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The top 10 most abundant transcripts are sufficient to characterize the organs functional specificity: evidences from the cortex, hypothalamus and pituitary gland

Yuichiro Nishida, Mayumi Yoshioka, Jonny St-Amand*

Molecular Endocrinology and Oncology Research Center, Laval University Medical Center (CHUL), Department of Anatomy and Physiology, Laval University, 2705 Boulevard Laurier, Quebec, Canada G1V 4G2

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Abstract

Using serial analysis of gene expression, we have identified the most abundant mRNA transcripts in parietal cortex, hypothalamus and pituitary gland in adult male mice. High mRNA abundance of neurogranin (cell signalling and communication) was characteristic of the cortex. The common molecular features of cortex and hypothalamus were high abundance of mRNA encoding mitochondrial enzymes such as reduced form of nicotinamide adenine dehydrogenase (NADH) 4 and cytochrome *c* oxidase 2 (energy metabolism), brain creatine kinase (energy metabolism) and myelin basic protein (cell structure). In the hypothalamus, mRNA levels of apolipoprotein E (lipid metabolism), prostaglandin D2 (cell signalling and communication) and secreted acidic cysteine-rich glycoprotein (extracellular matrix) were especially high. A common molecular feature of the hypothalamus and pituitary was high mRNA abundance of guanine nucleotide binding protein alpha stimulating complex locus (cell signalling and cell communication). The pituitary gland was characterized by high expression of genes encoding hormones such as growth hormone, pro-opiomelanocortin and prolactin, as well as neuronatin (cell differentiation) and four potential novel transcripts. Thus, these results show that the cortex, hypothalamus and pituitary gland can be specifically characterized according to their 10 most abundant transcripts. In addition, the current study serves as a basis for future studies on the potential novel transcripts and the transcripts with unclear functions despite their extremely high abundance, as well as studies on physiology and pathology of the two brain regions and pituitary gland.

Keywords: Transcriptome; Brain; Highly expressed genes; Neuroendocrine

1. Introduction

Almost all large-scale methods to measure gene expression including DNA microarray would not be suitable to quantify the abundance of mRNA species relatively to the total mRNA population (Novak et al., 2002), whereas serial analysis of gene expression (SAGE) enables to accurately measure the abundance of both known and novel transcripts on global scale (Velculescu et al., 1995). In general, there is an assumption that the most abundant transcripts are encoding for many kinds of ribosomal proteins, translation factors and housekeeping genes in all kinds of tissues or organs including brain (Adams et al., 1992).

Abbreviations: ACTH, adrenocorticotropic hormone; bp, base pair(s); CCD, comparative count display; cDNA, DNA complementary to RNA; ds, double strand; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; GH, growth hormone; GNAS, guanine nucleotide binding protein alpha stimulating; GNASXL, GNAS extra large; mt, mitochondria(l); NADH, nicotinamide-adenine dinucleotide and its reduced form; NESP, neuroendocrine secretory protein; nt, nucleotide(s); POMC, pro-opiomelanocortin; PPIA, peptidylprolyl isomerase A; SAGE, serial analysis of gene expression; SPARC, secreted acidic cysteine-rich glycoprotein.

* Corresponding author. Tel.: +1 418 654 2296; fax: +1 418 654 2761.
E-mail address: jonny.st-amand@crchul.ulaval.ca (J. St-Amand).

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Table 1
Top 10 most abundant transcripts in parietal cortex, hypothalamus and pituitary gland

Tag sequence	No. of tags									Description	Chr.	General function
	C	%	R	H	%	R	P	%	R	[UniGene cluster, GenBank accession no.]		
(a) Cortex												
ATGACTGATAG	**586**	0.59	**1**	489	0.49	**1**	257[a]	0.26	15	NADH dehydrogenase subunit 4 [NC_001569]	Mit: 11228-42	Energy metabolism
AGCAGTCCCCT	**546**	0.55	**2**	411	0.41	**2**	185[a]	0.19	19	Cytochrome *c* oxidase subunit 2 [NC_001569]	Mit: 7504-18	Energy metabolism
AGGACAAATAT	**488**	0.49	**3**	335	0.33	**5**	268	0.27	13	Cytochrome *b* [NC_001569]	Mit: 14543-57	Energy metabolism
CAGCTCTGCCT	**363**	0.36	**4**	29[a]	0.03	284	0[a]	0.00	–	Neurogranin [Mm.335065, AK002933]	9	Cell signaling/cell communication
AACGGCTAAAC	**311**	0.31	**5**	253	0.25	**8**	48[a]	0.05	81	16S ribosomal RNA	Mit: 2065-79	Protein synthesis
GCCTCCAAGGA	**309**	0.31	**6**	267	0.27	**7**	97[a]	0.10	34	Glyceraldehyde-3-phosphate dehydrogenase [Mm.288146, XM_132897]	6	Sugar metabolism
GCTGCCCTCCA	**276**	0.28	**7**	187	0.19	15	29[a]	0.03	151	Cytochrome *c* oxidase subunit 1 [NC_001569]	Mit: 6813-27	Energy metabolism
CATCCTTGATG	**248**	0.25	**8**	203	0.20	14	26[a]	0.03	179	Creatine kinase, brain [Mm.16831, NM_021273]	12	Energy metabolism
ATACTGACATT	**245**	0.24	**9**	141	0.14	20	41[a]	0.04	98	Cytochrome *c* oxidase subunit 3 [NC_001569]	Mit: 9322-36	Energy metabolism
GAGCGTTTTGG	**238**	0.24	**10**	226	0.23	11	61[a]	0.06	66	Peptidylprolyl isomerase A [Mm.5246, XM_122180]	11	Protein synthesis