

Asymmetric distribution of pallial-expressed genes in zebrafish (*Danio rerio*)

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Abstract

The left and right distribution of a set of twenty-six genes in the zebrafish pallium was examined by RT-qPCR experiments. The analysis comprised four general pallial markers (*eomesa*, *emx2*, *emx3* and *prox1*); eight genes, *dapper1*, *htr3a*, *htr3b*, *htr4*, *id2*, *ndr2*, *pkcβ* and *lmo4*, that have been described as asymmetric distributed in the brain of mammals (human and mouse); six genes, *arrb2*, *auts2*, *baiap2*, *fez1*, *gap43* and *robo1*, asymmetrically distributed in the mammalian cortex, that have been associated with autism in humans; and, eight genes, *baz1b*, *fzd9*, *limk1*, *tubgcp5*, *cyfip1*, *grik1a*, *nipa1* and *nipa2*, which have been associated with developmental dyscalculia, a brain disability linked to brain laterality in humans. We found a leftward bias in the expression of 10 genes (*dapper1*, *htr3a*, *htr3b*, *htr4*, *id2*, *ndr2*, *pkcβ*, *auts2*, *baiap2* and *grik1a*) and a rightward bias for 5 genes (*lmo4*, *arrb2*, *fez1*, *gap43*, *robo1*) in agreement with the data reported in mammals. We also found a rightward lateralization for *nipa1* and *nipa2*, whereas the remaining genes (*eomesa*, *emx2*, *emx3*, *prox1*, *baz1b*, *cyfip1*, *fzd9*, *limk1* and *tubgcp5*) were bilaterally distributed. These findings suggest a basic homology in the asymmetric expression of several pallial vertebrate genes.

KEYWORDS

autism-related genes, brain asymmetry, *Danio rerio*, developmental dyscalculia-related genes, telencephalic lateralization

Abbreviations: 18S, ribosomal RNA 18S; *arrb2*, arrestin beta 2; *auts2*, activator of transcription and developmental regulator AUTS2; *baiap2*, BAR/IMD domain containing adaptor protein 2; *baz1b*, bromodomain adjacent to zinc finger domain 1 B; *cyfip1*, cytoplasmic FMR1 interacting protein 1; *dapper1*, dishevelled binding antagonist of beta catenin 1; *emx2*, empty spiracle 2; *emx3*, empty spiracle 3; *eomesa*, eomesodermin homolog a; *fez1*, fasciculation and elongation protein zeta 1; *fzd9*, frizzled class receptor 9; *gap43*, growth-associated protein 43; *grik1a*, glutamate receptor, ionotropic, kainate 1a; *htr3a*, 5-hydroxytryptamine receptor 3a; *htr3b*, 5-hydroxytryptamine receptor 3b; *htr4*, 5-hydroxytryptamine receptor 4; *id2*, inhibitor of DNA binding 2; *kctd12.1/lev*, potassium channel tetramerization domain containing 12.1/leftover; *kctd12.2/ron*, potassium channel tetramerization domain containing 12.2/right-on; *kctd8/dex*, potassium channel tetramerization domain containing 8/dexter; LI, Index of Laterality; *limk1*, LIM domain kinase 1; *lmo4*, LIM domain only 4; *ndr2*, nodal-related 2; *nipa1*, nonimprinted in Prader-Willi/Angelman syndrome 1 homolog; *nipa2*, nonimprinted in Prader-Willi/Angelman syndrome 2 homolog; *pkcβ*, protein kinase C beta; *prox1*, prospero homeobox 1; RNA, ribonucleic acid; *robo1*, roundabout 1; RT-qPCR, reverse transcription-quantitative polymerase chain reaction; *tubgcp5*, tubulin gamma complex-associated protein 5.

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1 | INTRODUCTION

The two sides of the vertebrate brain appear as near-mirror images of each other, being grossly characterized by similar cell composition, subdivisions and connections. However, a large number of studies have revealed fundamental differences in the ability of the left and right side to perform different functions and to process specific information (Güntürkün & Ocklenbrug, 2017; Rogers & Vallortigara, 2015). Functional and anatomical differences (lateralization) are well-documented in all vertebrate taxonomic groups, from fish to mammals (see for reviews Güntürkün & Ocklenbrug, 2017; MacNeilage, Rogers, & Vallortigara, 2009; Rogers, Rigosi, Frasnelli, & Vallortigara, 2013; Rogers, Vallortigara, & Andrew, 2013; Vallortigara & Rogers, 2020; Vallortigara & Versace, 2017). It has been argued that possession of a slight asymmetry in the brain would confer biological advantages (Ghirlanda, Frasnelli, & Vallortigara, 2009; Ghirlanda & Vallortigara, 2004; Rogers, Zucca, & Vallortigara, 2004; Vallortigara, 2006; Vallortigara & Rogers, 2020). Impairment in the development of brain laterality has been linked to neurodevelopmental disorders such as autism (Paquet, Golse, Girard, Olliac, & Vaivre-Douret, 2017), developmental dyscalculia (Shalev, Manor, Amir, Wertman-Eiad, & Gross-Tsur, 1995) and developmental dyslexia (Milne, Syngeniotis, Jackson, & Corballis, 2002).

In the last twenty years, zebrafish (*Danio rerio*) has become a prominent model to study the molecular mechanisms of brain lateralization (Carl et al., 2007; Concha, Burdine, Russell, Schier, & Wilson, 2000; Duboc, Dufourcq, Blader, & Roussigné, 2015; Liang et al., 2000; Miletto Petrazzini, Sovrano, Vallortigara, & Messina, 2020). Research with zebrafish established that vertebrates laterality seems to be guided by four major pathways (nodal, fibroblast growth factors, notch and Wnt/beta catenin), which are involved in the positioning of some genes (*ndr2*, *lefty 1* and *pitx2*) on the left side of the forming neural tube (Carl et al., 2007; Concha et al., 2000; Essner, Amack, Nyholm, Harris, & Yost, 2005; Hüsken & Carl, 2013; Liang et al., 2000; Raya et al., 2003; Regan, Concha, Roussigne, Russell, & Wilson, 2009) and contributing to the generation of zebrafish thalamus asymmetries with the positioning of *kctd12.1/leftover* in the left and of *ktcd8/dexter* and *ktcd12.2/right-on* in the right primordium of habenular nuclei (Gamse et al., 2005; Gamse, Thisse, Thisse, & Halpern, 2003).

Disrupting of the signalling cascades from these pathways—and the consequent disorganization of the correct left-right laterality of zebrafish thalamus—leads to a loss of habenular responsiveness to either odour or light stimuli (Dreosti, Vendrell Llopis, Carl, Yaksi, & Wilson, 2014). In zebrafish transgenic line *frequent-situs-inversus* (*fsi*), the reversal of nodal signalling appears to reverse visceral and

diencephalic asymmetries and at least some behavioural asymmetries (Barth et al., 2005).

During the years, it has become apparent that very conserved gene expression patterns are present in forebrain, mid-brain and hindbrain of fish and other vertebrates (Wullimann et al., 2011; Wurst & Bally-Cuif, 2001), and similarities have been observed in the neurochemistry (Mueller, 2012; Panula et al., 2010; Schweitzer & Driever, 2009) and regional connectivity of thalamus (Mueller, 2012), optic tectum (Wullimann, 1994), hypothalamus (Herget, Wolf, Wullimann, & Ryu, 2014), cerebellum (Hashimoto & Hibi, 2012) and medulla oblongata (Kinkhabwala et al., 2011). Relatively little is known, however, as to telencephalic structures, in particular with respect to brain asymmetry.

In the earlier years of 2000s, the study on the molecular bases of brain lateralization converged on the hypothesis that an essential step is the breaking of the symmetry of brain structures as a result of an intrinsic genetic programme. Sun et al. (2005) and several other scholars (Guarneri et al., 1988; Larisch & Klimke, 1988; Moskal, Kroes, Otto, Rahimi, & Claiborne, 2006; Orman & Stewart, 2007; Ribasés et al., 2009; Samara et al., 2011) explored this hypothesis performing large, serial gene expression screening in the human, mouse and rat brains at different stages of development. These studies revealed that more than 500 genes are differentially expressed in the left and right brain in mammalian species. Among them, there are genes involved in the generation of left-side identity during vertebrate brain development, such as *id2* and *ndr2* (Carl et al., 2007; Concha et al., 2000; Essner et al., 2005; Hüsken & Carl, 2013; Liang et al., 2000; Raya et al., 2003; Regan et al., 2009) but also intracellular inhibitors of *Wnt* signalling cascade such as *dapper1* (Zhang, Gao, Wen, Ning, & Chen, 2006). The list also included three serotonin receptors (*htr3a*, *htr3b* and *htr4*) with a leftward asymmetric distribution in different areas of the mammalian brain (Andersen & Teicher, 1999; Fink et al., 2009; Sun et al., 2005), and during chick and frog embryonic development (Fukumoto, Keme, & Levin, 2005); the gene *pkcβ* which is leftward asymmetrical distributed in the mammalian amygdala and involved in different lateralized behaviours such as fear (Orman & Stewart, 2007), pain (Ji & Neugebauer, 2009) and olfactory discrimination (Cohen, Putrino, & Wilson, 2015); the gene *lmo4* which is one of the first genes described as differentially distributed in human and mouse cortex (Sun et al., 2005) and play a pivotal role in the definition of the shape of lateralized cortical functional areas in mouse brain (Huang et al., 2009; Li et al., 2013); and several other genes linked to autism, some leftward asymmetrical distributed, such as *auts2* and *baiap2* (Bedogni et al., 2010; Grabrucker et al., 2018; Toma et al., 2011) and others rightward asymmetrical distributed, such as *arrb2*, *fez1*, *gap43* (Bedogni et al., 2010; Toma et al., 2011) and *robo1* (Anitha et al., 2008).

Asymmetry of gene expression in telencephalic structures of zebrafish adult brain has not been explored. Pallial asymmetries have been examined in the scale-eating cichlid *Perissodus microlepis*. A study reported an asymmetry in the expression of 173 genes after food preference behavioural tests (Lee et al., 2017), whereas another study identified only three genes, belonging to signal transduction cascades, as differentially expressed in the left and right hemisphere in fish individually housed from capture to tissue extraction (Takeuchi, Ishikawa, Oda, & Kitano, 2018).

Here, we performed RT-qPCR experiments (reverse transcription–quantitative polymerase chain reaction) in order to investigate whether any left–right asymmetrical distribution in the expression of pallial genes could be observed in the dorsal telencephalon of adult zebrafish. Given the recent interest for the neural correlates of number (quantity) estimation using zebrafish as an animal model (Potrich, Sovrano, Stancher, & Vallortigara, 2015; Potrich, Rugani, Sovrano, Regolin, & Vallortigara, 2019; Messina et al., 2020; see Nieder, 2019 for a general review on neural mechanisms of numerical cognition), we also checked for the expression of eight genes (*baz1b*, *fzd9*, *limk1*, *tubgcp5*, *cyfip1*, *grik1a*, *nipa1* and *nipa2*) which have been associated with developmental dyscalculia in humans (Chai et al., 2003; Docherty, Yulia Kovas, Petrill, & Plomin, 2010; Maver, Čuturilo, Kovanda, Miletić, & Peterlina, 2019; Tassabehji, 2003), a specific learning disability that affects the natural predisposition to estimate quantity (Shalev, 2004) and that has been suggested to be linked with abnormality in brain asymmetry as well (Shalev et al., 1995). We also checked for the expression of three thalamic genes which have been well-characterized and that are known to be asymmetrically distributed in zebrafish (Concha & Wilson, 2001; Gamse et al., 2003, 2005) as a control for our procedures.

2 | MATERIALS AND METHODS

2.1 | Ethical regulations

All husbandry and experimental procedures complied with the European Legislation for the Protection of Animals used for Scientific Purposes (Directive 2010/63/EU) and were approved by the Scientific Committee on Animal Health and Animal Welfare (Organismo Preposto al Benessere Animale, OPBA) of the University of Trento and by the Italian Ministry of Health (Protocol n. 893/2018-PR and Protocol n. 135/2020-PR).

2.2 | Animals

Eleven adult (one year old) wild-type commercial mixed strain male zebrafish were used. Fish were maintained in an automated aquarium system (ZebTEC Benchtop, Tecniplast),

with 7-L plastic tanks, in standard conditions (28°C, light/dark cycle of 12 hr/12 hr, fed two times a day with artemia and one time with dry food) in accordance with the guidelines of animal welfare.

The zebrafish were killed by putting them in a bath of ice-cold water, and their brains were dissected in phosphate-buffered saline solution (PBS; Fisher BioReagents).

2.3 | Right and left brain tissue dissection and total RNA extraction

Before starting our analyses of left–right distribution of selected gene markers in the dorsal telencephalon of adult zebrafish, the left and right adult pallia were separately collected and the ventral subpallium was accurately removed from each side.

The left and right dorsal pallium, subpallium and left and right anterior thalamus were separately processed, and total RNA extraction was performed using the RNeasy Mini Kit (QIAGEN) according to manufacturer's instructions. Briefly, brain-derived tissues were homogenized in lysis buffer and loaded onto RNeasy spin columns, treated with DNase (RNase-Free DNase Set; QIAGEN) and eluted in RNase/DNase-free water. Collected total RNA was quantified using NanoDrop™ (Thermo Fisher Scientific). Reverse transcription was performed using the SuperScript™ VILO™ cDNA Synthesis Kit (Invitrogen, Thermo Fisher Scientific) according to manufacturer's instructions.

2.4 | Reverse transcription–quantitative polymerase chain reaction (RT-qPCR)

RT-qPCR experiments were performed using specific primer pairs commercially synthesized (Sigma-Aldrich/Merck). Primers were listed in Table 1. Triplicate reactions/sample were performed using the PowerUp™ SYBR™ Green Master Mix (2×) and a CFX96™ Real-Time System (Bio-Rad). The Δ Cq method was used for expression quantification (Messina et al., 2020). Data were normalized on the expression of the *18S* reference gene (Δ Cq), and the relative expression (to the reference gene) of each target was calculated.

2.5 | Index of laterality

An index of laterality (LI) was calculated as previously reported (de Kovel, Ligo, Fisher, & Francks, 2018). In short, the RT-qPCR normalized data deriving from the left hemisphere for each gene were compared with the amount deriving from the quantification of the same gene in the right hemisphere using the following formula:

TABLE 1 List of primers

Gene name	Gene ID		Primers	Amplicon size	Efficiency (%)
<i>18 S</i>	100037361	For	TCGCTAGTTGGCATCGTTTATG	85 pb	93.0
		Rev	CGGAGGTTCTGAAGACGATCA		
<i>kctd12.1/lov</i>	373865	For	AGTTCTTTTCAGCTGCGGGACCTTA	112 pb	98.3
		Rev	GCGACGGACAGTGTGCGAGAG		
<i>kctd8/dex</i>	568933	For	CATGCCATCAATTACGCAAC	112 pb	101.9
		Rev	CGGATCCCAGCTTTTCATTTA		
<i>kctd12.2/ron</i>	553403	For	GCCACTCAACTTTGCTCTCC	191 pb	99.7
		Rev	GAGGCTCGCTTTCTCTTTCTTTGA		
<i>eomesa</i>	64603	For	CTTATTGATCTCCGCCTTGC	147 pb	99.4
		Rev	TATTGGTGCTTTTCGGAGGAC		
<i>emx3</i>	30536	For	TTCACTCCATCATCGGGTTC	145 pb	93.7
		Rev	GCGTTTGACGAATTGGAGTC		
<i>emx2</i>	30537	For	TTTACATCCTCCCAACTCC	199 pb	94.6
		Rev	GGACTCGTTTCGTTTCCTTG		
<i>prox1a</i>	30679	For	TTACGAAGACGCTGTGATGC	195 pb	92.0
		Rev	AATGGTAAAAGGCACTCCTG		
<i>dlx2a</i>	30574	For	TTCAGCCACCACTTCATCAC	193 pb	95.0
		Rev	AACAGTGTCACGCCCAAATC		
<i>dlx5a</i>	30569	For	TCATACTCCACAGCGTATCACC	148 pb	90.0
		Rev	AGTAAATGGTTCGGGGCTTC		
<i>dapper1</i>	405799	For	TTCAGCGAGTGTGTTGTCCAG	127 pb	99.1
		Rev	AATCACACTCGGCACAACCTG		
<i>htr3a</i>	571641	For	TCGCTCAGCACAATGAGAAG	86 pb	101.7
		Rev	TTCACTGAGCAATCCACCAC		
<i>htr3b</i>	571632	For	AGTGAGCGAAGTGGATTG	83 pb	90.0
		Rev	GCTCCCATTCTCCATCATT		
<i>htr4</i>	101882850	For	TAGTTTGCGCTGACAGCAAC	83 pb	97.2
		Rev	AAGCTTTACCGGGTTTACGG		
<i>id2</i>	266599	For	GGCGTGTGAATGAGAAGATG	182 pb	97.6
		Rev	GATACCGCAGTCCAATTC		
<i>ndr2</i>	30292	For	CATGCTGCTGCTGTTTTTCAG	183 pb	101.8
		Rev	TTGTGCAGTGGTGTCTCTG		
<i>lmo4a</i>	114412	For	TTTGGTCACAGTGGAGCTTG	164 pb	98.2
		Rev	ATGGTGCCGTTGACATAGTG		
<i>pkcbeta</i>	393953	For	CAGGACGATGATGTCGAATG	182 pb	96.0
		Rev	TCCTTAAACTTGCCGACCTG		
<i>arrb2</i>	394099	For	CCCTTCAACTTCACGATTCC	127 pb	93.0
		Rev	CATCCACAGTTTTGGCACAG		
<i>auts2a</i>	368890	For	TGGCTCAAACCTGGAGAATC	181 pb	98.5
		Rev	TAACAGGAAGTGGGGATTGG		
<i>baiap2a</i>	678518	For	CAAAAGCAAAGGCGAGAGTC	183 pb	99.2
		Rev	GAAAGCGCTGTTTTGTAGCC		
<i>fez1</i>	406705	For	AAACACTCAACGGCAACCTC	159 pb	95.2
		Rev	CCGGTGAGTTTTCCATCATC		

(Continues)

TABLE 1 (Continued)

Gene name	Gene ID		Primers	Amplicon size	Efficiency (%)
<i>gap43</i>	30608	For	GACACATCACCCGGAAAAAG	151 pb	96.4
		Rev	TCATTTGCTGGGGAGTTAGG		
<i>robo1</i>	30769	For	ATCTCAATCCCGAAGTGCTG	118 pb	97.5
		Rev	TTTCCTGCTCACAGACGATG		
<i>baz1b</i>	571727	For	GCGTATCAGGAGGCAAAAAG	171 pb	96.3
		Rev	TCGTGAACCCATCCTTTCTC		
<i>fzd9b</i>	58023	For	TTCTGGACCTCATCGTTTC	145 pb	99.9
		Rev	TACAACCTCGCCATTCTCACG		
<i>limk1a</i>	735292	For	TACAGCCCTGAACACAAAACG	114 pb	103.5
		Rev	AACGTTCTGGATTGGCGTTC		
<i>tubgcp5</i>	553191	For	ACTTTGTCAACAGCCTGCAC	166 pb	102.4
		Rev	TGGCCTCCTTGACAAAACCTG		
<i>cyfip1</i>	336613	For	AACCAGGGTGCAAACATCTC	134 pb	99.3
		Rev	TAAAGCGCAGAAGACACACG		
<i>grik1a</i>	798001	For	ACGAGAAGATGTGGGCATTC	147 pb	99.7
		Rev	TGCAGTTTCTCTGGGTGATG		
<i>nipa1</i>	450042	For	AGTCTTGTGTTGGTGCCGTTC	119 pb	101.4
		Rev	TGGGTGAGTGAATGATGAGC		
<i>nipa2</i>	406399	For	CTTTGTGGTGTGCGACAG	176 pb	98.5
		Rev	CAGCGATGGCCTCTTAATC		

$$LI = \frac{\text{Left Hemisphere (L)} - \text{Right Hemisphere (R)}}{\text{Left Hemisphere (L)} + \text{Right Hemisphere (R)}}$$

2.6 | Statistical analyses

Statistical analyses on RT-qPCR data were performed using the Statistical Package for the Social Sciences (IBM SPSS Statistics; IBM). RT-qPCR comparisons between left and right dorsal pallium expressions were performed using a two-tailed *t* test for paired samples. Departures from chance level in the laterality index were estimated by one-sample two-tailed *t* tests. The Bonferroni–Holm correction was used for multiple testing comparisons.

3 | RESULTS

3.1 | Thalamic markers

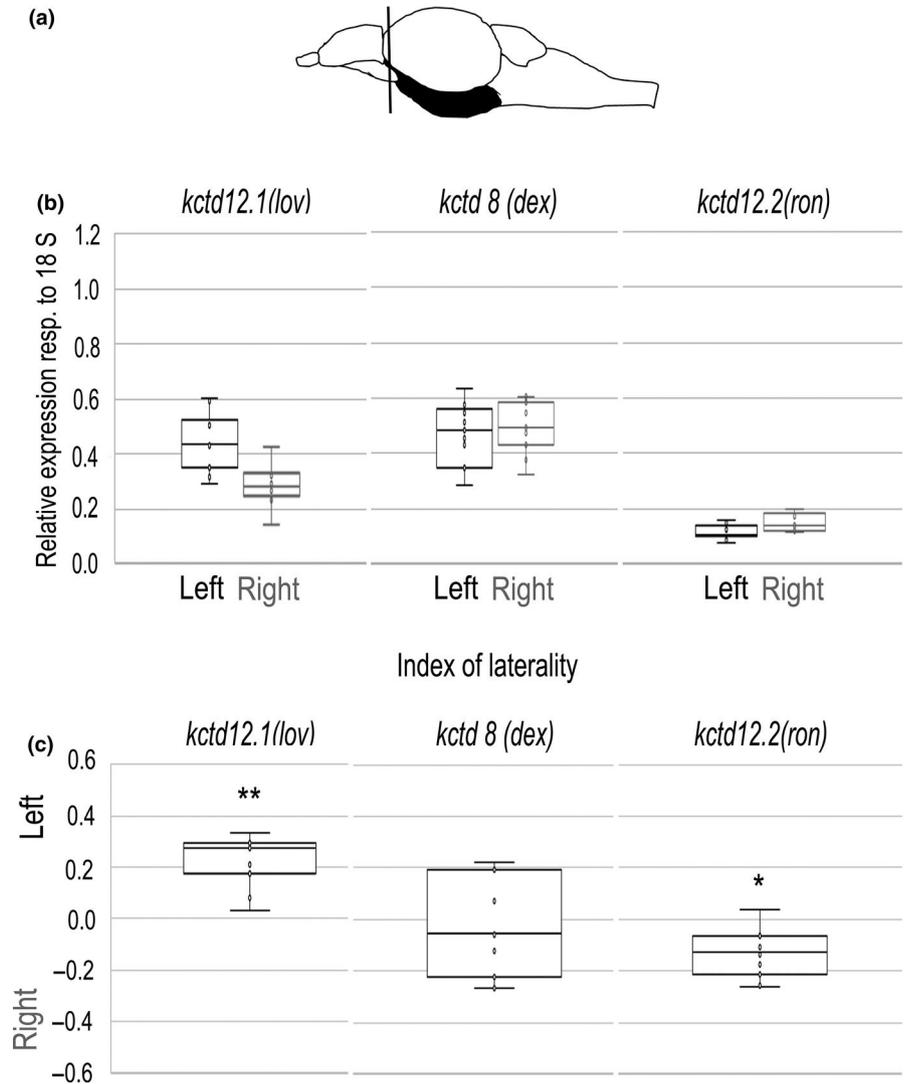
The thalamic markers *kctd12.1/leftover (lov)*, *kctd8/dexter (dex)* and *kctd12.2/right-on (ron)* were used to test brain asymmetry of the subjects examined in the present study. A predominant expression of *kctd12.1/leftover* on the left side of the adult thalamus and a predominant expression of *kctd12.2/right-on* the right side were observed, whereas

kctd8/dexter expression was symmetrically distributed (Figure 1b). See also Figure 1c for the index of laterality and Table 2 for the statistical analyses. Our results thus confirm the left–right patterning of genes in the thalamic structures of zebrafish brains which have been described in previous studies.

3.2 | Dissection of dorsal pallium and ventral subpallium of adult zebrafish brain

The samples collection (Figure 2a) and the results relative to dissections validation are shown in Figure 2b,c, in which total RNAs deriving from left and right dorsal (pallia) and ventral (subpallium) telencephalon were separately pooled and RT-qPCR was performed to test the distribution of six previously described telencephalic-positioning markers in the dissected area, that is *eomesa*, *emx2*, *emx3*, *prox1*, *dlx2a* and *dlx5a* (Ganz et al., 2011, 2014). *Eomesa* identifies the extent of pallium in tetrapods and fish (Brox, Puellas, Ferreira, & Medina, 2004; Bulfone et al., 1999; Ganz et al., 2014); *emx2*, *emx3* and *prox1* label the different pallial subdivisions of zebrafish brain (Ganz et al., 2014), whereas *dlx2a* and *dlx5a* are markers of subpallium in fish (Ganz et al., 2011). Results showed a predominant expression of *eomesa*, *emx2*, *emx3* and *prox1* in the dorsal tissues of telencephalon but not

FIGURE 1 RT-qPCR in the left and right thalamus of zebrafish. (a) Schematic representation of thalamic regions selected for the analyses. (b) RT-qPCR results for *kctd12.1/lov*, *kctd8/dex* and *kctd12.2/ron* in the left and right thalamus of zebrafish. (c) Index of laterality for *kctd12.1/lov*, *kctd8/dex* and *kctd12.2/ron*



of *dlx2a* and *dlx5a* (Figure 2b), and a predominant expression of *dlx2a* and *dlx5a* in the subpallial tissues with a marginal expression of the pallial markers *eomesa*, *emx2*, *emx3* and *prox1* (Figure 2c), showing that the pallium and subpallium were properly collected and separated.

A comparison between the expression of the four pallial markers (*eomesa*, *emx2*, *emx3* and *prox1*) in the left and right pallium was shown in Figure 2d. No differences between the left and right hemisphere were observed (see Table 2 for the statistical analyses).

3.3 | Asymmetric distribution of genes expressed in zebrafish pallium

A leftward bias in the expression of *dapper1*, *htr3a*, *htr3b*, *htr4*, *id2*, *ndr2* and *pkcβ* and a rightward bias in the expression of *lmo4* were observed (Figure 3 and Table 2).

A leftward bias for *auts2* and *baiap2* and a predominant right bias for *arrb2*, *fez1*, *gap43* and *robo1* were observed (Figure 4 and Table 2).

3.4 | Developmental dyscalculia-associated genes

As to genes associated with human developmental dyscalculia, we found that the genes *nipa1* and *nipa2* were predominantly expressed in the right hemisphere and the gene *grik1a* in the left hemisphere, whereas the genes *baz1b*, *cyfip1*, *fzd9*, *limk1* and *tubgpc5* were bilaterally distributed in the zebrafish pallium (Figure 5 and Table 2).

3.5 | Summary of left-right distribution of all tested genes

A summary of the results is shown in Figure 6, with the lateralization index of all twenty-six telencephalic genes that we characterized in our experiments. We found a leftward lateralization for ten genes (*dapper1*, *htr3a*, *htr3b*, *htr4*, *id2*, *ndr2*, *pkcβ*, *auts2*, *baiap2* and *grik1a*) and a rightward lateralization for seven genes (*lmo4*, *arrb2*, *fez1*, *gap43*, *robo1*, *nipa1* and *nipa2*); the others genes were bilaterally

TABLE 2 RT-qPCR results (group means with *SEM* are shown) of left- and right-side gene expression with statistical analyses and effect size

Gene	Left hemisphere	Right hemisphere	Paired <i>t</i> test	Effect size (Cohen's)
Thalamus				
<i>kctd12.1/lov</i>	0.453 ± 0.031	0.288 ± 0.021	<i>t</i> (10) = 7.526 <i>p</i> = .003	2.269174379
<i>kctd8/dex</i>	0.235 ± 0.016	0.249 ± 0.014	<i>t</i> (10) = -0.556 <i>p</i> > .999	-0.167640308
<i>kctd12.2/ron</i>	0.116 ± 0.007	0.152 ± 0.009	<i>t</i> (10) = -4.693 <i>p</i> = .027	-1.41499274
Telencephalon				
General dorsal markers in mammals				
<i>eomesa</i>	0.581 ± 0.064	0.598 ± 0.051	<i>t</i> (10) = -0.307 <i>p</i> > .999	-0.092563983
<i>emx3</i>	0.319 ± 0.047	0.322 ± 0.032	<i>t</i> (10) = -0.157 <i>p</i> > .999	-0.047337281
<i>emx2</i>	0.151 ± 0.015	0.158 ± 0.018	<i>t</i> (10) = -0.354 <i>p</i> > .999	-0.106735016
<i>prox1</i>	0.193 ± 0.017	0.195 ± 0.011	<i>t</i> (10) = -0.147 <i>p</i> > .999	-0.044322168
Differentially distributed				
<i>dapper1</i>	0.321 ± 0.028	0.215 ± 0.022	<i>t</i> (10) = 4.099 <i>p</i> = .044	1.235895001
<i>htr3a</i>	0.111 ± 0.008	0.062 ± 0.009	<i>t</i> (10) = 6.297 <i>p</i> = .002	1.898616937
<i>htr3b</i>	0.144 ± 0.021	0.087 ± 0.015	<i>t</i> (10) = 7.380 <i>p</i> = .002	2.225153723
<i>htr4</i>	0.805 ± 0.024	0.486 ± 0.032	<i>t</i> (10) = 7.689 <i>p</i> = .002	2.318320728
<i>id2</i>	0.428 ± 0.031	0.304 ± 0.026	<i>t</i> (10) = 8.7150 <i>p</i> = .002	2.627671368
<i>ndr2</i>	0.427 ± 0.033	0.322 ± 0.031	<i>t</i> (10) = 6.620 <i>p</i> = .002	1.996005101
<i>lmo4a</i>	0.154 ± 0.015	0.250 ± 0.015	<i>t</i> (10) = -4.879 <i>p</i> = .016	-1.47107385
<i>pkcbeta</i>	0.581 ± 0.035	0.458 ± 0.031	<i>t</i> (10) = 8.072 <i>p</i> = .002	2.434101085
Autism-related genes				
<i>arrb2</i>	0.314 ± 0.029	0.447 ± 0.039	<i>t</i> (10) = -4.931 <i>p</i> = .014	1.48675244
<i>auts2a</i>	0.659 ± 0.046	0.535 ± 0.027	<i>t</i> (10) = 5.832 <i>p</i> = .001	1.758414162
<i>baiap2a</i>	0.807 ± 0.034	0.655 ± 0.043	<i>t</i> (10) = 3.970 <i>p</i> = .036	1.197000038
<i>fez1</i>	0.357 ± 0.021	0.515 ± 0.037	<i>t</i> (10) = -6.790 <i>p</i> = .001	-2.04726203
<i>gap43</i>	0.517 ± 0.041	0.638 ± 0.055	<i>t</i> (10) = -5.270 <i>p</i> = .001	-1.588964786
<i>robo1</i>	0.785 ± 0.025	1.008 ± 0.034	<i>t</i> (10) = -7.388 <i>p</i> = .001	-2.227565814
Dyscalculia-related genes				
<i>baz1b</i>	0.666 ± 0.042	0.728 ± 0.055	<i>t</i> (10) = -1.095 <i>p</i> > .999	-0.330154922
<i>fzd9</i>	0.491 ± 0.066	0.485 ± 0.068	<i>t</i> (10) = 0.187 <i>p</i> > .999	0.056382621
<i>limk1a</i>	0.607 ± 0.032	0.563 ± 0.067	<i>t</i> (10) = 0.629 <i>p</i> > .999	0.189650636
<i>tubgcp5</i>	0.192 ± 0.014	0.219 ± 0.021	<i>t</i> (10) = -1.703 <i>p</i> = .595	-0.51347382
<i>cyfip</i>	0.685 ± 0.037	0.824 ± 0.053	<i>t</i> (10) = -2.795 <i>p</i> = .076	-0.842724208
<i>grik1a</i>	0.633 ± 0.062	0.399 ± 0.051	<i>t</i> (10) = 4.780 <i>p</i> = .004	1.441224227
<i>nipa1</i>	0.066 ± 0.003	0.085 ± 0.004	<i>t</i> (10) = -4.344 <i>p</i> = .003	-1.309765281
<i>nipa2</i>	0.228 ± 0.015	0.292 ± 0.023	<i>t</i> (10) = -4.997 <i>p</i> = .001	-1.506652189

distributed (*eomesa*, *emx2*, *emx3*, *prox1*, *baz1b*, *cyfip1*, *fzd9*, *limk1* and *tubgpc5*).

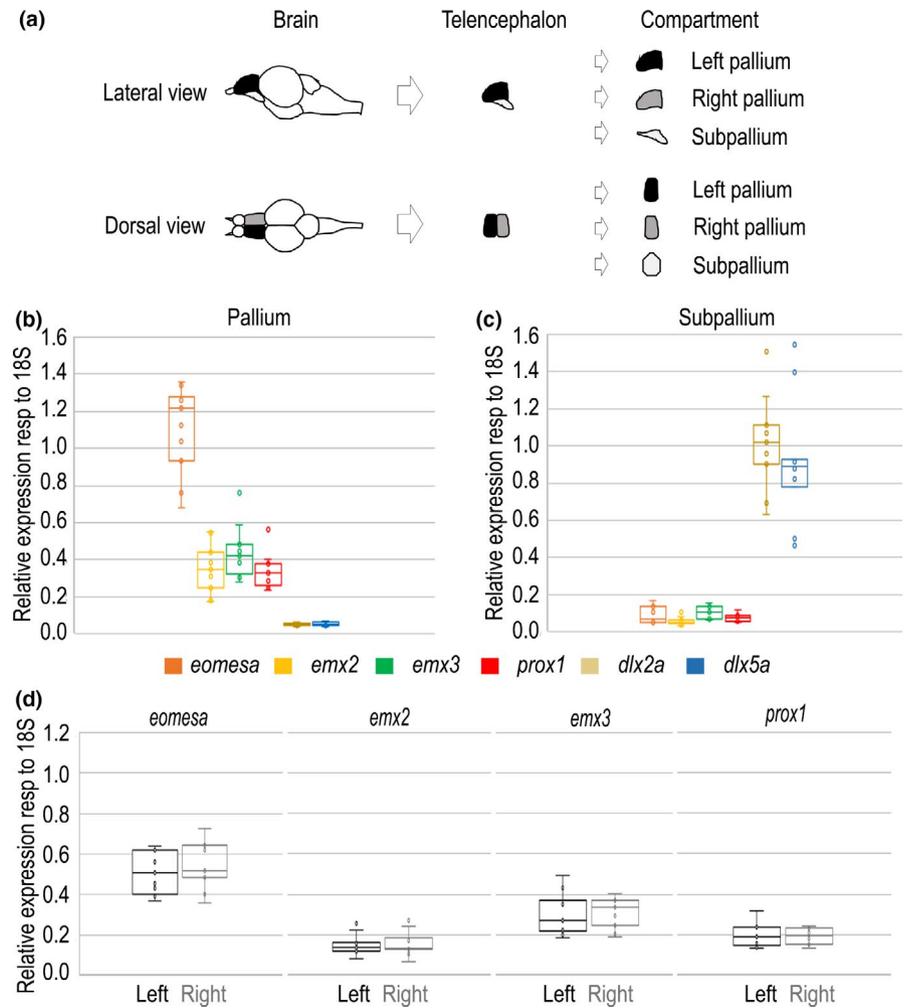
4 | DISCUSSION

Asymmetry of gene expression in the thalamus has been documented in zebrafish (Barth et al., 2005; Carl et al., 2007; Concha et al., 2000; Dreosti et al., 2014; Essner et al., 2005; Hüsken & Carl, 2013; Liang et al., 2000; Raya et al., 2003;

Regan et al., 2009). Here, we confirmed a predominant expression of *kctd12.1/leftover* on the left side (Gamse et al., 2003) and *kctd12.2/right-on* on the right side of the adult thalamus (Gamse et al., 2005). On the contrary, *kctd8/dexter* appeared symmetrically distributed in the adult thalamus (thought it seems to show a rightward bias during zebrafish embryonic development; Gamse et al., 2005).

We found a symmetrical expression of the general pallial marker *eomesa* (Brox et al., 2004; Bulfone et al., 1999; Ganz et al., 2014), but also of *emx2* (marker of dorsocentral

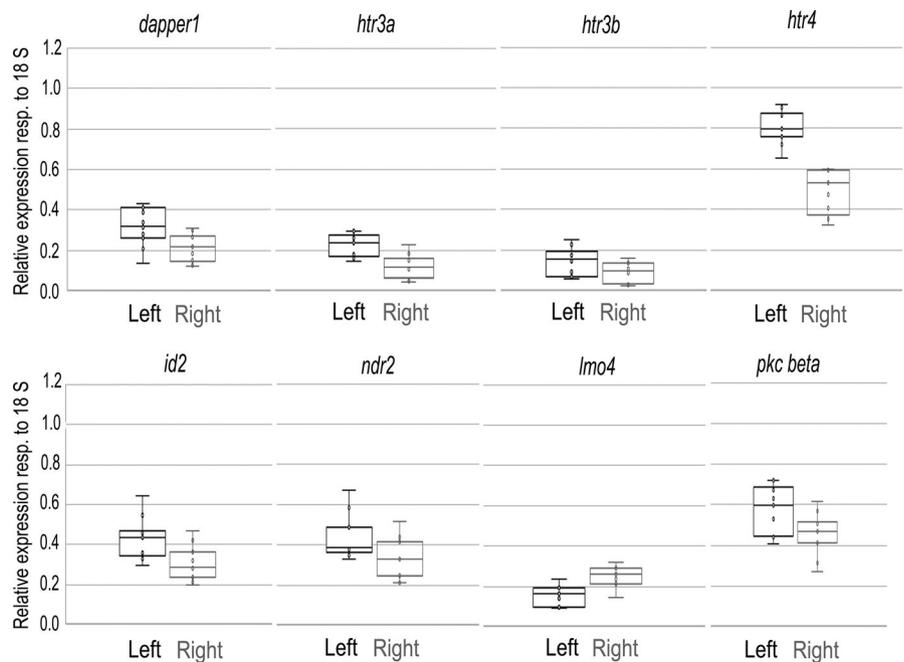
FIGURE 2 RT-qPCR in the telencephalon of zebrafish. (a) Schematic representation of the dissected telencephalic areas selected for the analyses: lateral view (top) and dorsal view (bottom). (b, c) RT-qPCR results for *eomesa*, *emx2*, *emx3*, *prox1*, *dlx2a* and *dlx5a* in (b) pallial (dorsal telencephalon) and (c) subpallial (ventral telencephalon) regions. (d) RT-qPCR results for *eomesa*, *emx2*, *emx3*, *prox1* and *dlx2a* in the left and right pallium [Colour figure can be viewed at wileyonlinelibrary.com]



pallium), *emx3* (marker of dorsomedial and dorsolateral pallium) and *prox1* (marker of dorsolateral pallium; Ganz et al., 2014).

A leftward bias in the expression of *id2*, *ndr2* and *dapper1* was observed in zebrafish, as reported in mammals (Sun et al., 2005). The asymmetric expression of these genes in the

FIGURE 3 RT-qPCR left and right expression of zebrafish pallial genes: *dapper1* (an inhibitor of Wnt signalling); *htr3a*, *htr3b* and *htr4* (serotonin receptors); *id2* and *ndr2* (two genes known to be involved in vertebrates laterality); *lmo4* (known to be involved in mammalian cortical development); and *pkcβ* (known to be differentially expressed in the mammalian amygdala)



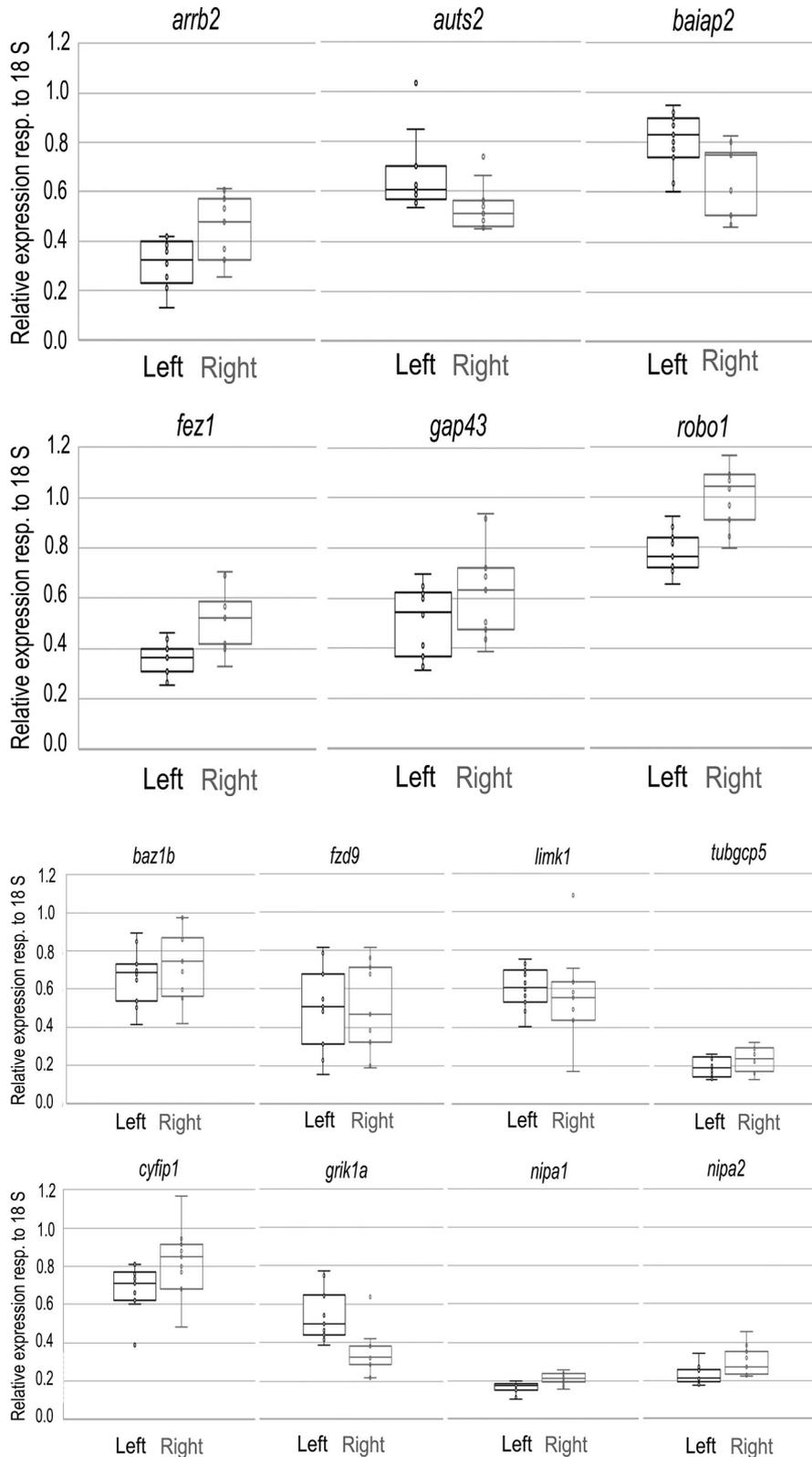


FIGURE 4 RT-qPCR left and right expression of zebrafish pallial genes *arrb2*, *auts2*, *baiap2*, *fez1*, *gap43* and *robo1* (these genes are left and right differentially distributed in the mammalian cortex and linked to autism)

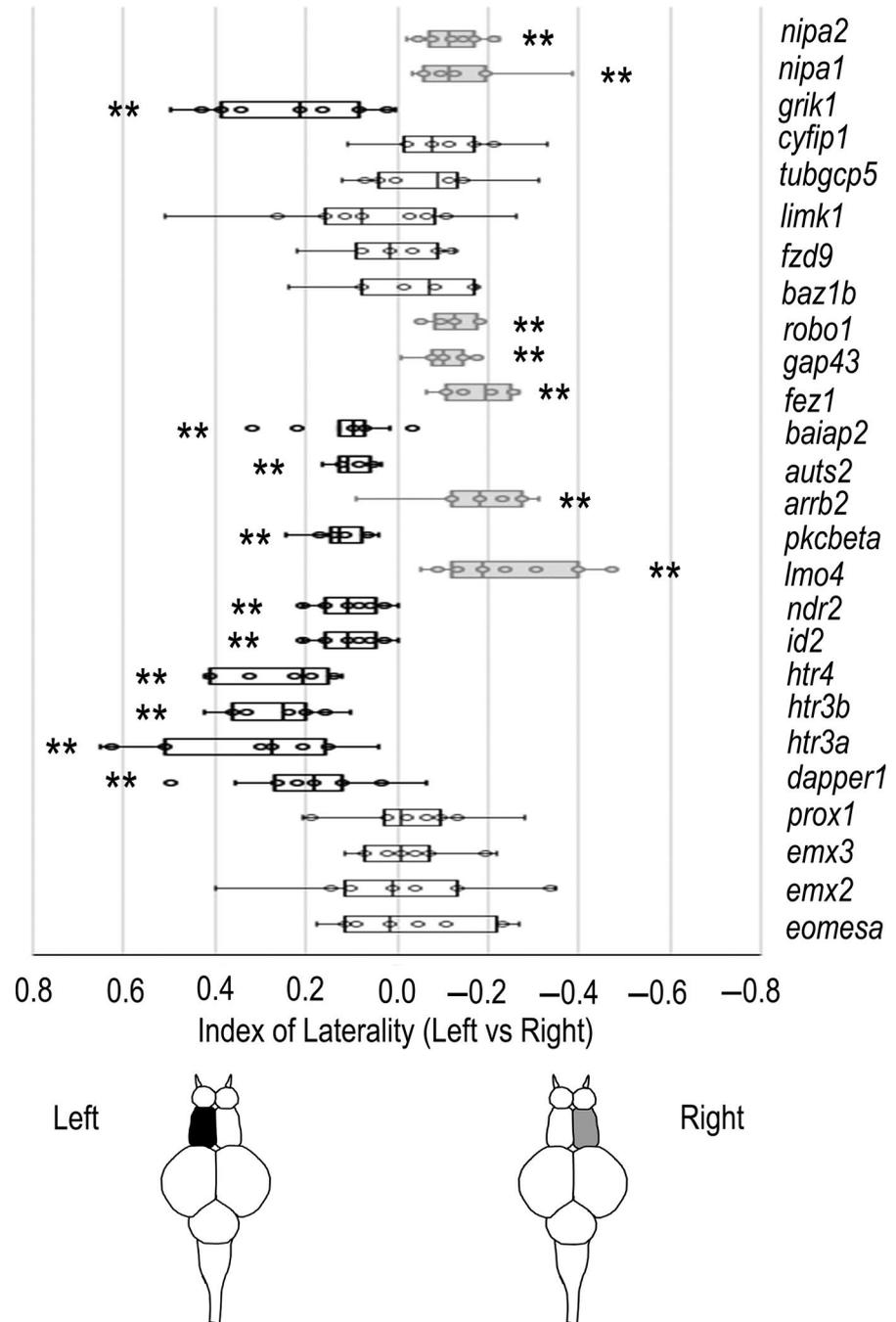
FIGURE 5 RT-qPCR left and right expression of zebrafish pallial genes *baz1b*, *fzd9*, *limk1*, *tubgcp5*, *cyfip1*, *grik1a*, *nipa1* and *nipa2* (these genes have been shown to be associated with human developmental dyscalculia and dyslexia)

adults opened the possibility that the *nodal* (*id2* and *ndr2*) and *Wnt* (*dapper1*) signalling pathway could play a role not only for the left–right patterning during early embryogenesis, but also in the maintenance of left–right asymmetry in the adult zebrafish brain (Carl et al., 2007; Concha et al., 2000;

Essner et al., 2005; Hüsken & Carl, 2013; Liang et al., 2000; Raya et al., 2003; Regan et al., 2009; Zhang et al., 2006).

A leftward asymmetric expression was found also for *htr3a*, *htr3b* and *htr4* similar to that observed in other taxonomic groups (human, Sun et al., 2005; chick and frog,

FIGURE 6 Laterality index for the genes tested in the left and right pallium of zebrafish (asterisks indicate significant departures from random distribution, $*p < .05$, $**p < .01$ two-tailed one-sample *t* tests)



Fukumoto et al., 2005). *htr3* and *htr4* receptors, but not other serotonin cascade members, guide brain laterality during early development of vertebrates, and the selective inhibition of these serotonin receptors leads to a randomization of brain laterality (Fukumoto et al., 2005). The conservative asymmetric distribution of serotonin receptors in different areas of mammalian (Andersen & Teicher, 1999; Fink et al., 2009; Sun et al., 2005), chick and frog (Fukumoto et al., 2005) and fish brain could become a useful marker to study the molecular basis of the laterality of the vertebrate telencephalon. Moreover, since *htr4* receptor was linked to aggressive behaviour (Kudryavtseva et al., 2017) and aggressive behaviour appears to be lateralized in different species

(Hews, Catsellano, & Hara, 2004; Hedayatirad, Nematollahi, Forsatkar, & Brown, 2017; review in Vallortigara, Rogers, & Bisazza, 1999), the magnitude of asymmetry in the distribution of this serotonin receptor could represent a key index to monitor this behaviour.

We also observed a leftward asymmetrical distribution of *pkcb* in the telencephalon of zebrafish, an asymmetry similar to that described in the mammalian amygdala (Orman & Stewart, 2007) and a rightward asymmetrical distribution of *lmo4* similar to that described for the mammalian cortex (Huang et al., 2009; Li et al., 2013; Sun et al., 2005). In particular, *lmo4* represents one of the first genes described as differentially distributed in human and mouse cortex (Sun

et al., 2005) and seems to play a pivotal role in the definition of the shape of lateralized cortical functional areas during mouse brain development (Huang et al., 2009; Li et al., 2013). The asymmetrical distribution of *lmo4* in zebrafish brain could represent a new tool to study the molecular mechanism through which anatomical brain asymmetries could be linked to lateralized functions.

Since in the last years the zebrafish became one of the animal model mostly used to study the molecular bases of autism, we checked for the distribution of some of the autism-related markers in the left and right hemisphere. We found a striking correspondence with the results obtained in humans (Sun et al., 2005; Sun & Walsh, 2006), that is a leftward distribution of *auts2* and *baiap2* and a rightward distribution for *arrb2*, *fez*, *gap43* and *robo1*. Differences were apparent with respect to mouse results (Grabrucker et al., 2018), in which *auts2* and *baiap2* revealed only a trend for a left bias, while *arrb2*, *fez1* and *gap43* were lateralized to the left and not to the right as it happens in zebrafish (present work) and humans (Sun et al., 2005; Sun & Walsh, 2006). The asymmetric distribution of some autism-related genes in vertebrates, including fish, represents an important support to the hypothesis of an involvement of brain laterality in the occurrence of autism spectrum disorders.

Finally, given the current interest for the neural correlates of quantity estimation in zebrafish (Messina et al., 2020; Potrich et al., 2015, 2019), we also checked for the expression of eight genes associated with developmental dyscalculia in human. We found clear asymmetries in the expression of *grik1a*, *nipa1* and *nipa2* genes in the left and right pallium of zebrafish, which confirm a possible link between brain laterality and the presence of such a disability as it has been described in humans (Shalev et al., 1995).

Recently, *robo1* was also associated with developmental dyslexia and dyscalculia (Mascheretti et al., 2014; Tran et al., 2014). The asymmetric distribution of *robo1*, with a greater magnitude with respect to other tested genes, could be another support to the hypothesis of an involvement of lateralized molecular mechanism in the insurgence of these disabilities. *robo1* is a factor downstream *baz1b*, another dyscalculia-associated gene (Tassabehji, 2003; Zanella et al., 2019), but appears as symmetrically distributed in our analyses. The inconsistency between *robo1* and *baz1b* data in our results could be related to the high variability in the expression levels of *baz1b* in the tested samples or to a role of *baz1b* as chromatin remodeler. Further analyses will be needed to clarify *baz1b* distribution between the left and right hemisphere of zebrafish and its relationships with *robo1* expression.

In conclusion, our results provide further evidence of a conservative distribution of pallial genes among vertebrates, which extend also to their pattern of asymmetric expression in the left and right side of the brain.

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CONFLICT OF INTERESTS

The authors declare no competing interests.

AUTHOR CONTRIBUTIONS

A.M. and G.V. conceived and designed the experiments. A.M., A.B. performed the experiments. A.M., A.B. and G.V. analysed and interpreted the data. G.V. contributed reagents/materials. All authors contributed to the manuscript writing.

DATA AVAILABILITY STATEMENT

Data are available in a submitted Supporting Information.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

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