Ambiguity Aversion and Familiarity Bias:

Evidence from Behavioral and Gene Association Studies

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Abstract It is increasingly recognized that decision making under uncertainty does not depend only on probabilities, but also on psychological factors. People display ambiguity aversion in preferring to bet on events with known probabilities rather than those for which probabilities are not known. People also tend to bet on uncertainty arising from a familiar source rather than from an unfamiliar source. Using 325 Beijing subjects, we conduct the first neurogenetic study of ambiguity aversion and familiarity bias in an incentivized choice experiment. For ambiguity aversion, 49.4% of the subjects chose to bet on the 50-50 urn despite the unknown urn paying 20% more. For familiarity bias, 39.6% of the subjects chose to bet on whether the temperature on a historic day in Beijing was even or odd rather than choose the corresponding bet with Tokyo temperature for the same day even though the Tokyo bet would pay 20% more. We genotype subjects for anxiety-related candidate genes and find the serotonin transporter polymorphism associated with familiarity bias but not ambiguity aversion while the dopamine D5 receptor gene and estrogen receptor beta gene are associated with ambiguity aversion only among female subjects. Our finding contributes to a deeper understanding of decision making under uncertainty beyond revealed preference.

Keywords: *Ambiguity Aversion, Familiarity Bias, Source Dependence, Genes, Dopamine, DRD5, Serotonin, 5-HTTLPR, Estrogen, ESR2, Experimental Economics, Neuroeconomics*

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We thank Wang Rui, Wu Qingyu, and Ye Qiaofeng for assistance in conducting the behavioral experiments, and Idan Shalev for doing genotyping. Financial support from the Hong Kong University of Science and Technology, as well as National University of Singapore is gratefully acknowledged. Financial support from the Research Grants Council, Hong Kong, the Hong University of Science and Technology, and the National University of Singapore is gratefully acknowledged.

Introduction

Many have attributed the study of probability to controversies on how best to engage in games of chance by Pascal and Fermat four hundred years ago. The subject developed rapidly during the 18th century, but it was not until the work of Kolmogorov (1956) in the 20th century that we have a precise definition of probability in terms of the relative frequency of an event which can be repeated. Around the same time, Ramsey (1926) initiated another strand of probabilistic thinking that is based on decision making and is applicable to non-repeatable events. For instance, if one is indifferent between betting on whether the trailing digit of the Hang Seng Index will turn up odd or else even the next day, one might say that these two events are, subjectively speaking, equally likely. Subjective probability was given an axiomatic foundation by Savage (1954) building on the expected utility model of von Neumann and Morgenstern (1944).

Implicit in both the objective and the subjective views of probability is the notion that a lottery is fully described by its outcomes and associated probabilities. In this light, it is remarkable that Keynes had offered a contrarian view in 1921 by positing an additional psychological consideration – "If two probabilities are equal in degree, ought we, in choosing our course of action, to prefer that one which is based on a greater body of knowledge?" He illustrated this observation with an example of two urns, one containing fifty black balls and fifty red balls while another contains one hundred balls of either color.

This example reappeared in Ellsberg (1961) who observed that people tend to be ambiguity averse in preferring to bet on the urn with known probabilities rather than one with unknown probabilities. The phenomenon of ambiguity aversion is puzzling since people tend to be

indifferent between betting on red or black for either urn, drawing either color ought to have the same subjective probability of one-half, regardless of the urn used. Over the past decades, ambiguity aversion has inspired an active literature in decision theory beyond the subjective expected utility model, e.g., by using a non-additive generalization of probability (see, e.g., Schmeidler, 1989; Tversky and Kahneman, 1992) and by assuming that decision makers have a set of prior probabilities in the absence of unique well-defined subjective probability (Gilboa and Schmeidler, 1989).

More recently, it is increasingly recognized that decision making under uncertainty depend not only on probabilities, but also on how uncertainty itself arises. This has been referred to as source dependence in Fox and Tversky (1995; see also Einhorn and Hogarth, 1986). In particular, they posit that people tend to prefer betting on risks arising from a more familiar source of uncertainty. Source dependence has given rise to another direction of research (see, e.g., Chew and Sagi, 2008; Ergin and Gul, 2009) in which the decision maker may have distinct attitudes towards risks arising from different sources of uncertainty. Here, a preference for betting on risks arising from a known or more familiar source may reflect a lesser degree of risk aversion than is the case for risks arising from an unknown or less familiar source of uncertainty.

Recently, ambiguity aversion and familiarity bias have been studied using neuroimaging (Chew, Li, Chark, and Zhong, 2008; Hsu et al., 2005; Huettel et al., 2006). Over the past year, there is an embryonic literature combining experimental economics and behavioral genetics to explore the genetic basis of economic decision making. Two recent twin studies, involving a Chinese and a Swedish population, suggest that genes may contribute significantly to economic risk taking (Cesarini et al., 2009; Zhong et al., 2009a). At the same time, findings of association between

economic risk taking and well-characterized functional genes have been reported in Crisan et al. (2009), Dreber and Apicella (2009), Kuhnen and Chiao (2009), Roe et al. (2009), Zhong, et al. (2009b, c), and Dreber et al. (2010). These findings, summarized in Table 1, involve risky decision making under a single source of uncertainty. The neurogenetic basis of ambiguity aversion and familiarity bias remains unexplored.

Several polymorphic repeat regions near well-characterized brain-expressed genes are of significant interest in personality genetics, psychopathology and social cognition. The dopamine D5 receptor (DRD5) polymorphic repeat has been robustly linked to attention deficit hyperactivity disorder (ADHD), risky behavior (such as substance abuse and drunk driving) and comorbid anxiety and mood disorders (McGough, 2005). The serotonin transporter (SLC6A4) is modulated by a polymorphic repeat, which has been shown to be associated with aversive behavior, neuroticism/harm avoidance and depression (Canli and Lesch, 2007). Estrogen receptor alpha (ESR1) and estrogen receptor β gene (ESR2) are also characterized by polymorphic repeats associated with gender-specific anxiety traits perhaps mediated by brain serotonin levels (Imwalle, Gustafsson, and Rissman, 2005). We hypothesized that these genes, linked to anxiety-related traits and characterized by polymorphic repeat regions, may contribute to ambiguity aversion and familiarity bias in decision making under uncertainty.

The paper is organized as follows. Section 2 introduces the methodology of behavioral genetics including a discussion on association studies using candidate genes. Section 3 presents the experimental design. Section 4 presents both behavioral and gene association results. Section 5 offers concluding remarks.

2. **Behavioral Genetics**

A gene is the basic unit of heredity in a living organism. The gene concept is an empirical construct preceding the molecular biology era and based on breeding experiments in plants (first by Gregor Mendel in 1866) and animals. At the beginning of the 20th century Mendel's genes were identified with chromosomes. In 1944 the gene was identified with DNA and is now known to represent a sequence of four bases (A, G, C andT) arranged in a linear order, and as shown by Watson and Crick in 1953, the DNA molecule is a double helix held together by complementary pairing of bases (A=T, G=C) providing the mechanism for molecular replication and heritability. A human chromosome is a single DNA double helical molecule. There are an estimated 25,000 genes distributed on the 23 pairs of chromosomes. Individuals inherit half of their DNA from each parent. Some genes have various forms, known as alleles representing variations in the sequence of the DNA bases. For example, sickle cell disease results from a particular allele coding for abnormal rather than normal hemoglobin and is due to a single base pair switch. Every individual has two separate copies of an allele at each locus, or location, on the chromosome, but each sperm or egg cell contains only one of these alleles. Thus a child has a 50% chance of receiving a particular allele from a particular parent.

In all organisms, genes encode protein in two major steps: First, the DNA is transcribed in the cell nucleus from DNA to messenger RNA; and, second, mRNA is translated into proteins in the cytoplasm. The process of producing a biologically functional molecule of either RNA or protein is called gene expression. Observable traits and behaviors of interest, referred to as phenotypes, are far downstream from the gene expression. While in some cases a single change in one letter of the DNA alphabet in a single gene alone can lead to a disease (such as Sickle Cell Anemia),

the vast majority of phenotypes are polygenic, meaning they are influenced by both multiple genes and different environmental factors.

Overall evidence that genes play a role in our ability to understand and manipulate social relationships mainly comes from studies of twins. The most common design compares monozygotic (MZ) and dizygotic (DZ) twins who were raised in the same family. MZ twins share all their genetic material, whereas DZ twins share approximately 50% of their genes. If we assume the environmental influences are the same for MZ and DZ twins for the phenotype of interest, then heritability is related to the difference in correlations between MZ twins and DZ twins. For the details of the twin method, readers can refer to Neale and Cardon (1992). Twin studies are informative regarding the percent of variance explained by genes, but not which specific genes or the number that contribute to the phenotype. For two decades the workhorse of human genetics has been genetic linkage combined with positional cloning which has produced remarkable success in identifying genes for rare Mendelian disorders (Risch, 2000). Today the completion of the Human Genome Project (HUGO) has allowed the use of the so-called SNP (single nucleotide polymorphism, a single change in one of the 4 DNA letters) map in testing association between phenotypes and genotype. Humans differ on the average every thousand base pairs (e.g. A→G) and this rich variation explains many differences in human behavioral traits. Another important source of variation in DNA are short-tandem repeat elements- regions of DNA that are variably repeated e.g. $(GCGCGCGCGCGCGC)_n$. Finally, relatively regions of DNA (>1kb) that are either duplicated or deleted, so-called copy number variations, are now recognized as a third source of variation perhaps rivaling that of SNPs in overall importance.

There are two general approaches today in genetic research of complex traits. One strategy is Genome Wide association studies (GWAS). The power of GWAS lies in it not being hypothesis driven. By default, GWAS engages the entire genome in the analysis. SNP frequencies are compared across cohorts or quantitative phenotypes to ascertain chromosomal regions that partially explain some of the phenotypic variance. A second widely-used approach is to start with candidate genes that are known to regulate specific proteins of interest and/or influence related behaviors that make 'biological sense'. For the studies of economic decision making, we shall focus on genes that affect neurotransmitter synthesis and reception, hormone regulation and transcription factors. Benjamin et al (2007) provides an excellent overview of the molecular genetics of economic behavior.

Association Study with Candidate Gene

The psychological factors underlying ambiguity aversion and familiarity bias have been linked to confidence and competence in Ellsberg (1961) and Fox and Tversky (1995). Brain imaging studies also identified the role of reward system - striatum and orbitofrontal cortx, as well as the amygdala, an important regulation of emotion system - that are activated by ambiguity aversion and familiarity bias (Hsu et al., 2005; Chew, Li, Chark, and Zhong, 2008). In choosing genes to examine, we were guided by guidelines indicating that (1) common variants are present in the population (2) these variants have been previously associated with either normal or abnormal behavior and (3) the genes encode elements of neurotransmitter systems that make sense to partially explain individual differences in ambiguity aversion and familiarity bias.

The dopamine D5 receptor (DRD5) gene, mapped to chromosome 4p15.1–p15.3, belongs to a group of dopamine receptors that stimulate the activation of adenylate cyclase through the

coupling of G-proteins. A number of studies have investigated the association between a dinucleotide [CA] repeat polymorphism, located 18.5 kb from the 5'end of the DRD5 gene, and ADHD. Presumably the 148 bp allele is in linkage disequilibrium with a functional allele of this gene. The DRD5 148 bp repeat has been robustly linked with ADHD (Lowe et al., 2004). In a meta-analysis of published studies involving European and Asian populations up to October 2005, Li et al. (2006) also show a strong association between the 148 bp allele and ADHD. Vanyukov and his colleagues (2000) have shown association between the 148 bp allele with risky behavior such as substance abuse and anti-social personality disorder and the association was gender sensitive.

Transcriptional activity of the human serotonin transporter (*SLC6A4)* is modulated by several variations, including a repetitive sequence, the *SLC6A4*-linked polymorphic region (*5-HTTLPR*), which is composed of a short and a long version resulting in different gene expression and function (Canli and Lesch, 2007). The contribution of SLC6A4 to individual differences in personality traits was initially explored in a population and family-based genetic study (Lesch et al., 1996) showing a significant association between the low-expressing 5-HTTLPR short variant and neuroticism. This trait is related to anxiety, stress reactivity and depression. In a recent study (Kuhnen and Chiao, 2009), subjects with the short allele of 5-HTTLPR were significantly more risk averse in a portfolio choice experimental setting. Meanwhile, Roiser et al. (2009) shows that subjects with the short allele of *5-HTTLPR* are more sensitive to the effect of loss-gain framing in decision making under risk at both the behavioral and neural levels.

Estrogen receptor alpha (*ESR1*) has a TA repeat located upstream from exon 1 which may influence its tissue specific expression. This repeat has been associated with high anxiety scores in men (Comings, Muhleman, Johnson, and MacMurray, 1999), conduct disorder (Comings et al.,

1999), and neuroticism in women (Westberg et al., 2003). The human estrogen receptor β gene (ESR2) with a polymorphic CA repeat in intron 5 has been shown to be associated with menopausal complaints including mood symptoms (Takeo et al., 2005). In rat pharmacological studies the anxiolytic properties of estrogens are ESR2 mediated (Lund, Rovis, Chung, and Handa, 2005). Similarly, in the absence of functional ESR2 receptors (ESR2 knockout), regardless of the presence of circulating estradiol in plasma, female mice exhibited enhanced anxiety and decreased concentrations of serotonin or dopamine in several brain regions (Imwalle, Gustafsson, and Rissman, 2005). These animal studies are consistent with some investigations involving human subjects. The polymorphic CA repeat in intron 5 of the ESR2 has been shown to be associated with menopausal complaints including mood symptoms (Takeo et al., 2005). Women with short CA repeats had a greater chance of psychological symptoms during menopause including mood disturbances, anxiety and depression. The short CA repeats have also been associated with osteoporosis suggesting a functional link between microsatellite and gene expression and that short alleles are associated with less expression (Geng et al., 2007). The association between ESR2 and ambiguity aversion in female also complements previous findings of ESR2's gender specific role in menopausal complaints including mood symptoms (Takeo et al., 2005), and depression (Geng et al., 2007).

We hypothesized that these genes, linked to anxiety-related traits and characterized by polymorphic repeat regions, may contribute to ambiguity aversion and familiarity bias in decision making under uncertainty. Since our initial analysis as well as prior research (Croson and Gneezy, 2009) provides evidence that women show greater ambiguity aversion and familiarity bias than men, these four genes, all associated with gender-sensitive phenotypes, are particularly attractive candidates.

3. **Experimental Design**

Subjects. 350 subjects were recruited in Beijing through internet, posters, and word of mouth. The first group was recruited in July 2007; the second group was recruited in February 2008. Demographics of the subjects are summarized as follows: mean age 28.2 +/- 10.8 (s.d.); 162 male, 188 female; 123 non-student subjects, 227 student subjects; 67 subjects with high school education, 194 subjects with college education, 89 subjects with postgraduate education; 325 Han Chinese, 25 non-Han Chinese. Only the 325 Han Chinese are included in analysis for current study to have a better control of population.

This study was approved by the Internal Review Board of the Hong Kong University of Science and Technology. Prior to running the experiment, subjects were each given a written informed consent form for donation of blood samples and for participation in the behavioral experiment. Subsequently, subjects participated in the behavioral experiment as described below. After the experiment, subjects donated 10 cc of blood each for genotyping, taken by nurses and doctors from hospitals in Beijing.

Experimental paradigm. Most experimental studies on the original Ellsberg paradox involve choosing between betting on the unknown urn versus betting on the known urn where betting correctly in either case would pay the same, in which case people tend to bet on the known urn. For our association study, in order to generate a more even split of individuals between those preferring to bet on the known urn versus those preferring to bet on the unknown urn, we increase the payoff associated with betting on the unknown urn. This calls for a judicious choice of a threshold difference. In the ambiguity aversion task, subjects choose between betting on a "known" deck consisting of 10 red cards and 10 black cards, and an "unknown" deck consisting

of 20 cards without knowing the composition of the red and black cards. For the known deck, a correct bet pays Y10 (about USD1.4). For the unknown deck, a correct bet pays Y12 with an increase of Y2 as a result of pretests.

In Fox and Tversky's (1995) experiment on familiarity bias, the bet is on whether the temperature in San Francisco/Istanbul is above/below a specific temperature. However, subjects may have different information about the cities, which could be a confounding factor for familiarity bias. Recently Abdellaoui et al. (2010) use the notion of exchangeability to elicit equal chance for the possible temperature range for cities. Chew et al. (2010) adopt the odd-even design to investigate source preference over almost objective events (Machina, 2004) such as whether the trailing digits of Dow Jones would be odd or even. We apply this design in this paper for bets on whether the temperature at a specific historical day of Beijing (Tokyo) would be odd or even. This procedure induces the same unambiguous probability of one half for odd versus even regardless of the city chosen. As with the case for ambiguity aversion, to generate an even split between those betting on Beijing and those betting on Tokyo, a correct bet on Beijing temperature pays Y11 which is Y2 less than the payout for a correct bet on Tokyo temperature.

Genotyping. The polymorphism for the *SLC6A4* 44bp deletion/insertion (*5-HTTLPR*) in the promoter region was characterized using PCR amplification procedure with the following primers: F5'-GGCGTTGCCGCTCTGAATTGC-3', R5'-GAGGGACTGAGCTGGACAACC-3'. PCR reactions were performed using 5µl Master Mix (Thermo scientific), 2µl primers (0.5 µM), 0.6µl Mg/Cl2 (2.5 mM), 0.4µl DMSO 5% and 1µl of water to total of 9µl total volume and an additional 1µl of genomic DNA was added to the mixture. All PCR reactions were employed on

a Biometra T1 Thermocycler (Biometra, Güttingem, Germany). PCR reaction conditions were as follows: preheating step at 94.0˚C for 5 min, 34 cycles of denaturation at 94.0˚C for 30 s, reannealing at 55˚C for 30 s and extension at 72˚C for 90 s. The reaction proceeded to a hold at 72˚C for 5 min. All reaction mixtures were electrophoresed on a 3% agarose gel (AMRESCO) with ethidium bromide to screen for genotype. It is in Hardy-Weinberg Equilibrium ($p < 0.9998$). The allele frequency is presented at Table 2.

Amplification of the *DRD5, ESR1* and *ESR2* microsatellites was achieved using the following primers: *DRD5*: forward: 5'- CGTGTATGATCCCTGCAG – 3'; reverse: 5'- GCTCATGAGAAGAATGGAGTG – 3'; *ESR1* (corresponds to the TA dinucleotide repeat in the 5' promoter region): forward 5'- AGACGCATGATATACTTCACC – 3'; reverse 5'- GTTCACTTGGGCTAGGATAT -3'. *ESR2* (corresponds to the CA dinucleotide repeat in intron 5): forward (fluorescent) 5'- GGTAAACCATGGTCTGTACC -3'; reverse 5'- AACAAAATGTTGAATGAGTGGG -3'. PCR reactions were performed using 5µl Master Mix (Thermo scientific), 0.5µl primers (0.5 µM), 0.4µl Mg/Cl2 (2.5 mM) and 3.1µl of water to total of 9µl total volume and an additional 1µl of genomic DNA was added to the mixture. All PCR reactions were employed on a Biometra T1 Thermocycler (Biometra, Güttingem, Germany). PCR reaction conditions were as follows: preheating step at 95.0˚C for 5 min, 30 cycles of denaturation at 95.0˚C for 30 s, reannealing at 55˚C for 30 s and extension at 72˚C for 40 s. The reaction proceeded to a hold at 72˚C for 10 min. The PCR product was analyzed on an ABI 310 DNA Analyzer. For ESR1, 16 alleles (178–208 bp) and for ESR2 15 alleles (141–169 bp) were identified and the distribution of allele frequencies is similar to previous reports (e.g., McIntyre et al., 2007). The allele frequency is presented in Table 3, Figure 1, and Figure 2 respectively.

4. Results

At the behavioral level, our specific choice of threshold payoffs induced 50.6% of the subjects to bet on the unknown deck in the card-deck task, and 60.4% of the subjects to bet on Tokyo in the temperature task. We find significant gender dependence with female subjects being significantly more likely to bet on Beijing (t-test, $p = 0.019$) in the temperature task and to bet on the known deck (t-test, $p = 0.011$) in the card-deck task. This is consistent with prior findings on the gender difference of decision under uncertainty (Croson and Gneezy, 2009). We do not find significant association between ambiguity aversion and familiarity bias (corr = 0.020, $p = 0.719$), a finding consistent with evidence from Hsu et al. (2005) (corr = – 0.143, $p = 0.579$, from Table S6). This suggests that familiarity bias and ambiguity aversion are distinct phenomena at the behavioral level.

As discussed in the recent study (Jakobsdottir et al., 2009), there are two basic statistical approaches for evaluating markers. The risk-based approach models risk as a function of marker(s), often with adjustment for covariates, and is commonly applied in genetic studies. In case-control studies, this is done with logistic regression, and the markers with the strongest effect on disease risk are those associated with the smallest p-values and most extreme odds ratios (ORs). The current investigation uses the latter method which is most commonly employed in genetic association studies. To test the effect of genotypes on our binary data, we use logit regression with robust standard error for genotype association analysis with Stata 8.0. Gender, age, and student status have been included as independent variables.

At the neurogenetic level, we find that alleles for each of the candidate genes is associated with one of two types of source preference – familiarity bias (*5-HTTLPR*) and ambiguity aversion

(*DRD5, ESR2*) – both of which are associated with more avoidant personality types. Subjects with the short *5-HTTLPR* allele tend to bet on Beijing (familiar) while subjects without the *DRD5* 148 bp allele were more likely to bet on the known deck as were subjects with the *ESR2* [CA] short alleles.

5-HTTLPR: The short allele of *5-HTTLPR* contributes significantly to familiarity bias ($p = 0.005$) (Figure 3A). This association is robust with respect to gender (*male*, $p = 0.057$; *female*, $p = 0.043$). No association is observed between *5-HTTLPR* and ambiguity aversion ($p = 0.315$).

DRD5: Although *DRD5* is not significantly associated overall with ambiguity aversion ($p = 0.212$) nor familiarity bias ($p = 0.928$), significant association is observed for ambiguity aversion in female subjects ($p = 0.01$) with the 148 bp allele contributing to ambiguity seeking (Figure 3B).

ESR1 and ESR2: Figure 1 and 2 display the distributions of *ESR1* and *ESR2* alleles, which were each divided into two groups of approximately the same size. For *ESR1*, 178-188 bp (48.2%) were classified as short (S), and 190-208 bp were classified as long (S). For *ESR2*, 141-157 bp (about 58.0%) were classified as short (S), and 159-169 bp were classified as long (L). No significant association is observed between *ESR1* and ambiguity aversion ($p = 0.497$) or familiarity bias ($p = 0.801$). However, significant association was observed between *ESR2* and ambiguity aversion ($p = 0.023$) with the short allele contributing to ambiguity aversion (Figure 3C), but no association was observed between *ESR2* and familiarity bias ($p = 0.672$). As anticipated, *ESR2* contributes significantly on ambiguity aversion in female subjects ($p = 0.046$), but not for male subjects ($p = 0.262$). These association results are summarized in Table 4 and Table 5.

5. **Concluding Remarks**

The remarkable works of Keynes, Knight, and Ramsey in the 1920s have enhanced our understanding of the nature of decision making under uncertainty with the suggestion that people may be ambiguity averse in preferring bets involving known probabilities to those based on contingencies without known probabilities. This was further studied in Ellsberg (1961) and subsequently extended to source dependence (Einhorn and Hogarth, 1986; Heath and Tversky, 1991; Fox and Tversky, 1995), which encompasses the phenomenon of familiarity bias in which people tend to prefer bets arising from a familiar source of uncertainty than those arising from an unfamiliar source.

Our odd-even design to elicit familiarity bias has the advantage of inducing the same unambiguous probability of half for each subject in both bets. A preference for the Beijing bet paying less than the Tokyo bet would support the idea that subjects strictly prefer betting on a more familiar source of uncertainty. This behavior is not compatible with non-expected utility models of decision making that are based on the hypothesis of global probabilistic sophistication , i.e., lotteries are fully captured by their underlying probabilities and outcomes (Machina and Schmeidler, 1992; Grant, 1995; Chew and Sagi, 2006). These include betweenness conforming preferences (Chew, 1983; Dekel, 1986; Chew, 1989; Gul, 1991) and rank-dependent preferences (Green and Jullien, 1988; Quiggin, 1982). While Choquet expected utility (Schmeidler, 1989) can account for ambiguity aversion via a non-additive capacity, this model reduces to Quiggin's rank-dependent utility in the presence of known probabilities if equally probable events assume the same capacity value. In this case, Choquet expected utility is incompatible with having a 'bias' in favor of one 50-50 lottery from a familiar source of uncertainty to another 50-50 lottery from a less familiar source and pays less. While this observation applies to cumulative prospect

theory which is defined in terms of Choquet expected utility, Tversky and Kahneman (1992, page 302) raised the intriguing possibility of the function, linking the non-additive capacity to an underlying probability, may itself depend on the source of uncertainty. Another strand of the literature that can account for Ellsbergian behavior involves the idea of multiple priors, e.g., Wald (1949), Hurwicz (1951), Gilboa and Schmeidler (1989) and Ghiradarto, et al (2004). For this approach to account for the nature of familiarity bias reported in this paper, one would need to assume that the event of odd or even have non-unique priors.

Ours is the first study that links ambiguity aversion and familiarity bias to three common polymorphisms which have been associated with anxiety-related traits and gender-sensitive phenotypes. Our results show that DRD5 (microsatellite marker) and ESR2 (CA repeat) are associated with ambiguity aversion, while SLC6A4 (5-HTTLPR indel) is associated with familiarity bias. Our results corroborates the view proposed in Ellsberg (1961) and Fox and Tversky (1995) that lack of competence and confidence contributes to ambiguity aversion and familiarity bias, specifically, that DRD5 (microsatellite marker) and ESR2 (CA repeat) are associated with ambiguity aversion while SLC6A4 (5-HTTLPR indel) is associated with familiarity bias. Taken together, our findings suggest distinct neurogenetic mechanisms modulating familiarity bias and ambiguity aversion. This corroborates the lack of significant correlation between ambiguity aversion and familiarity bias at the behavioral level.

Overall, alleles associated with familiarity bias and ambiguity aversion are the same alleles in many human studies, including studies using experimental economics paradigms (Crisan et al., 2009; Kuhnen and Chiao, 2009; Roiser et al., 2009), that are also associated with more avoidant personality types, especially neuroticism or harm avoidance (Cloninger, 1986). Personality is a

continuous trait and women score higher on harm avoidant traits than men (Zion et al., 2006) underpinning the idea that source dependence may have a link to this basic human personality trait. This notion is corroborated by current findings in personality neurogenetics. Intriguingly, the neurogenetic evidence appears to support a distinction between ambiguity aversion and familiarity bias at the specific gene level since ESR2 and DRD5 are associated solely with ambiguity bias whereas SLC6A4 is solely associated with familiarity bias. To summarize, we suggest that avoidant personality underlies source dependence which in turn drives familiarity bias and ambiguity aversion through partially distinct genetic mechanisms. Future studies would profitably examine other common polymorphisms and their role in source dependence.

In an imaging study of ambiguity aversion and familiarity bias, Hsu et al. (2005) found that the amygdala was more activated under ambiguity (unfamiliarity) condition than under risk (familiarity) condition. Chew et al. (2008) conducted a subsequent fMRI experiment on familiarity bias using an odd-even design that is close to what we use in the current study, and replicated amygdala activation in modulating familiarity bias. The emerging evidence regarding the role of 5-HTTLPR in mediating amydagla activation (Hariri et al., 2002; Roiser et al., 2009), together with the present study, suggests a neurobiological mechanism from 5-HTTLPR, amygdala activation, to familiarity bias. Specifically, genetically driven variation in brain activation may respond to human emotion arising from familiarity bias. This suggests that differential excitability of the amygdala to unfamiliar source of uncertainty may contribute to an increased fear and anxiety associated with the short allele of *5-HTTLPR*.

In their 1991 paper, Heath and Tversky suggest a link between familiarity bias and the home market bias in finance – “investors are sometimes willing to forego the advantage of

diversification and concentrate on a small number of companies with which they are presumably familiar". More recent empirical studies, e.g., Coval and Moskowitz (1999) and Huberman (2001), reveal an intriguing domestic "home bias" in terms of systematic under-diversification of stock holdings in companies that are closer to home even when all of them are US based. Through the Heath-Tversky observation, the results reported here point to a link between genetic variants of 5-HTTLPR and the home bias phenomenon and suggest a possible role of *5-HTTLPR* in modulating familiarity bias in other business settings, e.g., brand marketing.

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Study	N	Risk Attitude	Gene
Carpenter et al (2009)	140	Multiple-price list deign	DRD4
Crisan et al (2009)	36	Loss-gain framing	5-HTTLPR
Dreber et al (2009, 2010)	94	Portfolio choice	DRD4
Kuhnen & Chiao (2009)	65	Portfolio choice	5-HTTLPR, DRD4
Roe et al (2009)	67	Multiple-price list design	CHRNA4
Roiser et al (2009)	30	Loss-gain framing with fMRI	5-HTTLPR
Zhong et al (2009b)	325	Even-chance risks over gains and losses	Stin2, DAT1
Zhong et al (2009c)	325	Longshot risks over gains and losses	MAOA

Table 1. *Summary of recent studies of molecular genetic basis of decision making under risk*

Allele frequency		Genotype frequency		
s	*l*	*s/s*	*s/l*	*l/l*
69.8%	30.1%	51.7%	36.2%	12.1%

Table 2: *Allele and genotype frequency of 5-HTTLPR.*

Allele frequency		Genotype frequency		
148bp	others	148bp/148bp	148/others	others/others
30.1%	69.9%	11.0%	38.1%	50.8%

Table 3: *Allele and genotype frequency of DRD5.*

Genes	Pool			Male			Female		
	O.R.	*C.I.*	*p-value*	*O.R.*	*C.I*	*p-value*	*O.R.*	*C.I.*	*p-value*
DRD5	0.8	0.565, 1.134	0.212	1.298	0.755, 2.229	0.344	0.55	0.349, 0.866	0.01*
5-HTTLPR	1.188	0.860, 1.642	0.294	1.202	0.743, 1.943	0.453	1.213	0.773, 1.902	0.4
ESR1	1.108	0.823, 1.491	0.497	1.165	0.745, 1.822	0.502	1.047	0.702, 1.562	0.819
ESR2	1.45	1.051 2.001	0.023*	1.304	0.819, 2.075	0.262	1.589	1.007, 2.509	0.046*

Table 4. *Association results for ambiguity aversion with DRD5, 5-HTTLPR, ESR1 and ESR2.*

Genes	Pool			Male			Female		
	O.R.	*C.I.*	*p-value*	*O.R.*	*C.I*	*p-value*	*O.R.*	*C.I.*	*p-value*
DRD5	0.981	0.657, 1.466	0.928	0.785	0.401, 1.535	0.48	1.102	0.664, 1.830	0.706
5-HTTLPR	0.594	0.413, 0.856	0.005*	0.559	0.307, 1.016	0.057*	0.622	0.392, 0.986	0.043*
ESR1	0.958	0.687, 1.335	0.801	1.067	0.648, 1.756	0.799	0.88	0.562, 1.377	0.577
ESR2	1.083	0.747, 1.571	0.672	0.86	0.477, 1.551	0.618	1.299	0.792, 2.133	0.299

Table 5. *Association results for familiarity bias with DRD5, 5-HTTLPR, ESR1 and ESR2.*

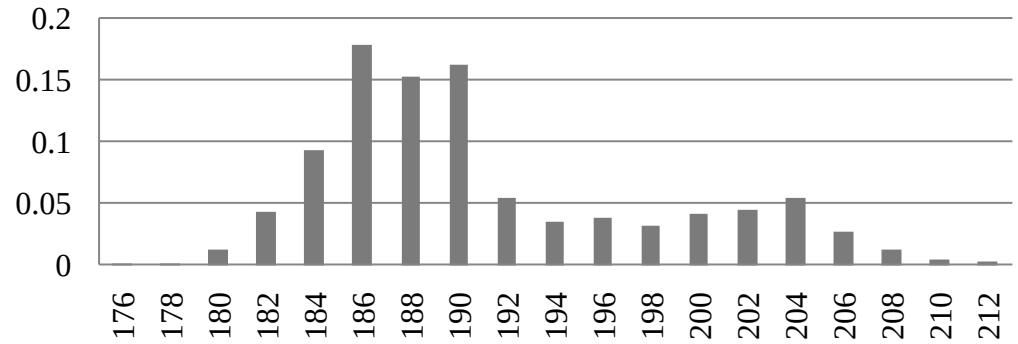

Fig 1: *Allele frequency of ESR1*.

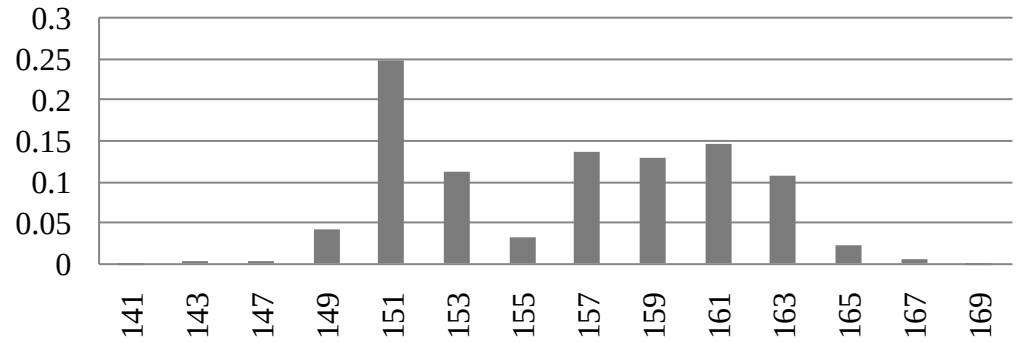

Fig 2: *Allele frequency of ESR2.*

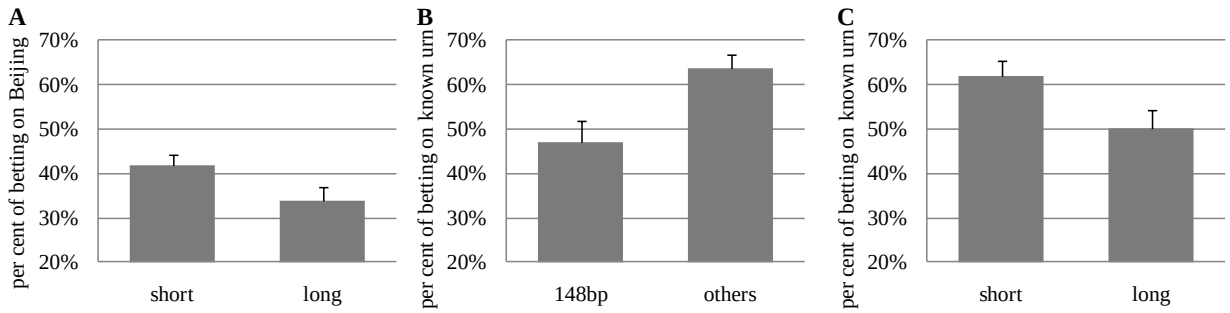

Fig.3 (A) *5-HTTLPR and familiarity bias.* Subjects with short allele tend to bet on Beijing. (B) *DRD5 and ambiguity aversion in female.* Female subjects without 148bp allele tend to bet on known deck. (C) *ESR2 and ambiguity aversion in female.* Subjects with short allele tend to bet on known deck.