COGNITIVE ENDOPHENOTYPES OF MODERN AND EXTINCT HOMININS ASSOCIATED WITH *NTNG* GENE PARALOGS

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ABSTRACT

A pair of gene paralogs, *NTNG1* and *NTNG2*, contributes to the Intellectual Quotient (IQ) test scores in a complementary manner. Single nucleotide polymorphisms (SNPs) of *NTNG1* are associated with attenuated verbal comprehension (VC) or processing speed (PS) while *NTNG2* SNPs affect working memory (WM), and perceptual organization (PO) forming cognitive endophenotypes in healthy and schizophrenia (SCZ)-affected human subjects. Regions of interest (ROIs), defined as 21 nucleotide (nu) long loci embedding the IQ-affecting mutation alleles, underwent dramatic evolutionary changes from mice through primates to hominin gene orthologs, and resulted in accelerated evolution of VC and WM/PO affecting ROIs. Mutation alleles associated with the higher VC and WM IQ scores are found in genomes of extinct hominins of Neolithic times, however, lower WM scores associated allele is detectable in Mesolithic hunters genomes. Protein sequence of *NTNG1* is 100% conserved among the archaic and modern extinct hominins while *NTNG2* underwent a recent selection sweep encoding a primate-specific S371A/V (~50,000 yrs BC), and a modern human (5,300 yrs BC) T346A substitutions. Hereby, we show that a 500 mln yrs old genomic duplication of a synapse primordial gene of an urochordate provided a substrate for further synapse elaborations and its ultimate capacitive expansion of what evolved into a vertebrate cognitive superior complexity – intelligence.

INTRODUCTION

In 1970 S.Ohno ingeniously proposed that new gene function can result from a gene duplication and following it gene paralogs SF (**Ohno, 1970**). Two gene paralogs, *NTNG1* and *NTNG2*, expressed predominantly in the brain (**Nakashiba et al., 2002**), and encoding Netrin-G1 and Netrin-G2 proteins, respectively, are localised pre-synaptically and segregate in a non-overlapping manner into distinct neuronal circuits (**Nishimura-Akiyoshi et al., 2007; Matsukawa et al., 2014**). They are related to the netrin family of axonal guidance cues (**Sun et al., 2011**) but differ in that they attach to the axonal membrane via a glycosylphosphatidylinositol (GPI) link (**Yu et al., 2013**; **Sevcsik et al., 2015**), a known lipid raft-associated membrane signaling cascade organiser (**Klotzsch and Schutz, 2013; Yu et al., 2013**). The first evolutionary precursor of *NTNG* as a single gene copy can be located in the genome of a primitive vertebrate tunicate/urochordate *Ciona intestinalis* (sea squirt, ENSCING00000024925), reported to be the first organism with the neural crest primordials (**Abitua et al., 2012**), multipotent brain progenitor cells (**Stolfi et al., 2015**), and neurogenic placodes, facilitating the transition from pelagic invertebrate life style to a predatory vertebrate (**Abitua et al., 2015**). The dramatic expansion of human cerebral cortex over the course of evolution (**Wise, 2008**; **Preuss, 2012**; **Geschwind and Rakic, 2013**; **Belmonte et al., 2015**) had provided new niches for accommodating either *de novo* or advancing pre-existed cognitive features and culminating in the positively selected human cognitive functions (**Joshi et al., 2015**).

IQ tests are a surrogate measure of general human cognitive ability characterising intelligence. They are often administered as WAIS-III/IV (**Wechsler, 1958**) and represent a cumulative score of 4 cognitive indices: VC, WM, PO and PS frequently referred as "cognitive domains" (**Deary et al., 2006**). IQ has been validated by factor analyses (**Glascher et al., 2009**), and a common factor (correlate) influencing each of them frequently

70 referred as *g*, or "general intelligence", proposed by Spearman in 1904 (**Spearman, 1904**),
71 and recently challenged as the only existing correlate (**Hampshire et al., 2012**). IQ is
72 affected by several mental disorders including schizophrenia (SCZ) characterized by severe
73 cognitive deficits in WM and behavioral flexibility and resulting in low performance in
74 several cognitive tests (**Forbes et al., 2009; Leeson et al., 2009**; **Barnett et al., 2010**). Since
75 both *NTNG* paralogs have been reported associated with SCZ (**Fukasawa et al., 2004**; **Aoki-**
76 **Suzuki et al., 2005**; **JSSLG et al., 2005**; **Eastwood and Harrison, 2008**; **Ohtsuki et al.,**
77 **2008**; **Zakharyan et al., 2011**; **Zhu et al., 2011**; **Ayalew et al., 2012**; **Wilcox and Quadri,**
78 **2014**) we investigated whether these gene paralogs contribute to human intelligence by
79 assessing the IQ of human carriers for the *NTNG1* and *NTNG2* SNP alleles against non-
80 carriers with and without SCZ.
81

RESULTS

Several *NTNG1* and *NTNG2* SNPs have been previously reported to be associated with SCZ (e.g. **Aoki-Suzuki et al., 2005**; **Ohtsuki et al., 2008**}. We have found that out of 11 SNPs tested, five affect the IQ scores and composite domains in human subjects (**Figure 1**, **Supplementary Table 1** (**ST1**)). SCZ patients carrying rs2218404 T allele (**Figure 1A-1**) of *NTNG1* (T/G and T/T genotypes, N = 25 patients) compared with G/G genotype (N = 36 patients) demonstrated attenuated full-scale IQ (FIQ, ANCOVA $p = 0.0057$ (F = 7.80)), and VIQ ($p = 0.0033$ (F = 8.87)). VC domain score was the main contributor to the VIQ decline ($p = 0.0050$ (F = 8.08), **Figure 1B-1**), with low scores across all parameters except comprehension (CH): vocabulary (Vc, $p = 0.020$ (F = 5.49)), similarities (SiM, $p = 0.041$ (F = 4.23)), and information (IF, $p = 0.0067$ (F = 7.50), **Figure 1B-1** lower panel). Thus, a point mutation in *NTNG1*, rs2218404, is associated with low VC affecting the VIQ via the attenuated Vc, SiM and IF subscores. The next *NTNG1* SNP found to affect IQ was rs96501, with attenuated PS in healthy human subjects C allele carriers (N = 45) vs T/T genotypes (N = 98, $p = 0.028$ (F = 4.89), **Figure 1B-1**) with no effect on SCZ patients. The contributing affecting score was symbol search (SS, $p = 0.053$ (F = 3.79), **Figure 1B-1**, lower panel) with digit symbol coding (DSC) being also attenuated but non-significantly ($p = 0.12$ (F = 2.40)). Three other SNPs mapped to *NTNG2* (**Figure 1A-2**) have been also shown to affect IQ. Healthy carriers of the *NTNG2* SNP rs1105684 A allele (N = 49) showed a lower FIQ ($p = 0.018$ (F = 5.70)), VIQ ($p = 0.029$ (F = 4.90)), and PIQ ($p = 0.048$ (F = 3.99)) when compared with the T/T genotypes (N = 96, **Figure 1B-2**). To check for a potential dosage-dependent effect of a mutation allele on IQ score, *NTNG2* SNP rs2149171 SCZ and healthy human subject cohorts were each split on 3 genotypes, respectively: C/C (N = 14 and 39), C/T (N = 29 and 73), and T/T (N = 15 and 30). The presence of the C allele as a single copy (C/T genotype) was strongly associated with a prominent attenuation in the IQ scores of SCZ

patients and was essentially identical to that produced by the C/C genotype when both are compared to the T allele carriers (FIQ: $p = 0.014$ (F = 4.35); VIQ: $p = 0.029$ (F = 3.60); PIQ: $p = 0.035$ (F = 3.42), **Figure 1B-2**). If in case of *NTNG1* located SNP rs2218404 the lower VIQ score was contributed mainly by the decreased VC domain scores for Vc, SiM, and IF (**Figure 1B-1**), in the case of *NTNG2* located rs2149171 the CH and WM domain scores were responsible for the VIQ decline in C allele carriers ($p = 0.012$ (F = 4.54) for CH and $p = 0.040$ (F = 3.27) for WM (N = 12 (C/C); N = 25 (C/T) and N = 14 (T/T)). Similarly to VIQ, where CH of rs2149171 complements the cognitive endophenotype produced by the T-allele of rs2218404, the PIQ attenuated score in the case of rs2149171 was due to lower PO score ($p = 0.050$ (F = 3.04), **Figure 1B-2**) in the C allele carriers. The third *NTNG2* located SNP found to affect the human IQ was rs2274855 (**Figure 1A-2**) with a cognitive endophenotype associated with the A-allele presence in SCZ patients (N = 33) vs G/G genotypes (N = 26) and resembling that of the described above C-allele of rs2149171. Accordingly, the attenuated scores were: FIQ ($p = 0.012$ (F = 6.44)), VIQ ($p = 0.018$ (F = 5.70)), and PIQ ($p = 0.036$ (F = 4.46), **Figure 1B-2**). Similarly to rs2149171 the lower VIQ score was due to declined CH ($p = 0.035$ (F = 4.49)) but unaffected VC that is contrary (complementary) to the rs2218404 endophenotype (**Figure 1B-1**). WM was robustly affected by the A-allele presence (N = 29; $p = 0.023$ (F = 5.28)) contributed by the low DS score ($p = 0.026$ (F = 5.04)) with LNS and AM being unaffected (**Figure 1B-2**, lower panel). The observed PO score was comprised by the declined matrix reasoning (MR, $p = 0.038$ (F = 4.34)), block design (BD, $p = 0.041$ (F = 4.23)) with picture completion being unchanged (**Figure 1B-2**, lower panel). Thus, all three aforementioned *NTNG2* SNPs affect the VIQ and PIQ in human subjects with the first one contributed by the CH subscore and WM and the latter by the PO score (**Figure 1C**). Contrary to this, the *NTNG1* located SNP (rs2218404) affects the VIQ through the lower Vc, SiM and IF scores and affecting the VC domain scores. Another SNP,

rs96501, affects PS domain, though in healthy subjects only. It can be concluded that both genes (as paralogs) contribute to the cognitive scoring produced upon the implemented IQ testing but in a cognitive domain-complementary manner, *NTNG1* is responsible for the VC and PS in human while *NTNG2* for the WM and PO domain scores (**Figure 1C**).

The robust link observed between a single SNP and affected cognitive domain IQ score (**Figure 1**) can be explained by some global dramatic perturbations caused by the presence of a mutated allele and/or a functinal importance of its context-dependent positioning on the gene (**Figure 2A** and **3A**). To determine a potential significance of the SNP alleles' epistatic environment we compared the nucleotide (nu) sequence within the immediate vicinity of a SNP allele positioning (50 nu upstream and downstream) in mice, primates and modern human. We compared all 11 SNPs used for the IQ screening and plotted the identity percent as a function of distance from the mutated allele position (**Figure 2B** and **3B**, see **Supplementary Materials** = **SM**). We found that the identity percent distribution over the analysed areas of $\pm$50 nu is not uniform and displays a SNP allele position-centred dramatic evolutionary changes pointing towards a potential functional significance of the immediate vicinity of a SNP as short as $\pm$10 nu and not further, referred from here and beyond as a Region Of Interest (ROI) for each specific SNP allele. We calculated the rates of evolutionary changes for each ROI as a percent identity change over the lapsed mln yrs of evolution (**Figure 2C and 3C**). Among the 6 *NTNG1*-located SNP ROIs three of them display accelerated rates of evolution from marmoset to chimpanzee (rs2218404, rs628117, rs96501) when compared to the mouse-marmoset rates, and rs2218404 (affecting VC in human subjects) additionally demonstrates an accelerated rate of evolution on the chimpanzee to human path (**Figure 2C**). As for the *NTNG2* located ROIs (**Figure 3-B**), rs1105684 is remarkably consistent at displaying high evolutionary rates around 0.8 and, together with rs2274855, both have identical rates at the mouse-marmoset and chimpanzee-

156 human paths, but differ dramatically at the marmoset-chimpanzee point (0.8 vs 0,
157 respectively). rs2274855 is the only *NTNG2*-nested SNP ROI which underwent an AE from
158 chimpanzee to human. Next we compared the DNA sequences of all 11 ROIs across mice,
159 primates and extinct hominins *NTNG* gene paralogs (see **ST2** for the datasets sources used
160 for the genes reconstruction). T-allele of rs2218404 is detectable in marmoset and in mouse
161 its position corresponds to adenosine (**Figure 2D**). G-alelle (associated with a higher VC
162 score comparing to the human T-allele carriers) is found in Mesolithic hunter Loschbour
163 (8,000 BC) but not in another ancient hunter Motala12 and is also present in other two
164 hominins belonging to the Neolithic period, Iceman and Eskimos (5,300 and 4,000 yrs BC,
165 respectively). rs628117 is the only *NTNG1*-related mutation near vicinity of which (±50 nu)
166 is located an intra-hominins (Es, Ice, Lo) mutation (**Figure 2B**, low left). The next, PS-
167 affecting, ROI of rs96501 displays an intricate path of T-allele evolution (associated with a
168 higher PS score) being anciently conserved from mice to primates but later substituted on the
169 less efficient (in terms of the generated IQ scores) C allele in Neanderthals, later again
170 replaced by the T allele in Mesolithic hunters and coming back during the Neolithic times
171 (**Figure 2D**). The first *NTNG2* SNP rs1105684 is located at the beginning of the gene and
172 affects WM in healthy human subjects (**Figure 3A**). The origin of the T-allele is evolutionary
173 bound to marmoset since its position in mice is occupied by another pyrimidine base C
174 (**Figure 3D**). Next on the gene are two SNP alleles for rs7851893 and rs3824574 which do
175 not affect IQ and similarly to rs1105684 are surrounded by highly conserved ROIs not only
176 in hominins and chimpansee (100% identity) but also in marmoset (except 1 mutation for
177 rs7851893). rs2149171 ROI (affecting the WM and PO scores) similarly to rs3824574 is
178 100% conserved across the all species (including the mouse) except the allele itself. The
179 attenuating IQ C-allele position is occupied in mice genome by T but present in Iceman and
180 Eskimos genes. A distinct evolutionary path is taken by another cognitive endophenotype-

associated and affecting WM and PO scores A-allele of rs2274855 and its ROI (**Figure 3D**). Its position in mice is likely to be occupied by the C pyrimidine base (the software places a blank instead of it) which is gradually substituted on purine G in chimpanzee and misplaced by the lower IQ score-associated A-allele in Mesolithic hominins. And 20 nu downstream of the centre of ROI is located a modern human-specific point mutation translated into the T346A protein substitution (as described below).

The distinct picture of evolutionary changes among the *NTNG1* and *NTNG2* nested SNPs has prompted us to compare evolutionary rates for the full-length proteins encoded by these gene paralogs, Netrin-G1 and Netrin-G2, respectively (**Nakashiba et al., 2000 and 2002**). Netrin-G1 undergoes only few changes in its amino acid (aa) composition with the maximum calculated rate of evolution reaching 0.05 when mice and marmoset proteins are compared, 0.01 among the primates, and 0.03 between chimpanzee and human due to a single point mutation A81S (**Figure 2E** and **SM:** Netrin-G1), absent in other primates. Netrin-G2 evolves 2.8 times faster between mouse and marmoset than its paralog Netrin-G1 and continues evolving with a steady rate of 0.05 from primates to human (**Figure 3E** and **SM:** Netrin-G2). We have also reconstructed both proteins from ancient (Neanderthals, Paleolithic time) and extinct hominins (Mesolithic and Neolithic times) and compared them with primates' and mice' Netrin-G orthologs (**Figure 2F** and **3F)**. Netrin-G1 is a highly conserved protein among the primates and hominins (**Figure 3F**). As for Netrin-G2, a mutation shared among the Neanderthals' and Mesolithic genomes, primates and mice (T346A) is absent in the Neolithic Iceman and modern human (the signal for Motala3, Motala1 and MezmayskayaNea is not clear due to low sequence coverage). Primates (marmoset and chimpanzee) share another mutation (S371A/V) preserved in mouse and absent in hominins (further details can be found in the **SM:** Results).

DISCUSSION

***NTNG* paralog SNPs and associated cognitive endophenotypes of human subjects.** Shortcomings of cognitive and information processing are key features of SCZ diagnosis (**APA, 2013**). They are manifested as impairments in PO, WM, VC and PS (see **Yoon et al., 2014** for references) frequently reported as attenuated scores upon IQ tests implementation. SCZ patients carrying a mutation allele for one of *NTNG* gene paralog SNPs form cognitive endophenotypes affecting the IQ scores (**Figure 1C**). The given endophenotypic groups comprise from subjects with either affected VIQ (via attenuated VC by *NTNG1* rs2218404 or WM by *NTNG2* rs2149171 and rs2274855) or affected PIQ (via attenuated PO by *NTNG2* rs2149171 and rs2274855). In two extra cases PS is affected by rs96501 of *NTNG1* and WM by rs1105684 of *NTNG2* (**Figure 1B-1** and **B-2**, respectively) but in healthy human subjects. Such intriguing non-overlapping effect on the IQ domains prompts us to conclude that *NTNG* paralogs complement each other function and represent an example of how a synapse-expressed genes affect the human cognitive abilities, perhaps through the precision of neuronal connectivity perturbations and concomitant miswirings. The observed phenomena of the affected WM is the most striking due to its multifaceted constructive nature (**Frydecka et al., 2014**) underlying many, if not all, cognitive tasks such as comprehension, reasoning and learning (**Baddeley, 1992**) and historically introduced by Baddeley as the reading span test (**Mackintosh, 2011**). Lack of the localization effect of *NTNG2* SNP mutation alleles, all three are located in different parts of the gene (**Figure 1A-2**) but associated with identical endophenotype (**Figure 1B-2**), points to a uniform nature of the *NTNG2* function distribution over the entire gene. An obviously non-coding nature of all five IQ-affecting alleles (rs2149171 despite being exon 4-located encodes a silent F246F mutation) corroborates an idea that anthropoid trait-associated loci lie outside coding protein areas (**del Rosario et al., 2014; Kellis et al., 2014**) and hints towards a potential of these alleles to perturb genes

regulatory functions, e.g. mRNA splicing, affecting downstream located pivotally functional *NTNG* elements such as Ukd-domain encoding exons 6 and 7 or a unique Netrin-Gs trait – GPI-link. Alternatively, or simultaneously, the *NTNG* SNP alleles may be embedded into an epistatic network of other genes influencing human cognitive traits (**Hemani et al., 2014**). However since it is usual for a SNP effect to be estimated using an additive model (assuming either independent and cumulative single contribution) to the mean of a trait with the small effect size the power to detect the epistatic environment drastically declines. Contrary to the genetic associations with gene expression having large effect sizes (**Hemani et al., 2014**), cognitive trait-associated effect sizes are reportedly small (**Plomin and Deary, 2015**), e.g. the largest effect sizes of the variance of intelligence scores accounted for only 0.2% (**Benyamin et al., 2014**), 0.5% on GWA studies of 1,583 adolescence (**Desrivieres et al., 2015**) or was predicted to be ~1% on 3,511 adults (**Davies et al., 2011**). Another GWAS of educational attainment (sharing a moderate correlate with intelligence), which included 126,559 individuals, reports on just 1% of the variance but only 0.02% in a replication sample (**Rietveld et al., 2013**). Our data support the preexisted conclusion that human cognitive traits modalities are not described by statistically large effect sizes.

Evolutionary elaborations of the embedding IQ-affecting mutations loci. Eleven previously published SCZ-associated SNPs were tested for their effect on IQ performance of human subjects and 5 of them were found to be associated with attenuated IQ cognitive endophenotypes (**Figure 1B-1** and **B-2**). ROIs of 3 of them (rs2218404, rs1373336 and rs2274855) underwent an AE from chimpanzee to human when compared to New World monkeys to apes (marmoset-chimpanzee) path (**Figure 2C** and 3**C**). Two of them affect IQ in humans (rs2218404 – VC and rs2274855 – WM, **Figure 1B-1** and **B-2**) while being located within the vicinity of exon 5 (2,275 nu downstream and 15 nu upstream, respectively) – a part of the lowest percent identity coding DNA among the *NTNG* gene paralogs (**Prosselkov**

et al., 2015). Presence of the evolutionary accelerated regions within the *NTNG* genes non-coding areas underscores them as contributors to the human-specific traits along with other genes (**Prabhakar et al., 2006**). However, not only ROIs of the IQ-affecting alleles but the alleles themselves demonstrate several unique evolutionary features (see **SM:** Discussion). To understand evolutionary forces driving the emergence of cognitive endophenotype-associated alleles we have deduced a set of rules outlined as follows. 1. An alternative (mutated) allele evolutionary appearance coincides with the lack of any other mutations within ROI (a conserved island rule); 2. positioning of the future mutation often represents a turning point of dramatic changes of an allele ROI (e.g. as seen in marmoset: rs2218404 (50-90%), rs628117 (30-80%), rs96501 (100-40%)); 3. an AE of ROI often precedes the emergence of a mutation allele (e.g. rs2218404: chimpanzee to human (k = 1.59), appearance of "G" in Loschbour; rs628117: marmoset to chimpanzee (k = 1.10), appearance of "T" in AltaiNea; rs96501: marmoset to chimpanzee (k = 0.83), appearance of "C" in AltaiNea; rs2274855: chimpanzee to human (k = 0.79), appearance of "A" in Motala12; 4. low identity percent (equivalent to subsequent substantial evolutionary changes) among the evolutionary species within the allele surrounding proximity of as long as $\pm$50 nu is not sufficient for the future mutated allele significance as a cognitive endophenotype determinant (as deduced by the IQ score) as seen for the rs1373336, rs1444042, rs4915045 and rs7851893 (none of them are IQ-affecting, though associated with SCZ, despite showing (very) low identity in mice). Rather some dramatic changes within the allele's immediate proximity of $\pm$10 nu (defined as a ROI) preceded or followed by more stringently conserved DNA are necessary (the conserved island perturbation rule). Currently we are unable to state that the IQ-associated alleles ROIs are regulatory loci and an important source of evolutionary innovation (**Rubinstein and de Souza, 2013**) but they may be the smallest functional blocks of a strong positive selection exerts its action upon similarly to the 20–30 nu clusters of strongly

conserved non-coding elements (CNEs), transcription factor binding sites (TFBS), RNA splicing and editing motifs (**Harmston et al., 2013**).

Extinct hominins and IQ-associated mutation alleles. Availability of archaic genomes allows excavation for the advantageous alleles that modern humans acquired from archaic extinct hominins such as Neandertals and Denisovans who used to live 230,000-30,000 years ago (Middle/Upper Paleolithic, Old Stone Age) defined by distinct morphological features (**Meyer et al., 2012**), and from modern extinct humans (hunters, farmers) from Mesolithic (Middle Stone Age, ~10,000 yrs BC, **Lazaridis et al., 2014**) and Neolithic (New Stone Age, ~5,000 BC, **Keller et al., 2012**; **Rasmussen et al., 2010**) periods. Though exhibiting several anatomical features, making archaic hominins different from the modern human, there are studies challenging the idea that reserve symbolism and abstract thinking was an exclusive prerogative of modern human (**Appenzeller, 2013**; **Wong, 2015**). The time Neanderthals used to live in is thought to be associated with the onset of cognitive fluidity involving the capacity to draw analogies (early paintings), to combine concepts (making tools) and to adapt ideas for new contexts (**Gabora and Russon, 2011**). Wynn and Coolidge believe that evolution of WM was central to the evolution of human cognitive traits consisted from few genetic mutations that led to "enhanced WM" 200,000-40,000 BC (**Balter, 2010**). Our work partially supports this idea showing the perseverance of higher WM score-associated alleles across the hominins such as T of rs1105684 and G of rs2274855 (**Figure 3D**) but a Neolithic appearance of rs2149171 T in Iceman previously found only in mice genome supporting the conclusion made by **Crabtree (2013**) that modern humans as species "are surprisingly intellectually fragile and perhaps reached a peak 2,000–6,000 years ago". Mesolithic period has been always considered as a key gate for the evolution of human languages (**Haak et al., 2015**) with our data showing that rs2218404 G-allele associated with a higher VC score (**Figure 1B-1**) emerges for the first time in the Loschbour hunter *NTNG1* gene (**Figure 3D**).

VC as a part of abstract symbol usage is associated with the global network efficiency (as a part of fronto-parietal network in **Song et al., 2008**; **Glascher et al., 2009**), and global communication and intellectual performance (**Pamplona et al., 2015**). From this point of view it is not surprising that appearance of the G allele in Loschbour and Iceman genomes coincides with the presence of PS enhancing rs96501 T allele (**Figure 3D**). A wealth of data has been collected characterising possible look and health status of archaic hominins and modern but extinct humans (for ref. see **Sarkissian et al., 2015** and **SM:** Discussion). Based on our own data we may also speculate that the extinct hominins may have had a lower VC comparing to us, and consequently, Neanderthals were unlikely able for a semantic communication due to a global network inefficiency VC is associated with; they have had similar to us PS (if they had lived beyond the Mesolithic period), and were likely to have had identical to modern human WM, corroborating the advanced evolutionary nature of this important human cognitive domain of a limited capacity and associated with intelligence.

CONCLUSION

Evolution of a novel function relies on enhanced genetic robustness through functional redundancy potentially provided by a gene duplication event. Further evolutionary outcome depends on the substrate availability (undergoing its own evolution) upon which the novel function(s) exerts its action. Nature does not create but tinkers to perfection provided to it material exploring available evolutionary tools. Half a billion years ago a gene duplication event had provided a plethora of such substrate thus converting the evolution itself into a "Creator" of new functions. Here we have described how a pair of twin genes got themselves involved into the human cognitive functioning believed to be emerged in a primordial state in primitive vertebrates prior to the first recorded gene duplication. Subsequent process of the function specialisation made *NTNG* paralogs to subfunctionalise into distinct cognitive

330 domains in a complementary manner (**Prosselkov et al., 2015**).

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MATERIALS AND METHODS

Ethics statement. This study was performed in accordance with the World Medical Association's Declaration of Helsinki and approved by the Osaka University Research Ethics Committee. A written informed consent was obtained from all subjects after the procedures had been fully explained.

Subjects. The procedures were performed as per established protocols at Osaka University as described previously (**Ohi et al., 2012**). The subjects consisted from 339 patients with SCZ and 716 healthy controls. The sex ratio did not differ significantly between the groups, but the mean age was significantly different. The subjects were all biologically unrelated Japanese and recruited from both outpatient and inpatient units at Osaka University Hospital and other psychiatric hospitals. Each patient with SCZ had been diagnosed by at least two trained psychiatrists based on unstructured clinical interviews, according to the criteria of the DSM-IV (**APA, 2013**). In case if the diagnosis of the two trained psychiatrists was discordant, it was resolved through the further negotiations on both specialist opinions. In case of unresolved diagnostic disputes, the patient was omitted from the study. Psychiatrically healthy controls were recruited through local advertisements and were evaluated by means of unstructured interviews to exclude individuals with current or past contact with psychiatric services, those who experienced psychiatric medications, or who were not Japanese. Controls for family history of a CD, such as SCZ, BD, or major depressive disorder were not included. Ethnicity was determined by self-report and was not confirmed by genetic analyses. Additionally, subjects were excluded from this study if they had neurologic or medical conditions that could have potentially affect their central nervous system, such as atypical headaches, head trauma with loss of consciousness, chronic lung disease, kidney disease, chronic hepatic disease, thyroid disease, active cancer, cerebrovascular disease, epilepsy, seizures, substance abuse related disorders, or mental retardation.

SNPs selection, genotyping, and genomic sequencing. This study was designed to examine the association of SCZ patients cognitive performance (through WAIS-III implementation, **Wechsler, 1958**) with *NTNG* genes. Venous blood was collected from the subjects. Genomic DNA was extracted from the whole blood using standard procedures. The SNPs (**Fukasawa et al., 2004**; **Aoki-Suzuki et al., 2005**; **JSSLG et al., 2005**; **Eastwood and Harrison, 2008**; **Ohtsuki et al., 2008**; **Zakharyan et al., 2011**; **Zhu et al., 2011**; **Ayalew et al., 2012**; **Wilcox and Quadri, 2014**) were genotyped using the TaqMan allelic discrimination assay (Applied Biosystems, Foster City, CA). No deviations from the Hardy-Weinberg equilibrium in the examined SNPs were detected ($p > 0.05$).

Statistical analysis. The effects of the diagnosis, genotype and their interaction on cognitive performances in the WAIS were analyzed by two-way analyses of covariance (ANCOVA). Diagnosis and genotype statuses were included in the model as independent variables (**ST1**). FIQ and each WAIS subscale score (VIQ, PIQ, VC, PO, WM, PS, Vc, SiM, IF, CH, AM, DS, LNS, PC, BD, and MR) were included as dependent variables. Sex, age and years of education were treated as covariates, as they were possible confounding factors. All p values are two tailed, and statistical significance was defined as $*p < 0.05$ and $**p < 0.01$.

Identity percent calculations and the definition of ROIs. The complete procedure is described in the **Figure 4** legend. Stretcher (**McWilliam et al., 2013**) was used for the alignments (the default values were: gap penalty – 16 (DNA) and 12 (protein), and the extend penalty – 4 (DNA) and 2 (protein)), for the percent identity calculations and evolutionary rates. A ROI was selected as a minimal area surrounding a SNP mutation allele incorporating the outmost evolutionary dramatic changes.

Mice, primates and hominins *NTNG* paralogs DNA and encoded aa sequences reconstruction. Genomes for mouse (GRC38.p3) and marmoset (C_jacchus3.2.1) were from Ensemble. Since chimpanzee's genome is based only on a single individual (CHIMP2.1.4,

Clint) and contains several questionable information we have reconstructed a consensus genome sequence for both *NTNG* genes based on 25 primate sequences of *Pan troglodytes* (**Prado-Martinez et al., 2013**). All datasets used for the *NTNG* paralogs DNA and encoded by them proteins reconstruction are listed in **ST2**. For details refer to **SM**.

SUPPLEMENTARY MATERIALS (**SM**)

Contain additional Results and Discussion, Supplementary Methods (ancient and primate genomes reconstructions), and Supplementary Tables (**ST1** and **ST2**) as a single compiled pdf file. Also included are human Netrin-G1 and Netrin-G2 alignments, as well as 101 nu alignments for all 11 ROIs across the all analysed species.

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COMPETING INTERESTS

Authors would like to express a lack of any competing interests associated with the work.

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