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Accumulation of CTCF-binding sites drives expression divergence between tandemly duplicated genes in humans

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From The Twelfth Asia Pacific Bioinformatics Conference (APBC 2014)
Shanghai, China. 17-19 January 2014

Abstract

Background: During eukaryotic genome evolution, tandem gene duplication is the most frequent event giving rise to clustered gene families. However, how expression divergence between tandemly duplicated genes has emerged and maintained remain unclear. In particular, it is unknown if epigenetic regulators have been involved in the process.

Results: We demonstrate that CCCTC-binding factor (CTCF), the master epigenetic regulator and the only known insulator protein in humans, has played a predominant role in generating divergence in both expression profiles and expression levels between adjacent paralogs in the human genome. This phenomenon was not observed for non-paralogous adjacent genes. After tandem duplication events, CTCF-binding sites gradually accumulate between paralogs. This trend was more prominent for genes involved in particular functions.

Conclusions: The accumulation of CTCF-binding sites drives expression divergence of tandemly duplicated genes. This process is likely targeted by natural selection. Our study reveals the importance of CTCF to the evolution of animal diversity and complexity.

Background

Gene duplication is a major driver for the emergence of organismal complexity and evolutionary innovations [1,2]. Tandem duplication is the most common route to the formation of clustered paralogous genes [3,4]. A newly duplicated gene must diverge from its progenitor gene in coding sequence or expression, or it will degenerate due to redundancy [1,5,6]. To acquire novel transcription patterns, tandemly duplicated genes need to interrupt expression similarity due to shared upstream *cis*-elements upon origin [3,7] and transcriptional interference contributed by physical proximity [8]. Despite the challenges, functionally important gene clusters consisting of paralogs with distinct expression patterns are found in a wide range of species, including human [9,10]. Therefore, it is important to understand the

origin and maintenance of expression divergence between tandem paralogs.

CCCTC-binding factor (CTCF), the only known human insulator protein, plays a master role in determining the transcriptional landscape of genomes. When bound to insulator sequences (CTCF-binding sites), CTCF can prevent repressive heterochromatin from spreading into neighboring regions [11,12]. In addition, CTCF interferes with enhancer-promoter communication [13] and guides long-range chromatin interactions [14]. Because changes in epigenetic marks play roles in regulatory divergence of duplicated genes [15-17], we hypothesize that CTCF also plays a role. Using human RNA-seq and ChIP-seq data (see Methods), we examined how CTCF drives regulatory divergence of duplicated genes, especially tandemly arrayed paralogs.

Results and discussion

In the genome, adjacent genes are coexpressed due to a common origin [18], cofunctionality [19], or deleterious

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transcriptional interference [8]. Using RNA-seq data from six human adult tissues [20], we measured gene expression dissimilarity between adjacent genes in terms of expression profile or expression level using $ExpD_{1-r}$ or $ExpD_{Euc}$ (see Methods), respectively. $ExpD_{1-r}$ focused on changes in the shape across the tissue dimension, while $ExpD_{Euc}$ focused on summed changes in abundance. We studied divergences in both profiles and abundances because previous studies have shown that the observations from the two aspects did not necessarily produce consistent results [21], possibly due to different underlying mechanisms controlling the properties [22].

Mammalian genes close to each other have similar expression profiles [8,19]. CTCF-binding sites can prevent undesirable crosstalk between active and inactive genomic regions [23]. DNA methylation upstream of a gene can inhibit its transcriptional initiation [24]. To determine if the effect of intergenic distance, the number of CTCF-binding sites, and DNA methylation is related to shared evolutionary origin, we measured $ExpD_{1-r}$ and $ExpD_{Euc}$ in non-paralogous adjacent genes. Non-paralogous gene pairs with a longer intergenic distance (d , calculated as the distance in nucleotides between the transcriptional start sites, TSS), more overlapping CTCF-binding sites ($\#CTCF$, see Methods), or a larger difference in upstream DNA methylation ($\Delta CpG_{O/E}$, see Methods) had greater $ExpD_{1-r}$ or $ExpD_{Euc}$ (see ρ in Table 1). Although d , $\#CTCF$, and $\Delta CpG_{O/E}$ were interrelated (d vs. $\#CTCF$: $\rho=0.521$, $P<10^{-300}$; $\#CTCF$ vs. $\Delta CpG_{O/E}$: $\rho=0.075$, $P<10^{-40}$; $\Delta CpG_{O/E}$ vs. d : $\rho=0.166$, $P<10^{-192}$), partial correlation analyses (see Methods) suggested that the effects of d , $\#CTCF$, and $\Delta CpG_{O/E}$ on generating expression dissimilarity between adjacent genes was independent. d had the largest direct influence on $ExpD_{1-r}$, and $\Delta CpG_{O/E}$ had the largest direct influence on $ExpD_{Euc}$. $\#CTCF$ had a weak but significant effect on $ExpD_{1-r}$ and an intermediate effect on $ExpD_{Euc}$ (see ρ_p in Table 1). Although CTCF binding can vary among cell types [25], when we define $\#CTCF$ using joint CTCF ChIP-seq peaks (see Methods) instead of overlapping CTCF peaks, the results did not change (Table S1 in Additional file 1).

Mechanisms generating coding sequence divergence, such as change in protein structure or splicing, between paralogous genes have been intensively investigated [2,26-28]. By contrast, mechanisms generating expression divergence have garnered less attention. Although $\#CTCF$ was not the strongest determinant of expression divergence in non-paralogous adjacent gene pairs (Table 1), for adjacent paralogs, $\#CTCF$ had the greatest direct influence on $ExpD_{1-r}$ and $ExpD_{Euc}$, followed by $\Delta CpG_{O/E}$ (see ρ_p in Table 2). Repeating analysis based on an independently generated and unpublished RNA-seq dataset including 16 human tissues (Illumina BodyMap 2.0 project, see Methods) produced a result consistent with Table 1 and 2 (Table S2 in Additional file 1), suggesting the robustness of the pattern found.

We classified adjacent paralogs into three groups according the orientations: head-to-head, head-to-tail and tail-to-tail [29]. Although reduced sample sizes resulted in reduced statistical significance, the pattern of the greatest impact $\#CTCF$ on expression divergences held regardless of the orientation of paralogs (Table 3). Using microarray expression data, a previous study found that intergenic distance was related to expression divergence for tandemly arrayed paralogs [30]. However, microarray data is known to have cross-hybridization related biases [17], and we found no direct association between intergenic distance and expression divergence for tandemly arrayed paralogs after controlling for $\#CTCF$ and $\Delta CpG_{O/E}$ (see ρ_p of d vs. $ExpD_{1-r}$ or $ExpD_{Euc}$, Table 2). Taken together, these results suggest that CTCF-binding sites play a very significant, if not primary, role in driving expression divergence of tandemly duplicated genes.

There are two hypotheses to explain the influence of CTCF-binding sites in driving expression divergence of tandem paralogs. First, tandem paralogs that arose in genomic regions with high densities of CTCF-binding sites nearby are more likely to be preserved due to immediate independence of gene regulation. Second, CTCF-binding sites accumulated over time to enhance independent gene regulation of tandem paralogs, especially those have been functionally diverged. If the first

Table 1 Rank correlations (ρ) and partial rank correlations (ρ_p) of the genomic properties with expression dissimilarities (measured by $ExpD_{1-r}$ or $ExpD_{Euc}$) of the non-paralogous adjacent genes

Genomic properties ^a	$ExpD_{1-r}$		$ExpD_{Euc}$	
	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}
d	0.180 ($<10^{-217}$)	0.130 ($<10^{-113}$)	0.112 ($<10^{-83}$)	0.040 ($<10^{-11}$)
$\#CTCF$	0.120 ($<10^{-98}$)	0.032 ($<10^{-7}$)	0.104 ($<10^{-72}$)	0.058 ($<10^{-22}$)
$\Delta CpG_{O/E}$	0.077 ($<10^{-39}$)	0.049 ($<10^{-16}$)	0.196 ($<10^{-258}$)	0.182 ($<10^{-227}$)

^a " d ", intergenic distance; " $\#CTCF$ ", number of overlapping CTCF-binding sites; " $\Delta CpG_{O/E}$ ", difference in upstream DNA methylation.

^b P values show the probabilities of the observations under the hypothesis of no correlation.

^c Spearman's partial correlation coefficient ρ_p is computed by controlling for the other two genomic properties listed in ^a

Table 2 Rank correlations (ρ) and partial rank correlations (ρ_p) of the examined genomic properties with expression dissimilarities (measured by $ExpD_{1-r}$ or $ExpD_{Euc}$) of the paralogous adjacent genes

Genomic properties ^a	$ExpD_{1-r}$		$ExpD_{Euc}$	
	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}
<i>d</i>	0.039 (0.164)	-0.011 (0.707)	0.100 (<10 ⁻³)	0.021 (0.461)
#CTCF	0.111 (<10 ⁻⁴)	0.103 (<10 ⁻³)	0.187 (<10 ⁻¹⁰)	0.159 (<10 ⁻⁷)
$\Delta CpG_{O/E}$	0.069 (0.015)	0.054 (0.023)	0.102 (<10 ⁻³)	0.094 (<10 ⁻³)

^a "*d*", intergenic distance; "#CTCF", number of overlapping CTCF-binding sites; " $\Delta CpG_{O/E}$ ", difference in upstream DNA methylation.

^b P values show the probabilities of the observations under the hypothesis of no correlation.

^c Spearman's partial correlation coefficient ρ_p is computed by controlling for the other two genomic properties listed in ^a

hypothesis is correct, there would be no correlation between the divergence time of paralogs (measured by d_S or T_{phy} , see Methods) and #CTCF. However, we observed a positive correlation between d_S or T_{phy} and #CTCF (Table 4), suggesting that the second hypothesis is correct. #CTCF had stronger rank correlation (ρ), which is positive, to d_S (or T_{phy}) than *d* and $\Delta CpG_{O/E}$ (Table 4). Partial correlation analyses further suggested that the increase of #CTCF with d_S (or T_{phy}) is not caused by the change in *d* or $\Delta CpG_{O/E}$ or their combined effect over time (see ρ_p in Table 4). By contrast, the insignificant partial correlation of *d* with respect to d_S (or T_{phy}) indicated that the increase *d* over time can be explained by the increase in the number of CTCF-binding sites and the associated changes in DNA methylation.

To determine whether tandem paralogs with specific functions tend to have a greater number of intervening CTCF-binding sites, we performed enrichment analyses in Gene Ontology (GO) terms. To eliminate the potential effect of duplicability in GO analysis [4], paralogous and non-paralogous gene pairs were analyzed separately.

To control for the potential effect of gene density [31], #CTCF/*d* was used instead of #CTCF (although using #CTCF produced a consistent result, which is not shown). Gene pairs in the top quartile of CTCF-binding site density (#CTCF/*d*) were compared against the bottom three quartiles. Enriched/depleted GO terms for the paralog group were substantially different from those in the non-paralog group (Table 5). Only two GO terms (GO:0010033, response to organic substance; GO:0031012, extracellular matrix) had the same enrichment status ("enriched") in both groups. Tandemly duplicated genes with a higher density of intervening CTCF-binding sites tended to specifically encode proteins involved in gene expression (GO:0010467, GO:0008134), metabolic processes (GO:0019222, GO:0006139, GO:0050790), or cellular processes (GO:0050794, GO:0051128, GO:0044249) through DNA binding (GO:0003677), SMAD binding (GO:0046332), growth factor binding (GO:0019955), or kinase interaction (GO:0019210, GO:0019887) in receptor complexes (GO:0043235) or intracellular regions (GO:0031012) (Table 5). This result implied that the densities of CTCF

Table 3 Rank correlations (ρ) and partial rank correlations (ρ_p) of the examined genomic properties with expression dissimilarities (measured by $ExpD_{1-r}$ or $ExpD_{Euc}$) of the adjacent paralogous genes of different orientations.

Genomic properties ^a	$ExpD_{1-r}$		$ExpD_{Euc}$	
	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}
Head-to-Head^d				
<i>d</i>	0.165 (0.072)	0.106 (0.250)	0.150 (0.109)	0.036 (0.700)
#CTCF	0.213 (0.020)	0.173 (0.058)	0.352 (<10 ⁻⁴)	0.327 (<10 ⁻³)
$\Delta CpG_{O/E}$	-0.024 (0.794)	0.001 (0.991)	-0.071 (0.443)	-0.054 (0.561)
Head-to-Tail^d				
<i>d</i>	0.005 (0.870)	-0.050 (0.110)	0.089 (<10 ⁻²)	0.016 (0.607)
#CTCF	0.100 (<10 ⁻²)	0.110 (<10 ⁻³)	0.151 (<10 ⁻⁵)	0.127 (<10 ⁻⁴)
$\Delta CpG_{O/E}$	0.083 (<10 ⁻²)	0.085 (<10 ⁻²)	0.109 (<10 ⁻³)	0.104 (<10 ⁻³)
Tail-to-Tail^d				
<i>d</i>	0.139 (0.110)	0.105 (0.230)	0.145 (0.096)	0.046 (0.602)
#CTCF	0.113 (0.195)	0.061 (0.482)	0.271 (<10 ⁻²)	0.202 (0.019)
$\Delta CpG_{O/E}$	0.050 (0.569)	0.018 (0.0835)	0.212 (0.014)	0.153 (0.078)

^a "*d*", intergenic distance; "#CTCF", number of overlapping CTCF-binding sites; " $\Delta CpG_{O/E}$ ", difference in upstream DNA methylation.

^b P values show the probabilities of the observations under the hypothesis of no correlation.

^c Spearman's partial correlation coefficient ρ_p is computed by controlling for the other two genomic properties listed in ^a

^d There were 120, 1003 and 133 head-to-head, head-to-tail and tail-to-tail adjacent paralogs, respectively.

Table 4 Rank correlations (ρ) and partial rank correlations (ρ_p) of the examined genomic properties with the divergence time of the paralogous adjacent genes.

Genomic properties ^a	d_s		T_{phy}	
	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}	ρ (P-value) ^b	ρ_p (P-value) ^{b,c}
All adjacent paralogs				
<i>d</i>	0.138 (<10 ⁻⁵)	0.057 (0.056)	0.141 (<10 ⁻⁶)	0.053 (0.060)
#CTCF	0.225 (<10 ⁻¹³)	0.189 (<10 ⁻⁹)	0.219 (<10 ⁻¹⁴)	0.178 (<10 ⁻⁹)
$\Delta CpG_{O/E}$	0.097 (<10 ⁻²)	0.089 (<10 ⁻²)	0.084 (<10 ⁻²)	0.073 (<10 ⁻²)
Adjacent paralogs associated with GO terms in which high #CTCF/<i>d</i> genes were specifically enriched				
<i>d</i>	0.086 (0.152)	-0.070 (0.245)	0.108 (0.072)	-0.038 (0.526)
#CTCF	0.292 (<10 ⁻⁶)	0.276 (<10 ⁻⁵)	0.273 (<10 ⁻⁵)	0.243 (<10 ⁻⁴)
$\Delta CpG_{O/E}$	0.122 (0.043)	0.079 (0.186)	0.132 (0.027)	0.092 (0.125)

^a "*d*", intergenic distance; "#CTCF", number of overlapping CTCF-binding sites; " $\Delta CpG_{O/E}$ ", difference in upstream DNA methylation.

^b P values show the probabilities of the observations under the hypothesis of no correlation.

^c Spearman's partial correlation coefficient ρ_p is computed by controlling for the other two genomic properties listed in ^a

binding sites between tandem paralogs were not contributed by the genomic background.

Genomic regions of high densities of CTCF binding sites can emerge through stochastic evolutionary processes. To examine if high CTCF-binding site density between tandem duplicates is the outcome of gradual CTCF-binding site accumulation by natural selection, we focused on the subset of 278 paralogous pairs in which at least one paralog had one of the abovementioned enriched GO categories. In this subset of tandem paralogs, ρ_p of #CTCF vs. d_s (or T_{phy}) after controlling for *d* and $\Delta CpG_{O/E}$ was stronger (#CTCF vs. d_s : $\rho_p=0.276$, $P<10^{-5}$; #CTCF vs. T_{phy} : $\rho_p=0.243$, $P<10^{-4}$) than that observed in the full set of adjacent paralogs (#CTCF vs. d_s : $\rho_p=0.189$, $P<10^{-9}$; #CTCF vs. T_{phy} : $\rho_p=0.178$, $P<10^{-9}$) (Table 4). When #CTCF was defined by joint CTCF ChIP-seq peaks rather than overlapping CTCF peaks, the results were similar (Table S3 in Additional file 1). Therefore, the trend to accumulate CTCF-binding sites following a tandem duplication event resulted in more CTCF-binding sites (both absolute number and density) between paralogs, especially for those with enriched GO-categories shown in Table 5.

Conclusions

Combining human genomic and transcriptomic data, this study demonstrates that CTCF and its binding sites play a major role driving the expression evolution of tandemly duplicated genes. Following tandem duplication events, CTCF-binding sites gradually accumulate between the paralogs to increase their divergences in expression profile and their divergences in expression level. The role of CTCF-binding sites is not limited to the insulation of DNA methylation domains, because the effects of #CTCF on $ExpD_{1-r}$ (or $ExpD_{EuC}$) were still significant even after controlling for $\Delta CpG_{O/E}$ (Table 2). Thus, CTCF, a conserved regulatory protein [32], affects

the expression evolution of adjacent genes in genomes from flies [33] to humans and is important for the evolution of organismal complexity in animals.

Methods

Annotation of the human genome (Ensembl v72), including gene coordinates, TSS, and paralog divergence, was retrieved through BioMart (<http://www.biomart.org/>) [34]. Orientation for each paralogous pair (head-to-head, head-to-tail, or tail-to-tail) was determined using strand information. For each paralogous pair, the rate of synonymous changes (d_s) was calculated using PAML [35], and the phylogenetic age (T_{phy}) was assigned according to Table S4 in Additional file 1 based on Ensembl's annotation of the most recent common ancestor [36]. A smaller d_s or T_{phy} indicated a more recent divergence time. The RNA-seq-based gene expression signals in the human brain, cerebellum, heart, kidney, liver and testis (GSE30352) [20] were obtained from NCBI Gene Expression Omnibus (GEO) (<http://www.ncbi.nlm.nih.gov/geo/>). The raw reads of RNA-seq data in 16 human tissues (adipose, adrenal, brain, breast, colon, heart, kidney, liver, lung, lymph node, ovary, prostate, skeletal muscle, testes, thyroid, white blood cells) by Illumina BodyMap 2.0 project were downloaded from GSE30611 of GEO and were processed following our previous studies [17,37] to obtain expression signals. Upstream DNA methylation for a gene was calculated based on the 500 nucleotides upstream of the TSS by $CpG_{O/E}=P_{CpG}/(P_C \times P_G)$, where P_{CpG} , P_C , and P_G are the frequencies of CpG dinucleotides, C nucleotides, and G nucleotides, respectively [17,38]. The difference in upstream DNA methylation, $\Delta CpG_{O/E}$, was calculated by the absolute value of the difference in $CpG_{O/E}$ between the two adjacent genes compared. In total, we obtained 30,164 non-paralogous and 1,256 paralogous gene pairs based on 32,164 human genes with detectable expression and estimable $CpG_{O/E}$.

Table 5 Enriched/depleted GO terms at level 4 for genes with high #CTCF/d flanking regions

Functional categories	Duplicate with 25% top #CTCF/d vs. rest of duplicates	Non-duplicates with 25% top #CTCF/d vs. rest of non-duplicates
	GO terms ^a (↑ or ↓ ^b , P-value ^c)	GO terms (↑ or ↓ ^b , P-value ^c)
Molecular functions	<p>DNA binding (GO:0003677) (↑, P<0.05)</p> <p>transcription factor binding (GO:0008134) (↑, P<10⁻²)</p> <p>SMAD binding (GO:0046332) (↑, P<0.05)</p> <p>growth factor binding (GO:0019838) (↑, P<0.05)</p> <p>kinase inhibitor activity (GO:0019210) (↑, P<0.05)</p> <p>peptidase inhibitor activity (GO:0030414) (↑, P<0.05)</p> <p>protein kinase regulator activity (GO:0019887) (↑, P<0.05)</p> <p>transferase activity, transferring acyl groups (GO:0016746) (↑, P<0.05)</p> <p>transferase activity, transferring glycosyl groups (GO:0016757) (↓, P<0.05)</p> <p>monooxygenase activity (GO:0004497) (↓, P<0.05)</p>	<p>transferase activity, transferring phosphorus-containing groups (GO:0016772) (↑, P<10⁻⁷)</p> <p>hydrolase activity, acting on acid anhydrides (GO:0016817) (↑, P<10⁻⁴)</p> <p>protein domain specific binding (GO:0019904) (↑, P<10⁻²)</p> <p>substrate-specific transmembrane transporter activity (GO:0022891) (↑, P<10⁻⁴)</p> <p>cytoskeletal protein binding (GO:0008092) (↑, P<10⁻⁷)</p> <p>phospholipid binding (GO:0005543) (↑, P<10⁻²)</p> <p>identical protein binding (GO:0042802) (↑, P<10⁻⁸)</p> <p>receptor binding (GO:0005102) (↑, P<10⁻⁹)</p> <p>heat shock protein binding (GO:0031072) (↑, P<0.05)</p> <p>oxidoreductase activity, acting on peroxide as acceptor (GO:0016684) (↑, P<10⁻²)</p>
Cellular components	<p>extracellular matrix (GO:0031012) (↑, P<10⁻⁶)</p> <p>intracellular (GO:0031012) (↑, P<0.05)</p> <p>receptor complex (GO:0043235) (↑, P<0.05)</p>	<p>extracellular matrix (GO:0031012) (↑, P<10⁻³)</p> <p>extracellular space (GO:0005615) (↑, P<10⁻⁸)</p> <p>endomembrane system (GO:0012505) (↑, P<10⁻³)</p> <p>membrane-bounded vesicle (GO:0031988) (↑, P<0.05)</p> <p>cell surface (GO:0009986) (↑, P<10⁻⁴)</p> <p>cell projection (GO:0042995) (↑, P<0.05)</p> <p>midbody (GO:0030496) (↑, P<0.05)</p>
Biological processes	<p>response to organic substance (GO:0010033) (↑, P<0.05)</p> <p>regulation of metabolic process (GO:0019222) (↑, P<10⁻³)</p> <p>regulation of catalytic activity (GO:0050790) (↑, P<10⁻²)</p> <p>regulation of cellular process (GO:0050794) (↑, P<10⁻³)</p> <p>regulation of cellular component organization (GO:0051128) (↑, P<0.05)</p> <p>nucleobase, nucleoside, nucleotide and nucleic acid metabolic process (GO:0006139) (↑, P<10⁻²)</p> <p>macromolecule biosynthetic process (GO:0009059) (↑, P<10⁻³)</p> <p>gene expression (GO:0010467) (↑, P<10⁻²)</p> <p>cellular biosynthetic process (GO:0044249) (↑, P<10⁻⁴)</p> <p>programmed cell death (GO:0012501) (↑, P<10⁻²)</p>	<p>response to organic substance (GO:0010033) (↑, P<10⁻⁵)</p> <p>lipid metabolic process (GO:0006629) (↑, P<10⁻⁶)</p> <p>defense response (GO:0006952) (↑, P<10⁻³)</p> <p>response to other organism (GO:0051707) (↑, P<0.05)</p> <p>carbohydrate metabolic process (GO:0005975) (↑, P<0.05)</p> <p>response to drug (GO:0042493) (↑, P<10⁻³)</p> <p>cell-cell signaling (GO:0007267) (↑, P<10⁻²)</p> <p>cytoskeleton organization (GO:0007010) (↑, P<10⁻³)</p> <p>regulation of developmental process (GO:0050793) (↑, P<10⁻⁴)</p> <p>regulation of immune system process (GO:0002682) (↑, P<10⁻⁴)</p>

^a Specifically enriched GO terms are highlighted in bold fonts

^b The symbol ↑ or ↓ represents the enrichment status of “enriched” or “depleted” of the GO term, respectively.

^c P values were Bonferroni-corrected for multiple tests

$ExpD_{1-F}$, which represents the dissimilarity in expression profile, was calculated by 1-Pearson's correlation coefficient of the expression signals of the six tissues. $ExpD_{EuC}$, which represents the summed difference in expression levels, was calculated by the Euclidean distance of the expression signals of the six tissues. CTCF-binding sites identified by ChIP-seq experiments [25] in 13 non-cancerous human cells (Table S5 in Additional file 1) were obtained from broadPeak data deposited as GSE30263 at NCBI GEO. We generated two sets of CTCF-binding sites. The number of overlapping CTCF-binding sites, which are CTCF-binding regions present in all examined cell types (Table S5 in Additional file 1), was determined using BEDTools [39]. The number of joint CTCF-binding sites, the union of CTCF-binding sites from all cell types, was determined using a custom Perl script. Enrichment analyses on GO terms were performed using FatiGO [40]. Partial correlation analyses were performed using modules of the "ppcor" package (v.1.0) [41] for R (<http://www.r-project.org/>).

Additional material

Additional file 1: Supplementary tables S1-S5.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

B.-Y.L. designed research; B.-Y.L. and A.Y.C. performed research; A.Y.C. analyzed data; B.-Y.L. wrote the paper. All authors read and approved the final manuscript.

Acknowledgment and funding

This work was supported by intramural funding from the National Health Research Institutes, Taiwan, and research grant (NSC 101-2311-B-400-001-MY3) from the National Science Council, Taiwan, to B.-Y.L.

Declaration

Publication of this article was funded by the intramural funding of National Health Research Institutes, Taiwan, and research grant (grant number NSC 101-2311-B-400-001-MY3) from the National Science Council, Taiwan, to BYL. This article has been published as part of *BMC Genomics* Volume 15 Supplement 1, 2014: Selected articles from the Twelfth Asia Pacific Bioinformatics Conference (APBC 2014): Genomics. The full contents of the supplement are available online at <http://www.biomedcentral.com/bmcgenomics/supplements/15/S1>.

Published: 24 January 2014

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doi:10.1186/1471-2164-15-S1-S8

Cite this article as: Liao and Chang: Accumulation of CTCF-binding sites drives expression divergence between tandemly duplicated genes in humans. *BMC Genomics* 2014 **15**(Suppl 1):S8.

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