

Correlation Analysis between English-Chinese Translation-Based Writing Error Types and Language Gene Polymorphisms for Chinese Graduate Students

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Abstract—In this paper, English-Chinese translation-based writing error types of twenty-one graduate students in the same class for the same course were collected to search for the correlation with language gene polymorphism as single nucleic polymorphism (SNP) of FOXP2 gene. Students' genome DNA was extracted from the finger-tip blood and subjected to DNA sequencing to characterize SNP information. Attention scores measured by Schulte grid were also included plus the class score. PCA (principal component analysis) correlation analysis indicated that attention score seems irrelevant to writing error types and SNPs, while two SNP alleles, rs2253478 (SNP3) and rs2396722 (SNP4), displayed preliminary correlation with writing error types. This study provided methodologically a scheme how to associate important learning behavior (phenotype) in classroom with students' genotype (SNPs in this study) as a preparation to develop genome-based personalized education protocol in the future.

Index Terms—language gene; English-Chinese translation; writing error; gene polymorphism; personalized education; genome

I. INTRODUCTION

It is well known that language ability is highly associated with learning performance of students. Also, there are lines of evidence that learning performance has solid genetic elements [1] that have not been clearly elucidated, though. Previously, most people may stick to a conventional idea that an individual's genetic DNA comes from parents and cannot purposely be changed in a life. But technology break-through is changing the world quickly, one example of which is gene editing technology and its fast influence around the world. Now more and more people realize that a person's genomic DNA may be editable in a very near future [2], and a poor learning capacity is not a thing that can't be changed forever. In

this situation, language gene, as a learning ability engineering target, is getting attention from scientists.

Lots of studies have been undertaken on the relationship between genes and human disease [3], but few on that between genes and learning behavior or capacity. One of the reasons is that it is only at the start point to tackle mechanisms of complicated phenotypes such as language behavior; another reason is to avoid personal discrimination (in the future). But the simple avoidance may not work, as the racial discrimination cannot be avoided simply by interruption of investigations on racial gene differences. Racial gene difference is an important base for precision medicine, while individual gene difference is a molecular base for personalized education/learning.

Innate learning ability difference between individuals is very large [1], [4], as seen when a student in an ordinary college is compared with one in Harvard University or MIT. The aim of education is to find one's advantage over one's shortcoming (disadvantage) and try to work in one's life by taking his own advantage(s), plus make some complementation for his disadvantage though proper education. By now, the content of education has little to do with personal genome in the classroom.

One important aspect is the digital nature of human life. Human genetic materials are composed of four bases, A (adenine), T (thymine), G (guanine) and C (cytosine). The total genetic materials in a cell are called genome. The genome encodes the whole life behavior through these four letters, so the whole lives, human and any other life forms, are basically digital [5], [6]. This nature means that human learning capacity and behavior and related molecular basis can be decoded completely, thus can be predicted largely by the human genome sequence.

Meanwhile, the world has been entering into the era of big data and artificial intelligence. Big data actually play a role of materials to construct the artificial intelligence, so the era is actually just the artificial intelligence. It has

been postulated that the era is coming very shortly, say, in just twenty years. When the whole society is running with technologies mainly derived from artificial intelligence and unexpected large scale of big data, human genome information will have no reason to escape the destiny of being fully exploited. At that time, people will likely rush for genome error correction and phenotype reconstruction. For example, one may want to change his hair color by gene modification, one may want to have an improved memory speed through genetic editing, one may want to change his speaking sound by re-editing his language genes, and some people may want to totally change his facial pattern by simply changing several genes. Revision of one's learning ability may become a commercial service. It is not sure where the technologies will bring us, but it is very likely that the relationship between learning behavior and a batch of human genes (including language genes) will be an important subject to be investigated and utilized.

Translation-based writing is an important learning performance in some college courses in China. In many examinations, students are often asked to translate English paragraphs into Chinese in a fixed time, but most students don't have enough translation training in formal classes. Translation score sometimes determines whether or not a student can be accepted as a graduate student. Some writing training is assigned as a course in graduate degree education, but generally such a course is not long enough and the training is generally inadequate.

During the past few years, translation-writing based errors have been steadily but differentially displayed by different students. So a postulation is always tackled by the authors if the differential behavior on translation-writing error type and frequency of different students has some genetic background. Because translation-writing skill is also generally linked with language ability, the authors planned this study to preliminarily investigate the correlation relationship between language gene single nucleic polymorphism (SNP) and translation-writing performance. FOXP2 gene [7], [8] was chosen for SNP analysis [9], [10]. Translation-writing errors, plus attention and course scores, were collected and analyzed.

II. MATERIALS AND METHODS

A. Language Gene Polymorphism Analysis

Sampling was undertaken from the graduate students who selected the course of Marine Systems Biotechnology. With the signed consent, the finger-tip blood was collected with Blood Glucose Device Kit for home usage (SANNUNO Company, China). The 50-100 μ l blood was collected from each student and stored at -80 degree refrigerator at once.

TABLE I. THE NAMELIST OF SOME LANGUAGE GENES [11], [12]

	Gene	Compromised ability when mutated (example)
1	FOXP1	Expressive language
2	FOXP2	speech

3	TPK1	Syntactic and lexical ability
4	DYX1C1	Reading, dyslexia
5	FLNC	Reading, language
6	TM4SF20	Language delay; communication disorder
7	DCDC2	Reading, dyslexia
8	ATP2C2	memory
9	ROBO2	Expressive vocabulary
10	ROBO1	Phonological buffer
11	KIAA0319	Reading, dyslexia
12	CNTNAP2	Early language development
13	RBFOX2	Reading, language
14	CMIP	Reading, memory
15	NFXL1	speech
16	CNVs	language

Human genome DNA extraction was undertaken using a Sangon Blood DNA Extraction Kit (B518253-0050). For each blood sample, the final genomic DNA was eluted with 100 μ l TE buffer (10mM Tris, pH 8.0, 1mM EDTA).

TABLE II. DNA PRIMERS TO DETECT FOXP2 GENE POLYMORPHISM [7]

SNP	Primers(5'-3')
rs923875 (SNP1)	F: CTTGGGAACTGAAGCCAG R: ACTCACCCAATATCATGCAATAG
rs10447760 (SNP2)	F: CTATTTCGATCGCTGTTTGCC R: GTGGCAGCTAGTTTGTGATG
rs2253478 (SNP3)	F: TAAAGAATAAAGACTGGGGTAAATGG R: TCAGGGACATTTTATTAATTTGACA
rs2396722 (SNP4)	F: GTCATCAATGTCACAGAGAACTTG R: AGACTGTACTTGTTCCTGGGAG
rs2396753 (SNP5)	F: TGGCTATGAAATAACAAGCACAAAC R: CCCAGTTATTGGCTCACTCTACC
rs1597548 (SNP6)	F: CAATTCACCAACAGTTGTACC R: GATGGCTACATCTGCTTTGAC
Rs6961558 (SNP7)	F: GAGCGCAGACACCTTTCGGTG R: CACTGAGGTCGGGTGTCACGG
rs17137124 (SNP8)	F: GGTTCCTACAGCAGTATCATGG R: TTATCTGCACCAATGGAAGG

Table I listed some known language genes in which FOXP2 attracted lots of attention. In this study, eight FOXP2 gene SNP sites [13] were chosen and subjected to eight pairs of polymerase chain reaction (PCR) primers (Table II); some primers were modified by simple allele-discriminating (SAP)-PCR method [14], [15]. Expected

DNA fragments were successfully amplified from fingertip blood DNA of the students under written consent (detailed data not shown, will be published later). SAP based technology can distinguish the two-base alleles without further DNA sequencing. But three or four-base SNP alleles need further DNA sequencing to acquire the base content.

Language gene amplification conditions were set up as follow [16]. The PCR system had a total volume of 12 μ L consisting of 1 μ L of template DNA, 6 μ L of NPK02 2 $\times$ buffer, 0.8 μ L of each primer (2 μ M), 0.2 μ L Taq DNA polymerase (5U/ μ L), and 3.2 μ L of distilled water. In the negative control, the template DNA was replaced by the same volume of water. The reactions started with an initial denaturing step at 95 $^{\circ}$ C for 5min, followed by 34 cycles of 95 $^{\circ}$ C for 30s, 60 $^{\circ}$ C for 60s, and 72 $^{\circ}$ C for 60s, and were appended with a 4 min elongation step at 72 $^{\circ}$ C. Amplified target bands (about 1500bp) were gel-purified using Sangon SanPrep kit (Cat#: SK8132). Purified DNA was then subjected to Sanger sequencing using the reverse primer of each amplified DNA fragment. The raw sequences were assembled by CExpress and edited by EditSeq to make sure of correct orientation. Successfully assembled DNA was subjected to Basic Local Alignment Search Tool (BLAST) analysis at the National Center for Biotechnology Information (NCBI) database (www.ncbi.nlm.nih.gov) in order to get taxonomic information. For 21 students, there were total 21 $\times$ 8=168 sequencing reactions and the sequences obtained were

aligned with MAFFT multiple sequence alignment tool (<http://www.ebi.ac.uk/Tools/msa/mafft>). From the MAFFT result the SNP site information for each student was clearly displayed.

B. Writing Assay and Writing Error Scores

Twenty-one students from a graduate class of 2018 autumn semester were selected with consent for this study. The class is frequently assigned for 20-min translation quiz from English to Chinese. The number of translation-writing errors of each quiz was accounted for word, phrase, grammar and sentence, respectively. A normalized error score was made by multiplying the number of word, phrase, grammar and sentence errors (Table 3 and Table 4). Note: the translation-writing errors were collected from eight quizzes and all eight scores of each student for word, phrase, grammar and sentence were added together and put into Table 3.

C. Attention Analysis

A Schulte table is a grid with randomly distributed numbers or letters used for development of peripheral vision, attention speed reading and visual perception [see Wikipedia]. The Schulte grid with 10 $\times$ 10 numbers was used in this study to quantify the attention level of each student. Students were required to focus on the grid center and find all the 100 numbers in 6 minutes with their peripheral vision, i.e. without moving their eyes (Table III and Table IV).

TABLE III. SUMMARY OF TRANSLATION-WRITING ERROR NUMBER AND OTHER SCORES (I)

st	wo	ph	gr	se	nes	cc	at1	at2	at3	at4	at5
st1	15	6	4	31	11160	74	54	75	55	68	55
st2	6	14	6	22	11088	77	47	38	50	45	52
st3	11	13	3	24	10296	77	47	40	46	42	43
st4	12	7	3	27	6804	75	66	60	64	63	70
st5	6	9	5	15	4050	77	53	60	52	59	57
st6	4	7	5	25	3500	77	62	30	61	40	45
st7	9	13	1	22	2574	82	32	44	33	47	55
st8	5	7	4	12	1680	78	57	49	59	51	54
st9	5	5	2	27	1350	80	58	42	57	45	56
st10	4	8	2	20	1280	79	80	59	77	62	70
st11	8	8	1	20	1280	80	60	38	62	42	41
st12	4	9	3	11	1188	80	46	44	50	47	45
st13	2	7	4	19	1064	81	62	36	58	45	48
st14	3	10	2	15	900	82	59	43	60	45	49
st15	4	11	1	13	572	83	71	55	72	59	70
st16	7	7	1	10	490	84	46	49	49	53	55
st17	5	4	1	12	240	86	77	53	78	60	62
st18	4	4	1	15	240	85	44	38	50	42	45
st19	3	5	1	13	195	88	70	66	64	58	66
st20	6	3	2	5	180	83	44	35	50	41	39
st21	5	4	1	6	120	87	47	49	51	52	55

Note: st: student; wo: word; ph: phrase; gr: grammar; se: sentence; nes: normalized error score; cc: class core; attention score: at1-at5.

TABLE IV. SUMMARY OF TRANSLATION-WRITING ERROR NUMBER AND OTHER SCORES (II)

st	at6	at7	at8	SN1	SN2	SN3	SN4	SN5	SN6	SN7	SN8
st1	50	45	54	C	C	G	C	T	G	A	G
st2	48	43	53	A	C	G	C	C	C	A	C
st3	43	56	50	A	T	G	C	T	G	A	T
st4	69	68	62	C	T	G	C	C	C	A	T
st5	55	65	57	T	T	A	C	T	C	G	G
st6	67	52	68	C	T	G	C	C	G	A	C
st7	48	52	50	A	C	G	C	G	C	A	C
st8	47	48	50	C	C	A	C	C	C	A	G
st9	45	70	52	C	T	T	C	A	C	G	T
st10	59	65	62	A	C	G	C	A	C	A	C
st11	58	47	61	T	T	G	C	C	G	A	C
st12	47	50	50	C	C	G	T	A	G	G	G
st13	66	43	74	T	C	A	T	C	C	G	T
st14	56	51	64	C	T	A	C	G	C	G	C
st15	66	76	64	C	T	T	C	A	C	A	G
st16	54	58	61	C	C	T	T	C	G	A	T
st17	67	67	68	T	C	G	T	G	G	G	C
st18	54	42	61	A	T	G	T	C	G	G	G
st19	56	70	62	A	C	G	T	C	C	G	T
st20	54	43	68	C	C	A	C	C	C	G	T
st21	49	61	46	T	T	A	T	C	C	G	G

Note: attention score: at6-at8; SN: SNP. Four bases, A,T,C and G, were assigned scores as 20,40,60 and 80, respectively, for SNP parameter to be conveniently used in the numerical PCA analysis.

D. Course Score

All the students were taught in a bilingual course "Marine Systems Biology and Technology", in which translation of course contents from English to Chinese was frequently trained and examined. In the final exam of the course, about 35% of the exam content was translation from English to Chinese. The final course score was also included for correlation analysis.

E. Correlation Analysis

The software Origin v10.5.1 was employed to analyze the potential correlation relationship between all parameters in this study.

III. RESULTS

1) Sentence error is the major error type: Among all 21 students, only one student's sentence error number is smaller than any of other three error types. So the sentence error is the dominant type for most students. Grammar error is much less than other error types. From figure 1, it is also clear that the sentence error is most correlated with SNP3 and SNP4. These two SNP sites are also most correlated with all four error types (discussed below). But the results in this stage have not pinpointed which alleles in the SNP3 and SNP4 are more correlated

with the sentence error and hopefully can be elucidated in the next study.

2) Attention score has little correlation with translation error: This preliminary investigation also revealed that attention score doesn't have much correlation with the four types of translation-writing error (Figure 1). This result may suggest, from another point of view, that translation-writing errors do have close relationship with language ability, because attention ability is not thought as directly language-related.

3) Attention score has little correlation with SNPs: Consistently with above result, attention was also not closely correlated with SNPs, except for SNP1. Though positively correlated between SNP1 and attention, this correlation is very weak as the arrow length of SNP1 is very short. Some SNPs of FOXP2 may be positively correlated with attention ability, because this gene is undoubtedly involved in other biological functions [17-19] besides language ability. In the past a few years, there were some reports about attention phenotype and its related genes [20-21], but none of them have been linked with language genes.

4) SNP3 and SNP4 seem more closely correlated with translation error: In this study, eight SNP sites of FOXP2 gene were scanned in the samples, and they are rs923875 (SNP1), rs10447760 (SNP2), rs2253478 (SNP3),

rs2396722 (SNP4), rs2396753 (SNP5), rs1597548 (SNP6), Rs6961558 (SNP7), and rs17137124 (SNP8). Interestingly, the allele rs2396722C of SNP4 was found more frequent in normal controls than in schizophrenic patients with auditory hallucinations, while conditional association between SNP rs2253478 and the poverty of speech was also detected [13].

IV. DISCUSSION

1) Potential significance between FOXP2 SNPs and translation-writing related error type and frequency: We hypothesized that FOXP2 polymorphism may confer vulnerability to the language related symptoms including translation-writing related error type and frequency. But a large scale sampling shall be essential to get a confirming conclusion.

2) Significance of the correlated FOXP2 SNP sites: this study found that the rs2253478 (SNP3) and rs2396722 (SNP4) showed more correlation with the translation-writing error types, but the biological meaning of these SNPs have been vague. It is postulated that these SNPs are all intron variants for FOXP2 gene (see dbSNP database at www.ncbi.nlm.nih.gov/snp), so they are not appearing in the FOXP2 protein itself, but may be involved in the gene expression process of FOXP2 gene.

3) Limitations of this study: In this small scale of study, we may get similar result no matter what the SNP determination result is for only 21 students. In order to escape from the situation like “garbage in-garbage out”, more SNPs or more samples are needed. So the result in this study is the only preliminary observation.

4) Effectiveness for translation error to describe the writing level: The writing ability contains at least word, phrase, grammar, sentence, paragraph and whole article. Apparently, translation-writing only mainly touches word, phrase, grammar, and sentence, and partially reflects the writing ability. However, it seems that translation-writing is good enough as a start point to tackle potential correlations between language ability and genetic components in students. It is highly anticipated to undertake similar studies to find language-performance related SNP patterns later on. In the near future, when gene-editing [22] is practical, modification of personal language gene related learning performance could also be expected.

5) Values of this study. This study works as a methodological example. Similarly, any interesting phenotype in language learning, for example reading quality-related parameters, such as reading continuity, sound stability, sound width, sound clearness, can be investigated in the context of its correlation with language gene SNPs. Note, if the average number of SNP for each language gene is ten, the total available SNPs are about 160 for the language genes in the Table I. Actually the known numbers of some language genes are much larger than the ten (SNPs and other types of DNA variants for each language gene can be checked out in dbSNP database). So a lot of experimental studies are to be undertaken in the future. As for the biological meanings

of the detected correlations, investigators have to spend probably a long time before they are fully understood.

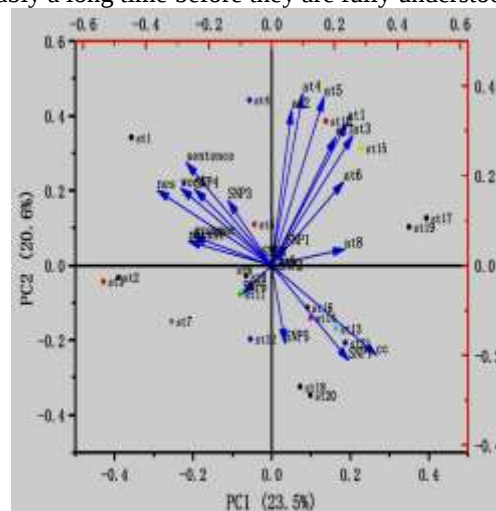


Figure 1. The correlation analysis result of multiple parameters in this study. st: student; nes: normalized error score; cc: class core; attention score: at1-at8; SN: SNP.

V. CONCLUSION

This study performed correlation analysis between English-Chinese translation-based writing error types and language gene polymorphisms for Chinese graduate students. First, this is one important direction for the future education by which any significant educational trait of a student can be studied similarly to get possible correlation and then to classify the targeted students for separate teaching regime development. This is about precision education we have to face soon. Second, this study provided an approach to establish potential correlation between target gene polymorphism in different individuals and any interesting learning phenotype (behavior) parameters. This is a useful approach, though probably not perfect yet. Data scale would be a key factor to grasp the real strong correlations. Third, specific SNPs have to be further confirmed and investigated using large dataset before they can be used as a start to develop personalized teaching curriculum.

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