L + \\ +\beta Y(1-a)(1-L_i) \quad (21)$$

$$(1-L_i) = \left[\sigma v\left(\frac{F_i}{F_t}, \phi\right) + a^2 L_t^{1-a} {F_i}^a {x_i}^a\right] \times \\ \times (1-\gamma)L[Y(1-a)(1-\beta)]^{-1} \quad (22)$$

Since in the steady state $F_i = 1 - L_i$

$$(1-L_i) = \left[\sigma v\left(\frac{1-L_i}{F_t}, \phi\right) + a^2 L_t^{1-a} (1-L_i)^a {x_i}^a\right] \times \\ \times (1-\gamma)L[Y(1-a)(1-\beta)]^{-1} \quad (23)$$

$$\frac{\partial \sigma v\left(\frac{1-L_i}{F_t}, \phi\right)}{\partial (1-L_i)} = \sigma \frac{\partial v\left(\frac{1-L_i}{F_t}, \phi\right)}{\partial (1-L_i)} = \left(\frac{\partial v\left(\frac{1-L_i}{F_t}, \phi\right)}{\partial (1-L_i)}\right)^2 \frac{\frac{F_{it}}{F_t},}{v\left(\frac{F_{it}}{F_t}, \phi\right)} > 0 \quad (24)$$

Since LHS and RHS of (23) are both increasing in $(1-L_i)$, $\phi = 1$ will be associated with higher equilibrium levels of $(1-L_i)$ and F_i, than $\phi = 0$, as a consequence, aggregate share of labor, devoted to the production of final good is inversely related to the fraction of agents with novelty-favorable alleles, thus, the share of labor devoted to research (and, as a consequence, steady state level of quality of intermediate goods and aggregate level of technology *F*) is directly related to the fraction of people with those alleles. This prediction will be empirically tested in the following sections.

It should be noted, that this model doesn't generate endogenous growth, however, it is simple and tractable and provides very intuitive results. One can assume different specifications of the law of motion of quality of intermediate products, which would allow for endogenous growth, for example, in scope of further research.

Chapter 3

METHODOLOGY

The main question of the paper is whether the frequency of certain alleles of DRD4 polymorphisms can explain the variation in the countries' technology adoption levels and some aggregate measures of innovations. To tackle this issue several regression specification are adopted. The baseline regressions will check whether will investigate the effect of each gene on the explainable variables:

$$Y_i = \beta_i FREQUENCY_i + \gamma_i Controls_i + \varepsilon_i \quad (1)$$

where *Y* is one of the measures of technology and innovations, *FREQUENCY* is the frequency of either 7R allele of VNTR polymorphism or C allele of 521 C/T polymorphism of DRD4, *Controls* is a vector of relevant control variables and *i* is a country index and ε is an error term. The frequency of genes in a population is supposed to be exogenous or at least predetermined. Genetic pool remains constant within a given population generation, there can be alterations only when genes are passed to the successors. If there are no mutations or genetic drift, the frequency of the alleles remains constant within the population according to Hardy-Weinberg principle. The alleles of the descendants are a sample of the alleles of their parents. These samples may differ due to some sampling errors, leading to a genetic drift (Barton et. al., 2007). However, if the population is large (like a population of the country) the speed of the genetic declines exponentially, it takes a lot of generations to change before the frequency of the alleles changes substantially. According to simulations conducted by Masel (2011), in the population of 5000, the frequency of two alleles with initial frequency is 50/50, it doesn't change over the subsequent 10 generations, which is approximately equal to 200 years speaking about human populations Thus the frequency of certain

alleles on modern population was predetermined a long time ago, they cannot be influenced by the modern level of technology and innovations of societies, thus, allele frequencies can be considered exogenous in equation (1).

The vector of controls includes the standard set of geographical variables, such as countries' absolute latitude and longitude and a dummy for countries, which do not have access to seas of oceans as in Gorodnichenko and Rolland (2011). Moreover, a relevant control is the measure of a diversity of population of a given country. Ashraf and Galor (2011) argue that genetic diversity may have a non-monotonic effect on economic development. On the one hand, heterogeneous population may benefit from a more diverse pool of productive knowledge and technologies. This hypothesis is supported by Hong and Page (2005) who develop a model in scope of which a group of heterogeneous agents better copes with finding a solution than a group of homogenous agents due to different perspectives, algorithms that are used for problem solving. To proxy ethnical diversity a measure of migration distance is used as in Ashraf and Galor (2011). It is assumed that all people migrated from the point of their origination in Africa (near the Ethiopian capital Addis-Ababa). The migration distance is calculated as the distance between Addis-Ababa and modern capital of the country, the migration route should be via land, if possible (for example, the migrants to Malaysia are assumed to move through Egypt, Saudi Arabia, Iran, Bangladesh, Myanmar and Thailand). The results are controlled for the population density. It is assumed that populations with higher density have more possibilities to spread the new ideas and technologies. Among other controls that may influence technological adoption progress are the quality of institutions, captured by the political regime and legal origin in the country, geographical barriers to diffusion – terrain ruggedness and percentage of land that lies near to ice-free coast. The level of human capital is supposed to influence technological level in the country, as well as the level of physical capital. One may argue that religion and the type of

culture, inherent to the society may also affect the innovative performance and technology adoption on the aggregate level. Due to limited number of observations it is impossible to account for all controls in one equation. Thus, a data reduction technique – principal components analysis – is used to decrease the dimensionality of the matrix of controls to or several vectors. This would help to eliminate the omitted variable bias, which reduces the reliability of previous estimations.

As was noted above, there is ambiguous evidence of the effect of *particular* genes on novelty-seeking behavior. To test the hypothesis that the process of technology adoption and innovations is guided by several rather than one gene, the specification in (1) is changed slightly so that now *FREQUENCY* represent a vector of allele frequencies for both 7R and C allele of corresponding DRD4 polymorphisms. All regression equations are estimated with heteroscedasticity robust standard errors. To check whether results are driven by outliers or not, a Huber (1964) estimation method is employed (HR).

Chapter 4

DATA DESCRIPTION

The main question of the paper is whether the presence of specific genetic markers may influence the process of technology adoption in the country. Thus the variables of interest should reflect technological advances of a particular state, which can be captured by the aggregate level of technology, measures of innovations in the economy and level of implementation of certain technologies.

Comin, Easterly and Gong (2010) developed an index that reflects country's technological advancement level as of 1500AD and 2000AD. The technology adoption index for 2000AD was calculated as the number of years a country lags behind the USA in particular technologies, taken from Comin, Hobijn and Rovito (2008) and normalized so that the score of the USA is unity.

There are numerous measures of innovations, which can be considered when studying technological advancement of the countries. First, OECD (2009) comprises a dataset of Main Science and Technology Indicators. The relevant variables that are considered are the number of researchers per thousand of population and the number of triadic (that are valid in Asia, USA and Japan) patents registered. Second, INSEAD (2009) computes a global innovation index based on innovation inputs (the measures such as education of the workers etc.) innovation environment and outputs (number of triadic patents). Thirdly, Economic Intelligence Unit (2009) constructed innovation performance index based on the measures of high-tech output, license fees, as a share of gross domestic product etc. Finally, Boston Consulting Group (2009) performed a survey to come up with a similar index of innovations, which comprises

innovation inputs (fiscal policies, innovation environment etc) and innovation outputs (reflected in R&D results, for example).

The most important explanatory variables in this paper are the frequency of specific genes in population. For the purposes of analysis of genetic influence on country-level of technology some aggregate measure of genetic markers has to be considered. Firstly, the frequency of C allele of 521 C/T polymorphism and 7R allele of 48VNTR polymorphism of DRD4 gene was calculated for separate ethnic groups based on population samples. There are several open databases that contain information on genetic frequencies: the Allele Frequency Database, the Human Genome Diversity Panel, the database of the National Center for Biotechnology Information. It is also possible to find the genetic frequency for certain ethnic groups in the articles which deal with genetic illnesses. For example, researchers who are interested whether a certain gene is responsible for a certain disease in the representatives of a particular ethnic group genotype two samples of people, first, the patients who suffer from the disease, second, a control group. The genotype of the second group is used when calculating the frequency of the gene for the whole population (if several studies are available for one ethnic group the frequency of the allele is computed as the average, weighted on the amount of control subjects in the survey – the sources of genetic data can be found in Appendix A). Secondly, the country-level frequency of the allele is calculated as the weighted average of frequencies of this allele in ethnic groups, which comprise countries population (the weights are the fraction of ethnic group in total population). The ethnical composition of nations is taken from Fearon (2003) and Alesina (2003).

The process of calculating allele frequencies can be illustrated using Ukraine, for example. The population of Ukraine consists basically of Ukrainians, but other ethnical groups, such as Russian or Jews, compose a substantial part of Ukrainian locals. Frequencies of 7R allele were calculated based on three studies: in the

study of Borinskaya et. al. (2003), two samples of Russians are genotyped, and one sample of Ukrainians, in Yirmiya et al. (2001) and Kotler et al. (1997) one may found the frequency of 7R allele for Jew people. Based on the sample size (the number of alleles that were investigated), the weighted average of allele frequencies was calculated for each ethnic group (see Table 1 for details).

Having the frequency of an allele in each group, one can calculate the frequency of the allele in a population, as a weighted average of group frequencies based on their share in total population of the country. For Ukraine the frequency of 7R allele thus equals to approximately 6%. The list of sources of genetic data as well as population frequencies of 7R and C allele can be found in Appendix A.

As was noted earlier, the heterogeneity of population may have an effect on the process of technology adoption. Among the possible candidates are the measures of genetic and ethnical diversity. Ashraf and Galor (2011) showed that genetic diversity may influence the economic development. However, it is more probably that ethnical diversity measures are more relevant for this as they directly influence the way people interact in the society. Fearon (2003) provides readers with three measures of ethnical diversity. Firstly, the measure of ethnical fractionalization of the country is constructed as $EF = 1 - \sum_i p_i^2$ where p refers to a fraction of a specific ethnical group in total population, i is an index for ethnical groups. Thus, if the country consists of one ethnical group its ethnical fractionalization score is 0, if of two groups, that correspond 50% of total population each – the score is 0.5, if three equal groups – 0.67 and so on. Since population diversity is supposed to differently influence the process of technological adoption on different continent, an interaction variable with a dummy for a continent was constructed. The second measure of ethnical diversity is cultural diversity, which accounts for cultural distance between groups. This measure takes into account the relatedness between the languages spoken by

ethnic groups populating the country. Finally, the third measure of diversity is taken by Fearon from Atlas Narodov Mira. The data for geographical controls is taken from Mayer and Zignago (2011). To calculate the density, country land area is taken from World Development Indicators database, constructed by the World Bank and population is taken from Maddison's Statistics on World Population, GDP and Per Capita GDP, 1-2008 AD. See Table 2 for descriptive statistics of main dependent and independent variables

Based on the standard deviation and range, it can be noted, that the frequency of 7R allele is more variable as the frequency of a C allele. The distribution of allele frequencies among countries can be seen on the map in Appendix B. What is interesting, 7R allele is more common in South American countries, than in East Asian, which is explained by the fact that indigenous population of South America is characterized by high frequencies of 7R allele. European nations have relatively medium level of 7R frequencies. With respect to the C allele, it should be noted, that East Asian countries are characterized by higher than average frequencies, while the population south-American countries (Columbia, Bolivia, Peru, Ecuador) have much lower frequencies of the allele.

The data on the political regime is taken from POLITY IV project (Monty and Jaggers (2002) constructed an index which reflects the level of totalitarity-democracy in the society). The data on legal origins was taken from La Porta et. al. (2008), a dummy for each type of legal origin was used (French, German, Scandinavian and Socialist). Data on terrain ruggedness as well as percentage of land that lies not further than 100 km from ice-free coast was taken from Nunn and Puga (2012). The ruggedness index incorporates information how much the elevation of different regions of the countries is different from each other thus creating obstacles to the free movement. Finally, the data on human capital is taken from Barro and Lee (2001). The variable of interest in this case is the

percentage of population which is older than 25 and has secondary education. Cultural variable is taken from Hofstede (2001), religion variables come from Barro and McCleary (2003) and indicate share of population who are adepts of one of the most widespread religions. Level of physical capital and values of social infrastructure is based on Hall & Jones (1999).

It should be noted, that the main drawback of the existing dataset is its small size. Genetic data is not available for every ethnic group, only countries for which the allele frequencies were known for a majority of population were considered in the analysis. Thus the selection of countries was not random which can lead to sample selection bias. Another source of bias may come from the fact that the regressors were calculated based on sample data. If these errors in independent variable are not correlated with the error term in regression equations, this may lead to attenuation bias.

Chapter 5

RESULTS AND DISCUSSION

This section contains empirical estimates of the association between population frequencies of C and 7R allele of DRD4 gene and aggregate measures of technological level and innovations.

Appendix C uses scatterplots to show correlations between the frequency of the certain allele and the measure of technology level or innovations. What can be inferred is that there is a positive relationship between the C allele and every measure of innovation or technology, used in the paper. However, the sign of a linear relationship between the dependent variable and a frequency of 7R allele is positive only in two cases of the cases (positive correlation with logarithm of technology adoption index and EIU Innovation Performance Index).

To check whether the discussed relationships are not accidental, different regression specifications were estimated. Tables 3 reports the estimated coefficients from a linear regression of technological measures on the frequency of 7R and C alleles. C allele is found to be significantly and positively correlated with the technology adoption index, patents per capita, innovation indexes of INSEAD and EIU. The results are economically significant as well. If, for example, population frequency of C allele increases by one standard deviation, or by 6.9%, log of technology adoption index increases by 0.21, or approximately half of a standard deviation. The number of patents per capita increases by 163% if the frequency of C allele increases by one standard deviation. Speaking about innovation indexes, if the frequency of C allele changes by 1 standard deviation, INSEAD and EIU indices change by approximately 4/10 of their standard deviations. To check whether these results are not driven by outliers, the same

regressions were estimated using Huber (1964) robust estimation method. The estimated results are reported in Table 4. The coefficient of influence of C allele on technology adoption index, number of patents per capita and INSEAD index remained roughly the same and significant. The influence on EIU index became marginally insignificant (t-statistics is 1.6).

However, these results may be biased due to the omitted variable bias. In purpose of elimination of selection bias, several specifications with different control variables were estimated. Firstly, results were controlled for geographical factors, such as absolute latitude (indicates the distance from equator, which may affect economic development through climate and associated diseases), absolute longitude (distance from Greenwich meridian is a proxy for distance from Great Britain, one of the most technologically advanced countries nowadays) and a dummy for landlocked countries (which are supposed to be less involved into the world economy due to lack of ports, and thus have less possibilities to keep up with the latest technological advancements). The results of corresponding regressions are reported in Table 5. With the inclusion of geographical controls, the effect of C allele on technology and innovations measures became less significant. The influence on technology adoption index became smaller by a fifth (increase in the frequency of C allele by one standard deviation increases technology adoption index by 0.45 standard deviations), however the influence on the number of patents per capita remained approximately the same. The influence of C allele on EIU index became insignificant, however, it becomes significant when HR regression is performed (see Table 6). With geographical controls, there is significant influence of frequency of 7R allele on technology adoption index (1 standard deviation change in allele frequency increases technology adoption index by 15-18%, which is, for example, the distance between Japan and Greece). Moreover, 7R allele becomes positively and significantly associated with EIU index.

As was previously argued, ethnic diversity may be a factor which could influence the level of technologies and innovations in the country. The effect is supposed to be non-monotonic, since a non-diverse country may lack competing ideas and solutions to existing problems, while a population of a very diverse country may not be able to come to a consensus due to cultural differences or lack of trust. There may be several means of controlling the non-monotonic effect of diversity. Firstly, a squared term of a diversity measure can be included into the regression. Secondly, one can construct an interaction term between a diversity measure and a continent dummy. For Africa it is expected, that the value of the coefficient of the variable should be negative, as its population is too diverse which hampers economic development, on the other hand, Europe and Asia may have reached an optimal moderate level of diversity, favorable for economic growth, thus the value of coefficient should be close to zero, finally, in America low degree of diversity may be detrimental for the development, thus the sign of the coefficient is expected to be positive. Therefore, the differences in the signs of coefficients will capture non-monotonic pattern of relationship between ethnic diversity and technology diffusion. As was noted earlier, three alternative measures of cultural diversity are employed: ethnic fractionalization (based on the weights of ethnic groups in population), cultural diversity (based on the distance between languages of ethnic groups) and the measure from Atlas Narodov Mira, composed by Soviet ethnographers. Tables 7 and 8 (Huber - robust) report the results of regressions with quadratic functional form. After controlling for ethnic diversity, the influence of frequency of C allele on technology adoption index was estimated to be statistically and economically significant (one standard deviation change in C allele frequency changes log technology adoption index by 0.5-0.6 standard deviations, based on the specification, not including regressions with Atlas Narodov Mira measure). It should be noted, that if Atlas Narodov Mira measure is used, some of the coefficients have negative and significant sign,

which contradicts to the main hypothesis of the paper. Based on the fact that this measure was constructed approximately 50 years ago, it may be outdated and not reflect the modern diversity patterns. The influence of frequency C allele on INSEAD and EIU indexes was found significant in most cases, the effect of 1 standard deviation change in C allele frequency ranged from 0.43-0.65 standard deviations on EIU index and 0.3-0.52 standard deviations on INSEAD index. The influence of 7R allele was majorly insignificant. The more or less robust and significant effect was found when the model is estimated using HR technique. Accordingly, one standard deviation increase in frequency of 7R allele changes the EIU index by 0.45-0.48 standard deviations.

Tables 9-10 contain the estimates of alternative specification with interaction variables between continent dummy and ethnic diversity measures. The effect of C allele on technology adoption index was proved to be of similar extent as estimated before. Interestingly, there is a large and significant effect of C allele frequency on the number of patents per capita (1 percentage point increase in allele frequency increases the number of patents per capita by 0.6%). However, when an outlier-robust regression is estimated, the value of the coefficient plummets and even becomes insignificant, in case when controlled for ethnical fractionalization. The effect of C allele on EIU index on average increased slightly, compared to other specifications. However, the effect of 7R allele in most cases remains insignificant. Final specification which includes the proxy for a diversity measure (migration distance) is represented in Tables 11-12. The influence of C allele becomes positive and significant in 5 out of 6 cases, the magnitude of influence on technological adoption index and INSEAD is comparable to previous estimates. Both allele frequencies now have significant and substantial effect on patents per million of population (the effect of one standard deviation increase in the frequency of allele ranges from over 2 standard

deviations increase in the ordinary OLS, to 4.5 standard deviations when Huber's estimation technique is employed).

Since the number of observations is low, it is impossible to include a full set of other possible control variables into the analysis. For this purposes, the dimensionality of the matrix of controls will be reduced using the principal components analysis. Among the considered variables are a proxy for the quality of institutions – political regime and legal origin capture whether the country has relatively extractive (for example, countries with totalitarian regime or social legal origin) or inclusive institutions. Moreover, Hall & Jones (1999) calculated an index of social infrastructure and accounts for the expropriation risk, corruption, law and order etc. Cultural controls include the dummy for a religion and a measure of individualism of a culture by Hofstede (2001), which is assumed to affect long-run economic growth (see Gorodnichenko and Roland 2010). The level of physical and human capital should also influence technological level in the country and the number of innovations. Finally, results are controlled for the physical barriers for technology diffusion – terrain ruggedness and percentage of land that lies within 100 miles from the shore and the density of the population as well as population density. Table 13 contains the results of estimations with the vectors, obtained from PCA analysis. To solve the tradeoff between the inclusion of more information and preserving degrees of freedom, two specifications with three and four principal components were estimated. In any case, the influence of frequency of C allele was in line with previous estimations. Other coefficients didn't show any robust pattern.

Table 14 contains the estimates of the coefficients of interest from all specifications of the econometric model. It can be inferred, that there is lack of evidence to suggest that there exists influence of 7R allele on technological level. However, the influence of C allele was found to be significant in most cases for

the level of technology, Economic Intelligence Unit and INSEAD measures of innovations. The effect is also economically significant, as 1 standard deviation increase in the frequency of C allele:

- increases technology adoption index by 0.4-0.7 standard deviations
- for significant coefficients, increases the EIU innovation index by 0.1-0.6 standard deviations
- for significant coefficients, increases the INSEAD global innovation index by 0.4-0.8 standard deviations.

Chapter 6

CONCLUSION

The purpose of this paper was to inspect whether population frequencies of 7R and C alleles of DRD4 gene influence aggregate the level of technologies and innovations in the country. The mechanism through which genes influence novelty-seeking behavior involves dopamine signal transmission. Dopamine is released when underlying action is associated with novelty seeking and serves as a kind of reward which activated dopamine receptors and lets the action to be performed. Different variations of dopamine encoding gene lead to different gene expression, which in turn shapes the way dopamine receptors behave.

According to the constructed economic growth model with three sectors and heterogeneous households (the source of heterogeneity was presence or absence of certain alleles which shift the utility function from innovative activity), frequencies of novelty-enhancing alleles have impact on aggregate level of technology (quality of products)

Population frequency C allele, which improves transcription activity, was found to be robustly associated with the level of technologies, captured by technology adoption index and measures of innovation by BCG and INSEAD. This association is economically significant as well. Another allele that was subject to analysis, 7R allele that increases resistance to dopamine antagonist, was not found to be robustly associated with technological measures or level of innovations.

One should cautiously treat the results of the estimation as they may be biased due to sample selection problems, errors in regressors. Low number of observations doesn't allow to control for all possible exogenous factors that may

influence the level of technology and innovations in the country. However, with the development of more advanced genotyping techniques, in future it should be possible to increase the sample of genotyped countries and obtain more reliable estimates.

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Table 1. Calculation of DRD 7R allele frequency for Ukraine

Ethnic group	Fraction in population	Average weighted allele frequency	Frequency of 7R allele	Allele sample size	Source
Jews	1%	19.7%	25%	136	Yirmiya et. al., 2001
			13%	108	Kotler et al 1997
Russians	22%	4.3%	4.4%	92	Borinskaya et. al., 2003
			4.2%	166	Borinskaya et. al., 2003
Ukrainians	73%	6.5%	6.5%	200	Borinskaya et. al., 2003

Table 2. Descriptive statistics

Variable	Obs	Mean	SD.	Min	Max
Frequency of alleles					
7R allele	27	13.9%	9.2%	0.0%	34.0%
C allele	27	40.6%	6.9%	26.1%	48.5%
Measures of technology and innovations					
Technology adoption index	24	0.62	0.22	0.25	1.01
Number of researchers per 1000 workers	17	6.53	3.45	0.78	13.96
Number of patents per capita	17	0.04	0.04	0.00	0.11
INSEAD: Global Innovation Index	26	3.66	1.07	2.05	5.28
EIU: Innovation Performance Index	23	7.48	1.89	4.58	10.00
BCG: Innovation Index	24	0.65	1.25	-1.37	2.45
Measures of ethnical diversity					
Ethnic fractionalization	24	0.22	0.19	0.00	0.68
Cultural diversity	26	0.31	0.22	0.00	0.74
ANM measure	26	0.19	0.17	0.00	0.66

Table 3. OLS: 7R and C alleles

	(1)	(2)	(3)	(4)	(5)	(6)
	Log of Technology Adoption Index	Log of researchers per 1000 Workers	Log of Patents per Capita	INSEAD index	EIU index	BCG index
7R allele	0.977	0.104	5.453	-1.740	-1.395	-0.654
	(0.777)	(2.700)	(7.254)	(1.757)	(4.818)	(2.217)
C allele	3.131***	6.324	27.26***	6.056**	11.40*	5.981
	(0.865)	(4.389)	(8.835)	(2.649)	(6.109)	(5.341)
Observations	25	18	18	27	24	16
R-squared	0.304	0.151	0.288	0.212	0.147	0.191

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 indicate significance level

Table 4 HR: 7R and C alleles, no controls

	(1)	(2)	(3)	(4)	(5)	(6)
	Log of Technology Adoption Index	Log of researchers per 1000 Workers	Log of Patents per Capita	INSEAD index	EIU index	BCG index
7R allele	0.967	-1.302	6.031	-1.649	-1.127	-2.508
	(0.854)	(1.402)	(7.507)	(2.468)	(5.586)	(1.496)
C allele	3.245***	-1.580	28.14**	6.573**	12.51	-3.665
	(1.087)	(2.846)	(12.38)	(3.166)	(7.787)	(3.236)
Observations	25	17	18	27	24	15
R-squared	0.293	0.072	0.259	0.201	0.138	0.221

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 indicate significance level

Table 5 OLS: of 7R and C alleles with geographical controls.

	(1) Log of Technology Adoption Index	(2) Log of researchers per 1000 Workers	(3) Log of Patents per Capita	(4) INSEAD index	(5) EIU index	(6) BCG index
7R allele	1.653*	-0.677	6.197	-0.428	0.570	0.360
	(0.822)	(3.484)	(9.020)	(2.445)	(7.022)	(2.999)
C allele	2.655***	5.439	28.18**	4.084	8.782	7.520
	(0.625)	(3.879)	(11.46)	(2.428)	(6.679)	(7.202)
Observations	25	18	18	27	24	16
R-squared	0.586	0.291	0.325	0.510	0.442	0.246

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 indicate significance level. The control variables are absolute latitude, absolute longitude and dummy for landlocked countries

Table 6. HR: 7R and C alleles with geographical controls

	(1) Log of Technology Adoption Index	(2) Log of researchers per 1000 Workers	(3) Log of Patents per Capita	(4) INSEAD index	(5) EIU index	(6) BCG index
7R allele	1.967***	-1.560	6.821	0.747	11.09**	-0.948
	(0.566)	(1.929)	(10.39)	(2.104)	(4.234)	(4.035)
C allele	2.208***	3.406	29.32*	2.956	13.32**	6.617
	(0.718)	(2.921)	(16.33)	(2.526)	(5.578)	(5.374)
Observations	25	17	18	27	24	15
R-squared	0.779	0.716	0.282	0.622	0.697	0.340

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level.. The control variables are absolute latitude, absolute longitude and dummy for landlocked countries

Table 7. OLS: 7R and C alleles with geographical and diversity controls I.

	(1)	(2)	(3)	(4)	(5)	(6)
	Log of Technology Adoption Index	Log of researchers per 1000 Workers	Log of Patents per Capita	INSEAD index	EIU index	BCG index
			Panel A:			
7R allele	1.092	-0.834	7.441	-1.174	2.092	2.433
	(0.952)	(3.763)	(8.716)	(2.708)	(6.628)	(4.023)
C allele	3.111***	5.499	23.78	6.002**	11.86*	6.987
	(0.669)	(4.745)	(14.07)	(2.560)	(6.627)	(8.014)
Observations	25	18	18	26	23	16
R-squared	0.634	0.293	0.392	0.562	0.498	0.297
			Panel B:			
7R allele	1.183	-1.153	5.058	-1.434	0.104	-1.252
	(0.992)	(3.342)	(10.59)	(2.986)	(7.103)	(3.079)
C allele	3.621***	7.700	32.57*	8.034**	16.91**	2.266
	(0.844)	(4.976)	(16.31)	(2.835)	(6.817)	(7.192)
Observations	25	18	18	26	23	16
R-squared	0.669	0.354	0.350	0.625	0.540	0.552
			Panel C:			
7R allele	0.967	-0.104	-0.938	-2.874	-4.303	-1.096
	(1.061)	(6.730)	(17.18)	(2.490)	(7.616)	(3.169)
C allele	2.927***	3.761	4.080	4.530	6.378	2.907
	(0.758)	(7.979)	(20.83)	(2.638)	(6.175)	(7.428)
Observations	24	17	17	25	22	16
R-squared	0.653	0.379	0.493	0.662	0.628	0.400

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity and its squared term (Panel A: ethnic diversity, Panel B: cultural diversity, Panel C: Atlas Narodov Mira diversity measure).

Table 8. HR: 7R and C alleles with geographical, diversity controls II

	(1)	(2)	(3)	(4)	(5)	(6)
	Log of Technology Adoption Index	Log of researchers per 1000 Workers	Log of Patents per Capita	INSEAD index	EIU index	BCG index
			Panel A:			
7R allele	0.869	0.0536	17.69***	0.204	9.995**	-1.180
	(0.591)	(0.852)	(1.140)	(2.067)	(4.139)	(3.322)
C allele	2.759***	3.528**	17.89***	4.686*	17.20***	-5.142
	(0.714)	(1.280)	(1.713)	(2.413)	(5.532)	(4.753)
Observations	25	17	17	26	22	12
R-squared	0.831	0.954	0.992	0.727	0.763	0.550
			Panel B:			
7R allele	0.613	-0.515	5.797	-3.431	9.263**	-2.545
	(0.847)	(1.585)	(11.82)	(2.397)	(3.896)	(3.175)
C allele	3.509***	5.379*	33.07	7.050**	14.45**	1.625
	(1.100)	(2.577)	(20.03)	(3.093)	(5.763)	(3.439)
Observations	25	17	18	26	23	13
R-squared	0.658	0.845	0.289	0.652	0.787	0.905
			Panel C:			
7R allele	1.346***	-6.356***	-25.54***	0.613	-0.503	-3.610
	(0.451)	(1.693)	(1.899)	(1.154)	(4.383)	(3.795)
C allele	1.998***	-3.959	-22.97***	2.686*	6.655	-0.178
	(0.556)	(2.657)	(2.981)	(1.408)	(5.799)	(5.319)
Observations	24	17	17	25	22	15
R-squared	0.896	0.944	0.988	0.897	0.768	0.644

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity and its squared term (Panel A: ethnic diversity, Panel B: cultural diversity, Panel C: Atlas Narodov Mira diversity measure).

Table 9. OLS: 7R and C alleles with geographical diversity controls II

	(1)	(2)	(3)	(4)	(5)	(6)
	Log of Technology Adoption Index	Log of researchers per 1000 Workers	Log of Patents per Capita	INSEAD index	EIU index	BCG index
			Panel A:			
7R allele	2.561*	16.70	66.80	5.627	14.60	15.35**
	(1.222)	(12.32)	(42.90)	(3.534)	(9.450)	(4.993)
C allele	3.161***	17.52	61.80*	6.828**	16.00	11.28**
	(1.020)	(10.73)	(32.32)	(3.036)	(11.79)	(3.375)
Observations	25	18	18	26	23	16
R-squared	0.671	0.456	0.486	0.646	0.587	0.647
			Panel B:			
7R allele	2.088	13.74	55.68	2.726	16.07*	15.25*
	(1.423)	(9.533)	(32.61)	(4.240)	(8.219)	(6.708)
C allele	3.157***	16.92	61.99*	7.535**	19.17**	12.56**
	(1.064)	(9.766)	(27.70)	(2.834)	(7.321)	(3.618)
Observations	25	18	18	26	23	16
R-squared	0.700	0.481	0.541	0.703	0.640	0.722

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity (interaction with continents) (Panel A: ethnic diversity, Panel B: cultural diversity).

Table 10. HR: 7R and C allele with geographical, diversity controls II

	(1)	(2)	(3)	(4)	(5)	(6)
	Log of Technology Adoption Index	Log of researchers per 1000 Workers	Log of Patents per Capita	INSEAD index	EIU index	BCG index
			Panel A:			
7R allele	1.378	5.860	9.196	-0.121	15.37***	11.56*
	(1.032)	(4.961)	(32.72)	(3.203)	(4.014)	(5.481)
C allele	2.263**	8.494*	11.53	1.687	21.21***	8.275
	(0.850)	(3.964)	(26.14)	(2.594)	(4.122)	(4.273)
Observations	23	17	17	24	22	15
R-squared	0.864	0.949	0.800	0.832	0.946	0.837
			Panel B:			
7R allele	1.136	-0.457	20.08	-2.122	9.044	11.94
	(1.216)	(2.953)	(23.73)	(3.369)	(9.800)	(6.871)
C allele	2.652***	3.377	39.75*	2.651	13.75*	9.738*
	(0.811)	(2.523)	(20.27)	(2.202)	(7.125)	(4.829)
Observations	24	17	17	24	21	14
R-squared	0.892	0.977	0.888	0.874	0.803	0.802

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity (interaction with continents) (Panel A: ethnic diversity, Panel B: cultural diversity).

Table 11. OLS: 7R and C allele with geographical controls, migration distance

	(1) Log of Technology Adoption Index	(2) Log of researchers per 1000 Workers	(3) Log of Patents per Capita	(4) INSEAD index	(5) EIU index	(6) BCG index
7R allele	2.404**	2.377	19.19*	2.999	6.043	4.807**
	(0.859)	(4.819)	(9.827)	(2.408)	(4.765)	(1.416)
C allele	3.057***	7.313	37.01**	6.463**	12.04**	8.657***
	(0.875)	(6.006)	(11.46)	(2.879)	(5.481)	(2.314)
Observations	24	17	17	25	22	15
R-squared	0.670	0.448	0.702	0.716	0.704	0.899

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity (log of migration distance) and its squared term.

Table 12. HR 7R and C allele, geographical controls and migration distance

	(1) Log of Technology Adoption Index	(2) Log of researchers per 1000 Workers	(3) Log of Patents per Capita	(4) INSEAD index	(5) EIU index	(6) BCG index
7R allele	2.134***	11.06***	48.98***	5.710**	2.489	7.530
	(0.581)	(2.438)	(6.346)	(2.027)	(4.075)	(4.359)
C allele	3.400***	17.46***	83.35***	9.282***	8.714	12.35*
	(0.639)	(3.420)	(8.788)	(2.157)	(5.143)	(5.625)
Observations	24	15	16	25	22	14
R-squared	0.855	0.945	0.948	0.811	0.773	0.726

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity (log of migration distance) and its squared term.

Table 13. OLS: 7R and C allele with geographical, diversity controls, and PCA vectors

	(1) Log of Technology Adoption Index	(2) INSEAD index	(3) EIU index
		Panel A:	
7R allele	1.675*	0.557	6.693
	(0.892)	(0.672)	(5.502)
C allele	3.947***	2.059**	15.29**
	(1.158)	(0.827)	(6.820)
Observations	22	23	22
R-squared	0.850	0.986	0.804
		Panel B:	
7R allele	0.132	-1.743	-0.600
	(0.917)	(2.267)	(6.466)
C allele	2.559**	4.648	8.626
	(1.047)	(3.479)	(6.769)
Observations	22	23	22
R-squared	0.791	0.832	0.742

Notes: Robust standard errors in parentheses, *** p<0.01, ** p<0.05, * p<0.1 significance level. The control variables are absolute latitude, absolute longitude, dummy for landlocked countries, measure of diversity (ethnic fractionalization) and its squared term. Panel A: three PCA vectors, Panel B: four PCA vectors.

Table 14. Summary of results

(1)	(2)	(3)	(4)	(5)	(6)	(7)
		7R allele			C allele	
	Log of Technology Adoption Index	EIU Index	INSEAD Index	Log of Technology Adoption Index	EIU Index	INSEAD Index
(3)	0.977	-1.74	-1.395	3.131***	6.056**	11.40*
(4)	0.967	-1.649	-1.127	3.245***	6.573**	12.51
(5)	1.653*	-0.428	0.57	2.655***	4.084	8.782
(6)	1.967***	0.747	11.09**	2.208***	2.956	13.32**
(7.a)	1.092	-1.174	2.092	3.111***	6.002**	11.86*
(7.b)	1.183	-1.434	0.104	3.621***	8.034**	16.91**
(7.c)	0.967	-2.874	-4.303	2.927***	4.53	6.378
(8.a)	0.869	0.204	9.995**	2.759***	4.686*	17.20***
(8.b)	0.613	-3.431	9.263**	3.509***	7.050**	14.45**
(8.c)	1.346***	0.613	-0.503	1.998***	2.686*	6.655
(9.a)	2.561*	5.627	14.6	3.161***	6.828**	16
(9.b)	2.088	2.726	16.07*	3.157***	7.535**	19.17**
(10.a)	1.378	-0.121	15.37***	2.263**	1.687	21.21***
(10.b)	1.136	-2.122	9.044	2.652***	2.651	13.75*
(11)	2.404**	2.999	6.043	3.057***	6.463**	12.04**
(12)	2.134***	5.710**	2.489	3.400***	9.282***	8.714
(13.a)	1.675*	0.557	6.693	3.947***	2.059**	15.29**
(13.b)	0.132	-1.743	-0.6	2.559**	4.648	8.626

Notes: This table contains estimated coefficients from reported regressions. *** p<0.01, ** p<0.05, * p<0.1 significance level. Column (1) indicates specification – number of table and panel in it. Columns (2)-(4) have coefficients of 7R frequency, columns (5)-(7) – of C allele frequency

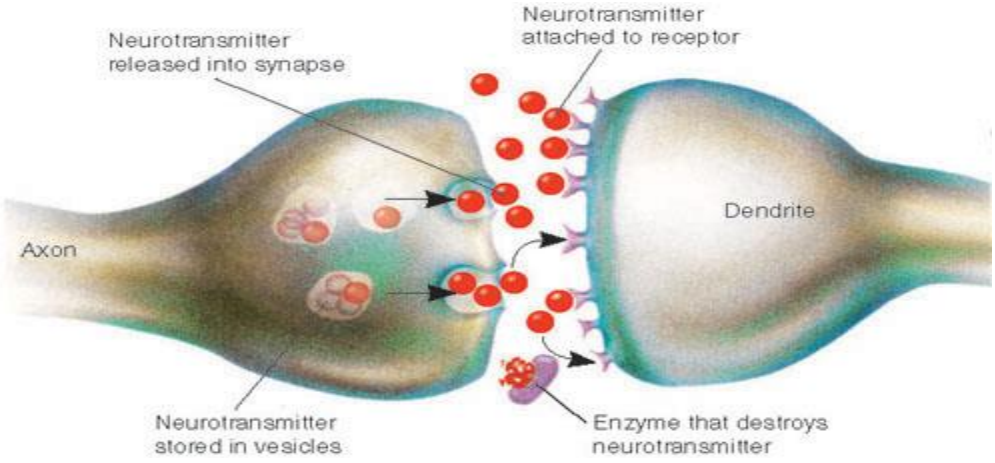

Figure 1. Synapse

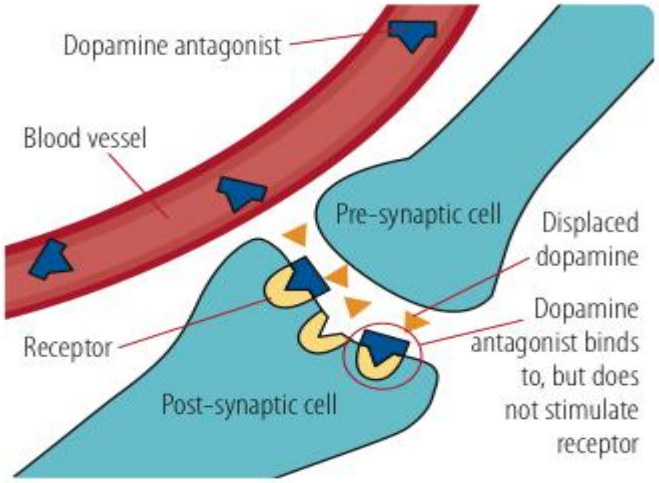

Figure 2. Action of dopamine antagonists

APPENDIX A. SOURCES OF ALLELE FREQUENCIES

Table A1. Sources of DRD4 frequency data - 7R allele

Continent	Population	Source	Allele sample size	7R allele frequency
Africa	Biaka	Chang et. al., 1996	124	14%
Africa	Mbuti	Chang et. al., 1996	74	16%
Africa	Bantu	Chang et. al., 1996	80	19%
Africa	San Bushmen	Chang et. al., 1996	44	0%
Africa	Yoruba	Naka et. al., 2011	112	30%
Asia	Druze	Chang et. al., 1996	50	6%
Asia	Indian Muslims	Gosh, Seshadri 2005	130	4%
Asia	Ezhavas	Gosh, Seshadri 2005	148	7%
Asia	Nairs	Gosh, Seshadri 2005	114	16%
Asia	Marathas	Gosh, Seshadri 2005	116	11%
Asia	Kachari	Chang et. al., 1996	36	11%
Asia	Kachari	Chen et. al., 1999	54	11%
Asia	Muslim	Bhaduri et. al., 2007	348	0%
Asia	Atayal	Chang et. al., 1996	56	0%
Asia	Han, Taiwan	Chang et. al., 1996	84	0%
Asia	Han, SFBA	Chang et. al., 1996	98	0%
Asia	Han in China	Li et. al., 1997	308	0%
Asia	Han in Taiwan	Hong et. al., 1997	86	0%
Asia	CHB: Han Chinese in Beijing, China	Naka et. al., 2011	88	0%
Asia	Japanese in the USA	Chang et. al., 1996	102	1%
Asia	japanese	Nanko et. al., 1993	100	1%
Asia	japanese	Inoue et. al., 1993	162	1%
Asia	japanese	Ono et. al., 1997	104	0%
Asia	japanese	Tanaka et. al., 1995	306	0%
Asia	JPT: Japanese in Tokyo, Japan	Naka et. al., 2011	140	1%
Asia	Koreans	Reist et. al., 2007	78	1%
Asia	Koreans	Kang et. al., 2008	146	0%
Asia	Filipinos	Reist et. al., 2007	670	0%
Asia	Cambodians, Khmer	Chang et. al., 1996	50	0%

Table A1. Sources of DRD4 frequency data - 7R allele (Cont.)

Continent	Population	Source	Sample size	7R allele frequency
Asia	Malay	Chang et. al., 1996	24	17%
Asia	Tatars	Borinskaya et. al., 2003	166	3%
Asia	Kazakhs	Borinskaya et. al., 2003	152	0%
Asia	Israeli Arabs	Kotler et. al., 1997	112	11%
Asia	Sephardic Jews	Kotler et. al., 1997	108	13%
Europe	Danes	Chang et. al., 1996	64	16%
Europe	Finns	Chang et. al., 1996	66	6%
Europe	Finns	Lahti et. al., 2005	4298	16%
Europe	Finns	Adamson et. al., 1995	226	17%
Europe	Hungarian	Nemoda et. al., 2010	356	19%
Europe	Hungarian	Ronai et. al., 2000	1196	20%
Europe	Swedes	Chen et. al., 1999	130	16%
Europe	Swedes	Geijeter 1997	130	16%
Europe	Spanish	Chen et. al., 1999	64	14%
Europe	Spanish	Pérez de Castro et. al., (1994)	92	11%
Europe	German	Strobel et. al., 2003	230	19%
Europe	German	Szantai et. al., 2005	394	15%
Europe	German	Franke et. al., 2000	120	16%
Europe	Italian	Szantai et. al., 2005	212	13%
Europe	Italian	Szantai et. al., 2005	190	14%
Europe	Italian	Seretti et. al., 1999	942	15%
Europe	Italian	Seretti et. al., 1998	158	15%
Europe	Dutch	Bakker et. al., 2004	198	17%
Europe	Dutch	Bakermans-Kranenburg et. al., 2008	148	28%
Europe	Dutch	Colzato et. al., 2010	128	31%
Europe	Polish	Dragan et. al., 2006	400	27%
Europe	Greeks	Roussos et. al., 2010	504	14%
Europe	Ukrainians	Borinskaya et. al., 2003	200	7%
Europe	Russians VUR	Borinskaya et. al., 2003	92	4%
Europe	Russians CR	Borinskaya et. al., 2003	166	4%

Table A1. Sources of DRD4 frequency data - 7R allele (Cont.)

Continent	Population	Source	Sample size	7R allele frequency
Europe	Croatia	Oruc et. al., 1997	142	17%
Europe	Israelites	Yirmiya	68	25%
Oceania	New zeland (Caucasians)	Mill et. al., 2002	1760	19%
North America	Pima, Arizona	Chang et. al., 1996	70	22%
North America	Pima, Mexico	Kidd, unpublished	104	17%
North America	Maya, Yucatan	Chang et. al., 1996	100	39%
South America	Quechuan (Peru)	Chang et. al., 1996	44	45%
South America	Mapuches	Martinez-Marignac & Bianchi, 2006	44	11%
South America	Ayore´os	Martinez-Marignac & Bianchi, 2006	8	63%
South America	Lenguas	Martinez-Marignac & Bianchi, 2006	16	19%

Table A2. Sources of DRD4 frequency data – C allele

Continent	People	Source	C allele	Allele sample size
Africa	Biaka	ALFRED	34.8%	138
Africa	Hausa	ALFRED	33.3%	72
Africa	Ibo	ALFRED	42.0%	88
Africa	Mbuti	ALFRED	47.0%	66
Africa	Yoruba	ALFRED	39.3%	150
Africa	Jews, Ethiopian	ALFRED	53.2%	62
Africa	African Americans	ALFRED	24.0%	156
Asia	Druze	ALFRED	40.7%	140
Asia	Jews, Yemenite	ALFRED	41.9%	86
Asia	Ami	ALFRED	32.5%	80
Asia	Atayal	ALFRED	16.3%	80
Asia	Chinese	Ho et. al., 2008	40.3%	168
Asia	Chinese	Lai et. al., 2010	42.8%	300
Asia	Chinese	Li et. al., 2000	44.5%	644
Asia	Han	Xing et. al., 2003	39.1%	412
Asia	Han	ALFRED	41.3%	422
Asia	Han	ALFRED	32.6%	92
Asia	Japanese	ALFRED	35.3%	116
Asia	Japanese	Okuyama et. al., 2000	46.8%	94
Asia	Japanese	Okuyama et. al., 1999	41.0%	538
Asia	Japanese	Okuyama et. al., 2000	41.0%	294
Asia	Japanese	Mitsuyasu et., al., 1999	53.5%	172
Asia	Japanese	Mitsuyasu et., al., 2006	37.1%	478
Asia	Japanese	Ujike et. al., 2009	45.3%	486
Asia	Korean	Lee et. al., 2003	46.0%	202
Asia	Cambodians, Khmer	ALFRED	26.1%	46
Europe	Danes	ALFRED	45.7%	94
Europe	Finns	ALFRED	40.0%	70
Europe	Finns	Ekelund et. al., 2001	42.1%	382
Europe	Hungarian	Szantai et. al., 2005	46.5%	1196

Table A2. Sources of DRD4 frequency data – C allele (Cont.)

Continent	People	Source	C allele	Allele sample size
Europe	Hungarian	Ronai et. al., 2001a	43.0%	
Europe	Hungarian	Nemoda et. al., 2010	47.5%	178
Europe	Hungarian	Ronai et. al., 2001b	20.2%	218
Europe	Irish	ALFRED	34.8%	184
Europe	Russians	ALFRED	18.8%	96
Europe	Russians	Golimbet et. al., 2005	44.0%	220
Europe	German	Strobel et. al., 2003	40.0%	230
Europe	German	Strobel et. al., 2002	49.9%	552
Europe	Swedish	Johnsson et. al., 2001	42.0%	776
Europe	UK	Munafo et. al., 2006	45.2%	
Europe	Spanish	Kramer et. al., 2007	47.1%	1312
Oceania	Melanesian, Nasioi	ALFRED	43.2%	44
Oceania	Micronesians	ALFRED	27.8%	72
Oceania	New Zeland	Joyce et. al., 2003	41.4%	292
NorthAmerica	Cheyenne	ALFRED	26.4%	106
NorthAmerica	Pima, Arizona	ALFRED	6.0%	100
NorthAmerica	Pima, Mexico	ALFRED	20.6%	102
NorthAmerica	Pima, Mexico	ALFRED	23.4%	192
NorthAmerica	Maya, Yucatan	ALFRED	13.7%	102
NorthAmerica	USA	Nemoda et. al., 2010	39.4%	198
SouthAmerica	Karitiana	ALFRED	4.9%	102
SouthAmerica	Surui	ALFRED	10.9%	92
SouthAmerica	Ticuna	ALFRED	37.3%	134

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Table A3. Calculated allele frequencies by countries.

Country	7R allele	C allele	Country	7R allele	C allele
ECUADOR	34.01%	28.50%	ARGENTINA	14.78%	42.92%
BOLIVIA	32.15%	26.08%	ITALY	14.53%	
POLAND	27.26%		DENMARK	14.00%	45.70%
IRELAND	25.60%	34.80%	CYPRUS	13.90%	
MEXICO	22.22%	29.95%	GREECE	13.90%	
NETHERLANDS	21.71%		CHILE	13.41%	31.79%
AUSTRALIA	21.48%		GREAT BRITAIN (United Kingdom)	13.17%	45.18%
NEW ZEALAND	19.40%	39.47%	ISRAEL	12.57%	
HUNGARY	19.26%	44.81%	MALAYSIA	11.80%	
SOUTH AFRICA (Zuid Afrika)	18.75%		UKRAINE	5.98%	
CROATIA (Hrvatska)	17.00%		RUSSIAN FEDERATION	4.29%	36.34%
UNITED STATES	16.95%	40.94%	PHILIPPINES	4.29%	
PARAGUAY	16.64%	45.57%	SINGAPORE	2.77%	40.64%
GERMANY (Deutschland)	16.57%	46.99%	KAZAKHSTAN	2.75%	
SWITZERLAND (Confederation of Helvetia)	16.28%	46.99%	BANGLADESH	1.09%	
SWEDEN	15.99%	42.00%	JAPAN	0.48%	42.11%
FINLAND	15.65%	41.83%	CAMBODIA	0.00%	26.26%
DOMINICAN REPUBLIC	15.41%	46.98%	CHINA	0.00%	40.64%
VENEZUELA	15.33%	47.02%	KOREA (Democratic Peoples Republic of [North] Korea)	0.00%	48.50%
COLOMBIA	15.25%	37.48%	KOREA (Republic of [South] Korea)	0.00%	48.50%
SPAIN	15.17%	47.10%	TAIWAN (Chinese Taipei for IOC)	0.00%	
COSTA RICA	15.02%	47.03%	NIGER		33.30%
CANADA	14.97%		NIGERIA		38.50%
UGANDA	14.79%		CHILE		31.79%
			PERU		27.99%

APPENDIX B. FIGURES

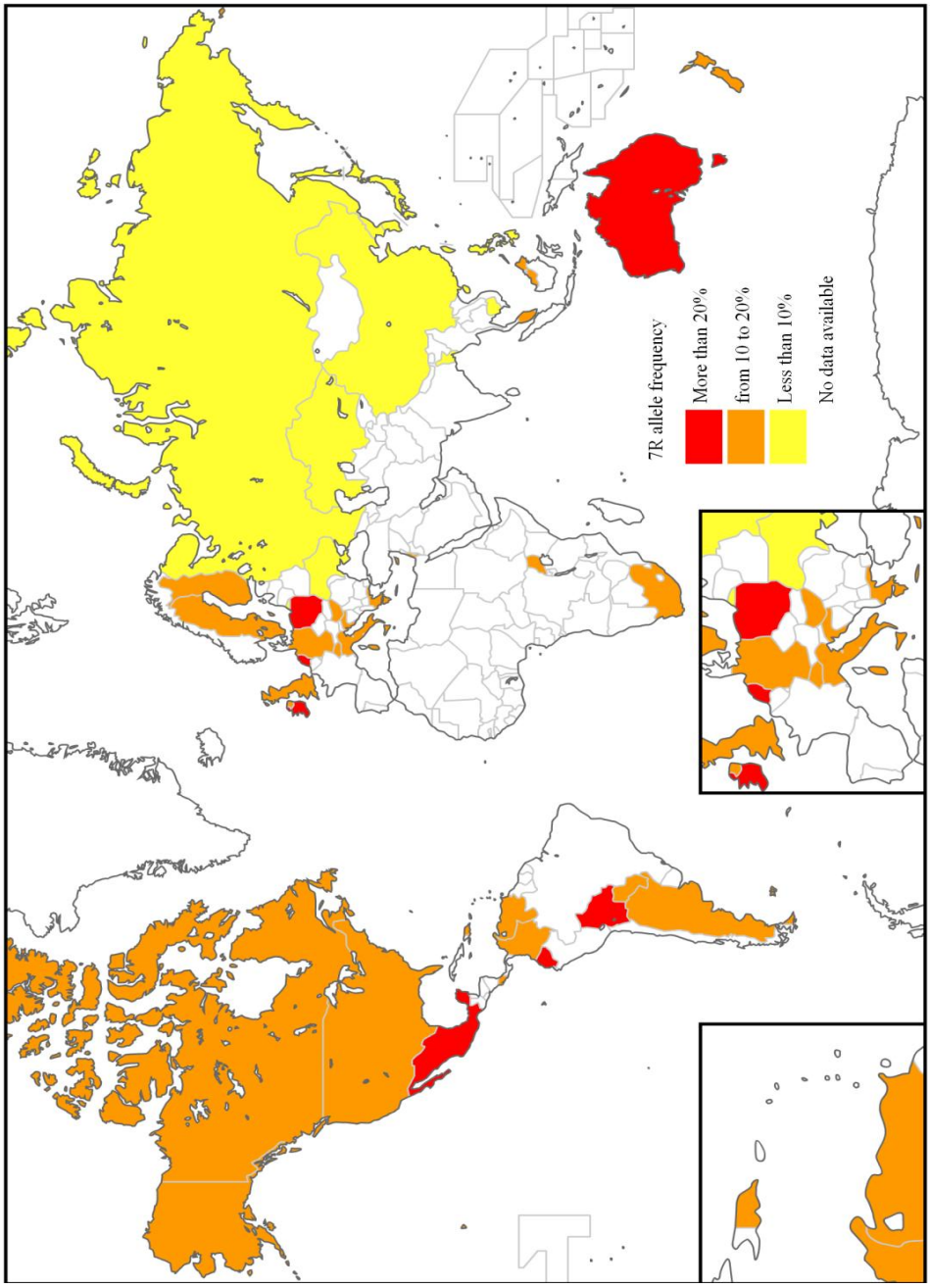

Figure B1. Distribution of 7R allele frequencies

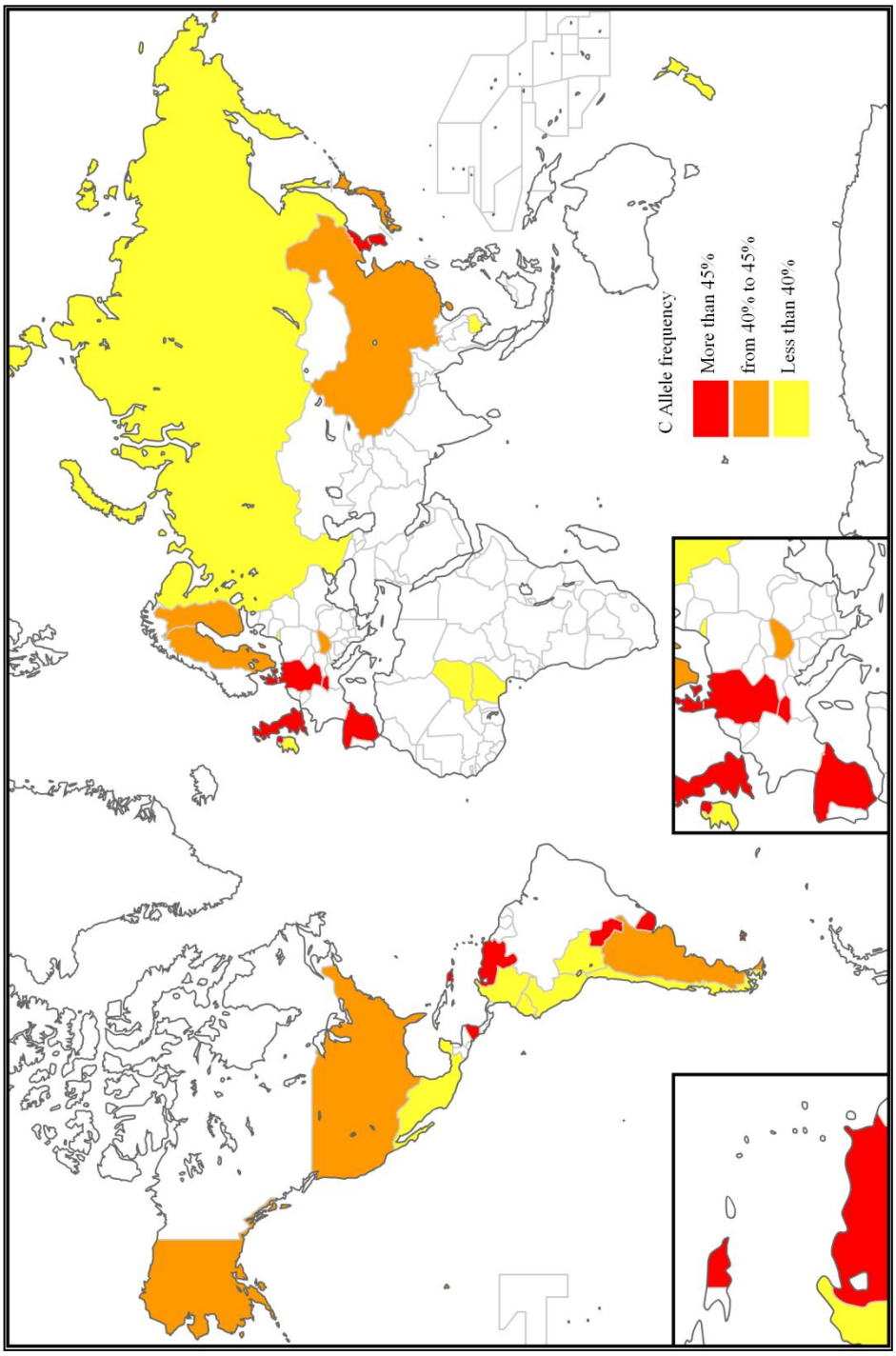

Figure B2. Distribution of C allele frequencies

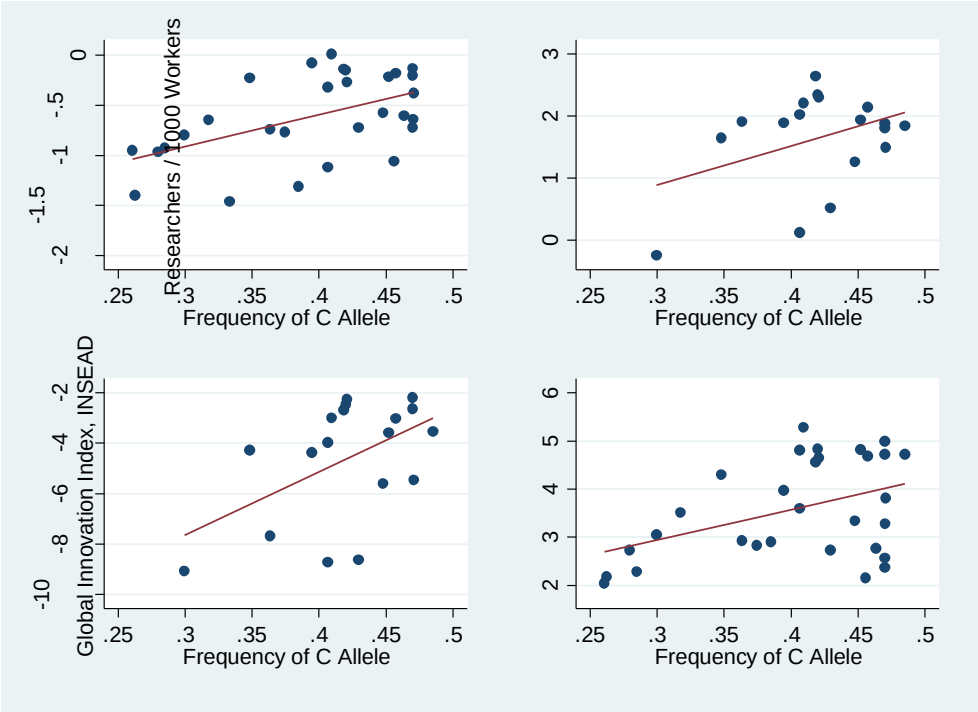

Figure B3. Scatterplots: C allele and technology measures

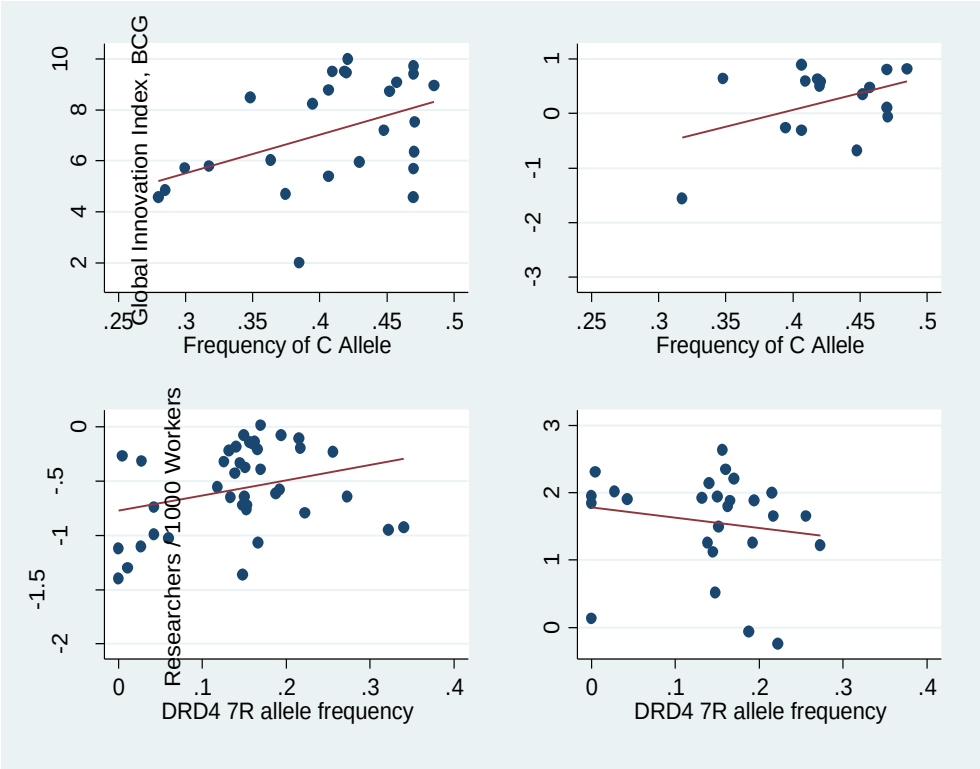

Figure B4. Scatterplots C and 7R alleles and technology measures

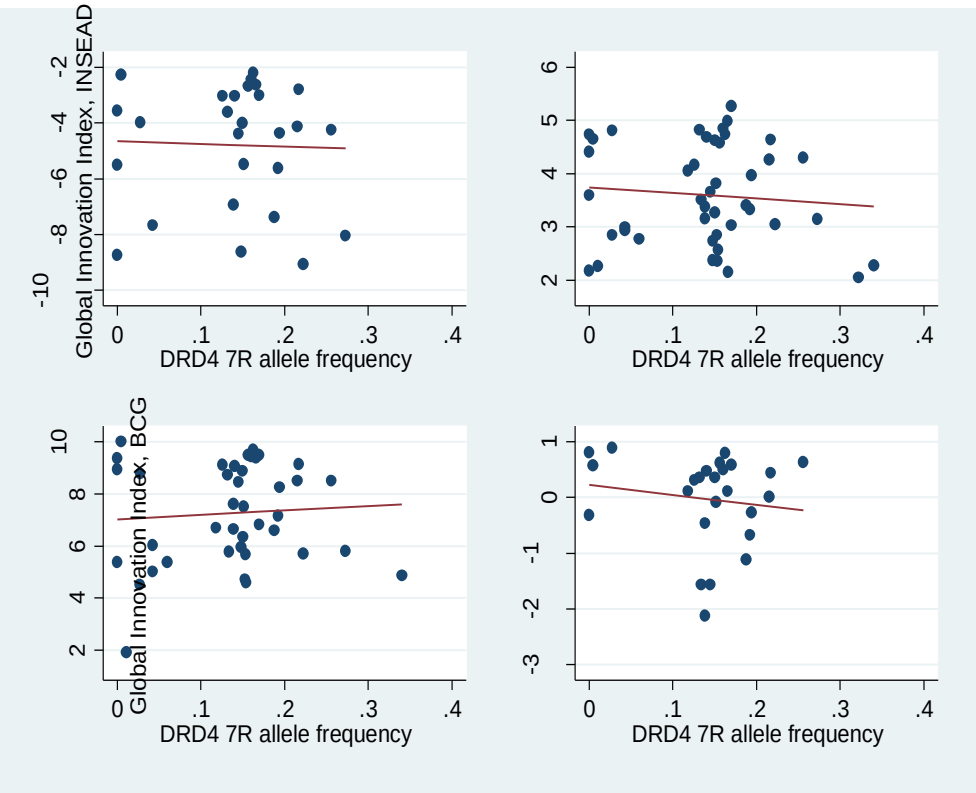

Figure B5. Scatterplots: 7R allele and technology measures