Ovariectomy Alters Gene Expression of the Hippocampal Formation

in Middle-Aged Rats 2 3 Miklós Sárvári¹, Imre Kalló^{1,2}, Erik Hrabovszky¹, Norbert Solymosi³ and Zsolt Liposits^{1,2*} 4 5 6 ¹Laboratory of Endocrine Neurobiology, Institute of Experimental Medicine, Hungarian Academy of 7 Sciences, Budapest, Hungary; 8 ²Faculty of Information Technology and Bionics, Pázmány Péter Catholic University, Budapest, 9 Hungary; 10 ³Department of Animal Hygiene, Herd-Health and Veterinary Ethology, University of Veterinary 11 Medicine, Budapest, Hungary. 12 13 Abbreviated title: OVX-regulated hippocampal gene expression in rats 14 15 Key terms: hippocampus, rat, middle-age, ovariectomy, microarray, PCR, pathway analysis 16 **Word count:** 3,268 17 Number of figures and tables: 7 18 19 20 Corresponding author and person to whom reprint requests should be addressed 21 Miklós Sárvári, PhD 22 Institute of Experimental Medicine, Hungarian Academy of Sciences, 23 Szigony u. 43, 1083 Budapest, Hungary 24 e-mail: sarvari.miklos@koki.mta.hu 25 26 **Disclosure Statement:** The authors have nothing to disclose 27

Abstract

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Ovarian hormones regulate the transcriptome of the hippocampus and modulate its functions. During menopause, this complex signaling declines, leading to impaired learning and memory. This study was undertaken to clarify the effects of long-term, surgical ovariectomy (OVX) on the rat hippocampal transcriptome. At age of 13 months, intact control and ovariectomized groups were formed. All animals were sacrificed 5 weeks after gonadectomy, hippocampal formations were dissected and processed for transcriptome analysis, Microarray and PCR studies identified 252 and 61 genes, respectively, whose expression was altered in the lack of ovarian hormones. Pathway analysis revealed impact on neuroactive ligand-receptor interaction, endocannabinoid and estrogen signaling, among others. Network and interaction analyses of proteins encoded by OVX-regulated genes revealed upregulation of growth/ troph/transcription factor signaling assembly (Mdk, Fgf1, Igf2, Ngf, Ngfr, Ntf3, Ntrk1, Otx2, Hifla, Esr1, Nr4a3), peptides/peptide receptors (Cartp, Kl, Ttr, Gnrhr), neurotransmission (Grm1, Gria4, Gls, Slc18a2, Kcj6) and genes serving immune functions (C3, Ccl2, Itgam, Il1b). Downregulated clusters included neuropeptides and their receptors (Adcyap1, Cbln2, Cck, Cckbr, Crhr1 and 2, Oprd1, Nts, Penk, Sstr1, Vip), neurotransmitter signaling (Htr2c, Chrna3, Chrm4, Grm8, Hrh3, Slc17a6) and potassium channels (Kcnk9, Kcnj9, Kcnma1, Kcnc2). Several transcription factors (Rxra, Thrb), solute carriers and defense molecules (Apital, Bcl2, Clql3, Ilr3a, Sod1, Sncb) also underwent downregulation. The findings indicate that surgical gonadectomy carried out at middle-age robustly changes the hippocampal transcriptome that alters neurogenesis, synaptic plasticity, immune modulation causing cognitive dysfunctions.

Introduction

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The ovarian hormone supply is crucial for development of the brain and maintenance of its diverse functions (1-3). The proper physiological performance of the ovary is guaranteed and regulated by the hypothalamo-pituitary neuroendocrine unit (4). Aging results in a decrease in the production of ovarian hormones, including the gonadal sex steroids estradiol and progesterone (5,6). During menopause, the ovarian hormone supply to the brain, including the hippocampal formation, gradually weakens causing impairments in learning ability, memory processing and spatial navigation (7.8). These events negatively influence quality of life in menopause, therefore, various strategies of hormone replacement therapy (HRT) have been introduced (9,10). Current efforts are aimed at HRTs with low health risk consequence and high effectiveness (11-13). The timing of HRT has been found crucial (14,15) in order to keep the brain's responsiveness to ovarian hormones and prevent structural disintegration of the neural tissue. In experimental neuroscience, middle-aged, ovariectomized animals have been widely used as models of menopause including primates (16,17) and rodents (18-23). The beneficial role of HRT has been shown in counter-balancing hippocampus-related dysfunctions. These studies indicate that declining ovarian hormone signaling to the hippocampal formation promotes neuroinflammation (24), disturbs synaptic signaling and plasticity (25-29), alters neurogenesis (26,30,31) and decreases the efficacy of cellular neuroprotective mechanisms (32-34). Although many HRT studies used the ovariectomized animal model, the impact of surgical, long-term OVX per se upon the hippocampal transcriptome and functions has not been fully elucidated yet. We hypothesized that ablation of ovarian hormones by gonadectomy in middle-aged, female rats results in malfunction of the related hormone receptors leading to modification of gene expression and altered functions. Therefore, in this study, the hippocampal transcriptomes of intact control and long-term ovariectomized, middle-aged rats were compared using microarray and quantitative real-time PCR. The predicted networking of proteins encoded by OVX-regulated genes was also analyzed. We identified clusters of differentially-regulated genes, indicating that gonadal hormone ablation might alter essential hippocampal functions.

Material and Methods

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Experimental animals

All experiments were performed with permission from the Animal Welfare Committee of the Institute of Experimental Medicine (IEM, Permission Number: A5769-01) and in accordance with regulations of the European Community (Decree 86/609/EEC). Female Harlan-Wistar rats were purchased from Toxicoop (Budapest, Hungary) and housed on a 12h light/12h dark cycle in the animal care facility of IEM. The rats were used as breeders and retired at their age of 8 months, then housed individually for the subsequent months. At their age of 13 months, 14 animals were deeply anesthetized and shamoperated or ovariectomized bilaterally (18,35). Two experimental animal groups were formed: intact control group (n=6) and ovariectomized group (n=8). Both groups were kept on phytoestrogen-free diet (Harlan Teklad Global Diets, Madison, WI). Intact middle-aged female rats show the initial signs of reproductive aging manifested in persistent vaginal cornification, tonic estrogen secretion and low plasma levels of progesterone (36). Accordingly, our middle-aged intact females had low serum E2 level (12 pg/mL). In contrast, ovariectomized middle-aged animals had only residual serum E2 (2 pg/mL), significantly decreased uterus weight and significantly increased body weight indicating progressing reproductive senescence and clear signs of menopause. Five weeks after the surgical intervention all animals were terminated, the brains were quickly removed from the skull and placed into an ice-cold rat brain matrix. A three millimeter thick coronal slice was dissected with two blades positioned at bregma levels -3.8 and -6.8. Between these levels the targeted part of the hippocampal formation was easily separable from the neighboring brain areas (the thalamus and the corpus callosum), it was lifted from the slice and processed for transcriptome analysis. Affymetrix Rat Genome 230PM Strip Arrays

Hippocampal formations from 14 animals were prepared and total RNA was isolated and analyzed as described previously (24). RNA quality was measured and samples displayed high RNA integrity numbers (RIN > 8.2) on Agilent's Bioanalyzer Nano RNA chips (Santa Clara, CA, USA). Four samples from each group were individually examined by oligonucleotide microarray including amplification, target labeling, hybridization, staining and scanning steps, which were carried out as described earlier (26). In brief, using 25 ng of total RNA Whole Transcriptome Amplification (WTA) library preparation and amplification for 17 cycles were performed following distributor's (Sigma-Aldrich) recommendations. 8 µg cDNA was fragmented by DNase I and biotinylated by terminal transferase obtained from the GeneChip Mapping 250K Nsp Assay Kit (Affymetrix Inc, Santa Clara, CA, USA). Hybridization, washing, staining and scanning of Affymetrix Rat Genome 230 PM Strip arrays were performed following the manufacturer's recommendations. Scanned images (DAT files) were transformed into intensities (CEL files) using the AGCC software (Affymetrix).

Quantitative real-time PCR

Custom TaqMan microfluidic cards (Applied Biosystems, Foster City, CA, USA) were designed to study mRNA expression by real-time PCR. Fourteen samples were examined. Reverse transcription and PCR were carried out by using Applied Biosystems' High Capacity cDNA Reverse Transcription Kit and TaqMan Universal PCR Master Mix II, respectively. PCR data evaluation were performed as described previously (24). The ViiA7 RUO 1.2.1 (Applied Biosystems) software and relative quantification against calibrator samples ($\Delta\Delta$ Ct) were used for data evaluation. Intact control was the calibrator sample. Glyceraldehyde-3-phosphate dehydrogenase (Gapdh) and hypoxanthine guanine phosphoribosyl-transferase (Hprt) were used as housekeeping genes. Expression of these genes did not vary among experimental groups. A computed internal control corresponding to the geometric mean of cycle threshold (Ct) values of Gapdh and Hprt was used for Δ Ct calculation. Relative quantity (RQ) was calculated according to RQ=2^(- $\Delta\Delta$ Ct) equation.

Data analysis

Microarray data analysis, including GC robust multi-array average (GCRMA), statistical and data mining work, were carried out as published earlier (25,26). In brief, raw data were preprocessed for analysis using GCRMA. For selection of differentially expressed genes, fold change values were used and linear models combined with empirical Bayesian methods were applied. Obtained p-values were adjusted by the false discovery rate (FDR)-based method. Genes that met the selection criterion of fold change (FC) >1.5 were considered OVX-regulated. For statistical analysis of real-time PCR results we used one-way ANOVA. Pathway analysis was constructed by using the <u>KEGG database</u>; http://www.genome.jp/kegg). Putative protein-protein interactions were evaluated by the web-based STRING 10 platform (http://string-db.org, as reported previously (25).

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Results

Modification of hippocampal transcriptome in response to long-term OVX

135 Microarray study

The comparison of hippocampal transcriptomes from middle-aged intact (M) and middle-aged ovariectomized (M-OVX) rats revealed that chronic ablation of gonadal hormones by surgical OVX results in differential expression of genes. At FC > 1.5 criterion, more than 200 genes were differentially regulated. Downregulated genes (145) outnumbered upregulated (107) ones. The full list of genes is shown in **Supplemental Table 1** providing the probe set ID, gene symbol and name, corresponding FC and adjusted P values. Top up- and downregulated genes selected at FC >1.7 are listed in **Table 1**. Top upregulated genes encode peptides like cocaine- and amphetamine-regulated transcript (Cartpt) and transthyretin (Ttr), peptidases (Sppl2a, Usp25, Prcp), adhesion proteins (Vcl, Pcdh20), proteo- and glucosaminoglycans (Spock3, Fndc3a), ion channel (Trpm7), signaling molecule (Ptpn3) and transcription factors (Hifla, Klf3) among others. In the top downregulated category, differentially regulated genes encode potassium channels (Kcnma1, Kcnj9, Kcnk9), serotonin receptor (Htr2c), neuropeptide (Adcyap1), members of G-protein coupled signaling mechanisms (Gpr123, Rgs17 and Rgs4), retinoid acid signaling molecule (Crabp1), components of growth factor signaling (Igfbp4, Nov), members of solute carrier family (Slc39a7, Slc17a6) and transcription factor (Etv1). Quantitative real-time PCR study In this study, the putative differential expression of 62 genes was examined by TaqMan-based PCR. Target selection was aimed at validation of the microarray result and also getting further insight to basic molecular mechanisms of neuronal networks of the hippocampus affected by OVX with special reference to synaptic plasticity, neurogenesis and immune modulation. The PCR results are listed in Table 2 and grouped in the aforementioned functional categories. In the clusters of synaptic plasticity and neurogenesis, both up- and downregulated genes were noted, on the other hand, most defense genes

were upregulated. Neuropeptide and neurotransmitter signaling mechanisms shape neuronal plasticity

of the hippocampal formation, accordingly, a large number of genes encoding various components of

these signaling pathways were seen robustly changed by long-term OVX. In case of peptide signaling,

Cartpt, Ttr, Cck, Vip and Penk were involved. Altered expression of genes encoding neuropeptide receptors was revealed for Crh1r and Crh2r, Gnrhr, Cckbr, Sstr1 and Oprd1. Regarding the involvement of classic neurotransmitter signaling mechanisms, differential expression was found in case of cholinergic (Chrm4, Chrna3), glutamatergic (Grm8, Slc17a6), serotonergic (Htr2c) and histaminergic (Hrh3) systems. Neurogenesis in the subgranular layer of the hippocampal formation is highly regulated by growth and troph factors, and this process is mirrored in changes of transcriptional activity. OVX influences both mechanisms with a particular strong impact on growth/troph hormone signaling. To the most important contributors of this cluster belong nerve growth factor (Ngf, Ngfr, Ntf3, Ntrk), insulinlike growth factor (Igf2, Igfbp4) and fibroblast growth factor (Fgf1) signaling systems. Regarding the regulation of transcription, Otx2 as classical transcription factor, whereas Esr1, Rxra and Thrb as ligand-activated nuclear transcription factor genes responded to OVX. Alteration in the expression of Sgk1 mRNA has extraordinary importance because of its wide-based regulatory potential. The gene cluster affiliated with processes of immune response and defense, covered predominantly upregulated genes like C3, Il1b, Tlr3, Tlr4, RT1-A1, Ccl2 and Aif1 among others.

174 KEGG pathway analysis of OVX-regulated genes

The top KEGG pathways changing in response to chronic OVX in middle-aged rats were summarized in **Table 3**. Neuroactive ligand-receptor interaction (ID: 4080, counts: 15), retrograde endocannabinoid signaling (ID: 4723, counts: 9), transcriptional misregulation in cancer (ID: 5202, counts 10), apoptosis (ID: 4210, counts: 7) and proteoglycans in cancer (ID: 5205, counts 11) pathways appeared at false discovery rate lesser than 0.005. Estrogen (ID: 4915) and thyroid (ID:4919) hormone signaling pathways also emerged. The influence on cholinergic (ID: 4725), glutamatergic (ID: 4724), adrenergic (ID: 4262) and serotonergic (ID: 4726) signaling pathways was also raised.

Predicted networking of hippocampal proteins encoded by OVX-regulated genes

In order to elucidate the interrelationship of genes, the predicted interaction and networking of proteins encoded by OVX-regulated changes were performed using the STRING 10 platform. The analysis was based on microarray and PCR results, carried out at confidence value 0.6. and the non-interacting genes were omitted. The networking of proteins coded by OVX-regulated genes is depicted in **Supplementary Figure 1**. Clusters of peptides serving neuropeptide and neurotransmitter signaling are explicit, similar

to protein assemblies regulating transcription. The OVX-regulated genes were sorted into up- and downregulated clusters (**Tables 4 and 5**) and the STRING analysis was implemented for both groups (**Figure 1 and 2**). Thirty-four upregulated, interacting proteins were sorted into 3 functional categories including growth/troph factors/transcription regulation, peptides/transmitters/ion channels/signaling and immune response/defense (**Table 4**). The downregulated group consisted of 47 proteins that were grouped in 4 operative categories such as peptides/transmitters/receptors/ion channels/signaling, solute carriers, growth factors/transcription regulation and immune response/defense (**Table 5**).

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Discussion

OVX modulates neurotransmission

Modulation of peptidergic signaling

Ablation of the ovaries affected interneurons of the hippocampal formation that responded mainly by downregulation of neuropeptide expression and also some of their genuine receptors. Cholecystokinin (Cck), neurotensin (Nts), vasoactive intestinal peptide (Vip) and preproenkephalin (Penk) are wellestablished and characterized constituents of certain hippocampal interneurons (37-45). Cck exerts excitatory role on CA1 pyramidal neurons (46,47) via its B type receptor that was also altered after OVX. Vip also increases excitatory transmission to CA1 pyramidal neurons by disinhibition of their dendrites (48). Nts targets interneurons enhancing GABAergic activity by modulating L-type calcium channels (49). OVX influences the opioid peptide signal transduction in the hippocampus as exemplified by decreased expression genes encoding Penk and its cognate receptor Oprd1. Enkephalins are known to modify the activity of hippocampal circuits (50,51). Opioid inhibition of GABA release from terminal boutons of interneurons has previously been reported (52). These changes suggest that OVX modulates interneuron function via downregulation of neuropeptides resulting in declining excitatory transmission in the hippocampus. Adcyap1 (PACAP) derives from both interneurons and principal neurons of the hippocampal formation. It exerts effects on CA1 pyramidal neurons by inhibiting the slow afterhyperpolarizing current (53). Increased PACAP level may also serve neurogenesis (54,55) and support neuroprotection (56,57). Accordingly, decreased Adcyap1 expression can affect the function of principal neurons, neurogenesis and protective mechanisms. Marked downregulation of Adcyap1 can't be restored by estradiol replacement (26). Decreased levels of type 1 and 2 CRH receptors indicate alteration in CRH signaling. Activation of these receptors has been reported to reduce the amplitude of hippocampal population spike and prevent the onset of long-term potentiation (LTP) (58). Downregulation of genes for CRHR subtypes decreases CRH-CRHR signaling and the impact of stress response on LTP. Estradiol replacement significantly increases Crhr2 expression. Regarding the upregulated category, the peptides CART, transthyretin, klotho and the Gnrhr were involved. The increase of CART and klotho seems to be advantageous for the hippocampus because of their renowned pro-cognitive effects (59,60). Increase in activation of Gnrhr may result in excitation of pyramidal neurons (61,62) although data on the expression of its ligand GnRH are controversial (63,64). Estradiol replacement (26) and DPN administration (25) do not affect Cck, Nts and Vip, but activate Crhr2 and suppress Cart mRNA expression. Disturbances in neurotransmitter signaling In middle-aged rats, OVX affected transmitter signaling via glutamate, acetylcholine, serotonin and histamine in the hippocampus, mainly by regulating the expression of their receptors (65). In case of glutamatergic signaling, Gria4, Grm1 and also Gls were upregulated, whereas Grm8 and Slc17a6 downregulated. Grm1 and AMPA receptors occur in the hippocampus enriched in association with postsynaptic densities of neuronal elements communicating via synapses (66-69). Vesicular glutamate transporter 2 was reported to play a crucial role in the proper development of mature pyramidal neuronal architecture and plasticity, and in the processes of cognition (70). Striking decrease of Slc17a6 expression affects glutamatergic signaling and cognition in the hippocampus after OVX. The signal transduction by serotonin is influenced via the downregulated Htr2c. Its activation regulates anxiety and release of acetylcholine in the hippocampus (71,72). Estradiol replacement and DPN administration restore Htr2c mRNA expression after OVX. Acetylcholine is a potent modulator of hippocampal circuits and has a pivotal role in cognition (73). Regarding the modulation of fast-synaptic neurotransmission, OVX influenced Chrna3. Its expression in the hippocampus has been reported earlier (74) and the present data indicate its downregulation. Similar to that, the expression of Chrm4 was also downregulated. Suppression of Chrm4 may affect synaptic transmission via alteration of glutamate

release probability. Hippocampus-dependent memory and synaptic plasticity are modulated by the

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244 estradiol milieu of the hippocampus (75-78). OVX also downregulated the expression of Hrh3. 245 Antagonizing H3 receptor has been shown to increase the release of acetylcholine in the dorsal 246 hippocampus and improve parameters of cognitive disorders (79). 247 Vesicular monoamine transporter 2 (*Vmat*2) showed upregulation after OVX, an event that influences 248 the transport of dopamine, epinephrine, norepinephrine, serotonin and histamine from the cytosol into 249 synaptic vesicles of neurons and plays role in their vesicular release of transmitters by exocytosis. Mice 250 mutant for *Vmat2* display symptoms of depression (80). 251 Modifications of potassium channels 252 Effect of OVX was overwhelmingly manifested in altered expression of different potassium channels. 253 The regulatory influence of estradiol has previously been described in case of slow Ca²⁺-activated K⁺ 254 current and large-conductance, voltage- and calcium-activated potassium channels (81,82). The single 255 upregulated gene was Kcnj6 that codes an ATP-sensitive, inwardly rectifying K+ channel that is 256 regulated by G proteins and closed by the rise of intracellular ATP levels. Downregulated genes included 257 Kcnj9, Kcnk9, Kcnma1 and Kcnc2. These alterations may lead to decreased synthesis of Kcnj9 (G 258 protein-activated inward rectifier potassium channel 3) which regulates resting membrane potential and 259 initiation of action potentials, Kcnk9 (Task 3 potassium channel) whose current is highly sensitive to 260 changes in extracellular pH, Kcnma1 (BK, large conductance calcium-activated potassium channel) and 261 Kcnc2 (Shaw-related K⁺ channel). Estrogenic regulation of BK (83) and G-protein-gated inwardly 262 rectifying K⁺ (GIRK) (84) channels has previously been reported. The present results indicate that 263 ablation of gonadal hormones in middle-aged rats changes the expression of all four functional types of 264 potassium channels in the hippocampus (85) that depending on their cell type and cellular domain 265 specific expression can modulate the excitability of hippocampal neurons. Long-term DPN treatment 266 attenuates the decrease in *Kcnma1* expression. 267

OVX interferes with mechanisms involved in neurogenesis

268 *Influence on growth/troph hormone signaling*

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OVX substantially influenced growth factor signaling within the hippocampus of middle-aged rats by dominantly upregulating the expression certain growth factors and their receptors. In the nerve growth factor family, Ntf3 and Ngf showed enhanced expression after OVX. In addition, two neurotrophin receptor genes, *Ngfr* (coding for p75) and *Ntrk1* (coding for TrkA) showed a similar, upregulated state. Neurotrophin signaling (86) has a key importance in neurogenesis and synaptic plasticity of the hippocampus (87-90). Two components of IGF signaling mechanisms were altered by OVX, the upregulated *Igf2* and the downregulated *Igfbp4*. Igf2 is a potent regulator of neurogenesis (91) and it also controls memory consolidation and enhancement (92). The differentially expressed *Fgf1* has been shown to support neuroprotective mechanisms (93) and facilitate LTP (94). *Mdk*, the retinoic acid-responsive, heparin-binding growth factor gene also showed higher expression after gonadectomy. Mdk was reported to block kainic acid-induced seizure and concomitant cell death (95). We found slight upregulation of neutrophin and growth factor genes after OVX. In previous studies we demonstrated that estradiol and DPN increase further mRNA expression of many growth factor genes in the hippocampus of ovariectomized rats which may contribute to the enhanced neurogenesis after replacement (96).

284 Impact on transcriptional regulation

Orthodenticle homeobox 2 (*Otx2*) and hypoxia inducible factor 1 alpha subunit (*Hif1a*) were both upregulated by OVX. *Otx2* shows altered expression in the hippocampus after tricyclic antidepressant treatment (97), whereas *Hif1a* responds to global ischemia (98). Aryl hydrocarbon receptor nuclear translocator 2 (*Arnt2*) was downregulated. Its encoded protein complexes with Hif1a and the complex regulates oxygen-responsive genes. Members of the nuclear receptor superfamily were also influenced by OVX resulting in upregulation of *Esr1* and *Nr4a3* (neuron-derived orphan receptor 1). Downregulation characterized the expression of *Thrb* and *Rxra*. The changes suggest that ablation of ovarian hormone supply to the hippocampus interferes with estrogen, thyroid hormone and retinoic acid signaling mechanisms that are basic transcriptional regulators of diverse hippocampal functions (28,99,100).

OVX affects defense mechanisms

- 296 Modulation of the immune system
- We have previously reported the impact of OVX and treatment with ERα and ERβ specific agonists on the innate immune system of the hippocampal formation in middle aged rats (24). In accordance with that PCR study, here we confirm the differential expression of macrophage markers (*Aif1*, *RT1-EC2*),

phagocytic receptors (CD11b, Fcgr3a), recognition receptors (Tlr3, Tlr4), complement system (C3, Cfh) proinflammatory cytokine IL-1β (Il1b) and an IL3 receptor subunit (Il3ra). These upregulated genes reflect the sensitization of microglia and increased level of complement components leading to an increased proinflammatory stage in the absence of gonadal hormone signaling to the hippocampus. Chronic estradiol and DPN administrations attenuate OVX-dependent upregulation of microglia-related genes (24). In a recent study, the role NLRP3 inflammasome activation was shown in development of estrogen deficiency-related affective disorders (101). Effects on neuroprotective mechanisms

Long-term OVX decreased the expression of genes encoding Bcl-2 (Bcl2) and superoxide dismutase (Sod1). These events are known to lead to increased apoptotic activity and enhanced level of the reactive superoxide radical, O²-. The neuroprotective role of Bcl-2 and Sod1 in the hippocampal circuits has been widely explored (102-107). Decreased synthesis of synuclein beta after OVX may promote alpha synuclein accumulation and trigger neurodegeneration (108,109). Estradiol replacement (26) and longterm DPN treatment (25) activate transcription of genes involved in protection against oxidative stress and detoxification such as Sod3, Gpx1, Gstm2, Gsta4, but do not increase Bcl2 and Sod1 expression in the hippocampus.

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To sum up, the present study demonstrated extensive transcriptional changes in the hippocampus after OVX in middle-aged rats. Ablation of the ovarian hormone supply influences the machinery of transcription, growth factor signaling, channels of synaptic communication, immune and neuroprotective mechanisms modulating neurogenesis, synaptic plasticity and immunomodulation. Some but not all changes can be restored by estradiol replacement. Regarding the translational value, the results suggest the careful consideration and risk evaluation of the effects of oophorectomy (and menopause) on basic neuronal operation and cognitive performance of the hippocampus in middle-aged individuals (110-112).

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Table 1. List of top hippocampal genes regulated by long-term OVX in middle-aged rats

Probeset ID	logFC	FC	adj. P	Symbol	Description
Upregulated Gen	es				
1394252_PM_at	1.194	2.288	0.356	Spock3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3
1368585_PM_at	1.188	2.278	0.141	Cartpt	CART prepropeptide
1391387_PM_s_at	1.158	2.232	0.479	Slbp	stem-loop binding protein
1391208_PM_at	1.087	2.124	0.178	Pcdh20	protocadherin 20
1380805_PM_at	1.060	2.084	0.310	Pvrl3	poliovirus receptor-related 3
1393247_PM_at	0.974	1.965	0.462	Zfp26	zinc finger protein 26
1378679_PM_at	0.963	1.949	0.446	Usp25	ubiquitin specific peptidase 25
1390812_PM_a_at	0.961	1.947	0.159	Rerg	RAS-like, estrogen-regulated, growth-inhibitor
1398355_PM_at	0.950	1.931	0.456	Trpm7	transient receptor potential cation channel, subfamily M, 7
1380279_PM_at	0.934	1.911	0.410	Prcp	prolylcarboxypeptidase (angiotensinase C)
1383396_PM_at	0.929	1.904	0.460	Fndc3a	fibronectin type III domain containing 3a
1375676_PM_at	0.915	1.886	0.460	Lin7c	lin-7 homolog C (C. elegans)
1374959_PM_at	0.894	1.858	0.457	Ngo2	NAD(P)H dehydrogenase, quinone 2
1389479_PM_at	0.890	1.853	0.419	KIf3	Kruppel-like factor 3 (basic)
1395744_PM_at	0.886	1.849	0.477	Sppl2a	signal peptide peptidase-like 2A
1389362 PM_at	0.856	1.811	0.246	Ptpn3	protein tyrosine phosphatase, non-receptor type 3
1382171_PM_at	0.851	1.804	0.515	Tsc22d2	TSC22 domain family, member 2
1387076_PM_at	0.850	1.802	0.460	Hif1a	hypoxia-inducible factor 1, alpha subunit
1375538_PM_at	0.835	1.784	0.519	VcI	vinculin
1376319_PM_at	0.834	1.783	0.061	Sema3c	semaphorin 3C
1382390_PM_at	0.809	1.752	0.469	Fubp3	far upstream element (FUSE) binding protein 3
1367598_PM_at	0.793	1.733	0.616	Ttr	transthyretin
1372905_PM_at	0.782	1.720	0.530	VcI	vinculin
1377651_PM_at	0.774	1.710	0.445	Trio	triple functional domain (PTPRF interacting)
Downregulated (c.p.o tanodonal contain (* 11 ta moradan g)
1370472 PM a at	-0.802	0.574	0.445	Kcnma1	K large conductance Ca-activated channel, subfamily M, α 1
1391074_PM_at	-0.807	0.574	0.440	Crabp1	cellular retinoic acid binding protein 1
1367768_PM_at	-0.807	0.572	0.440	Lxn	latexin
1383386_PM_a_at	-0.814	0.569	0.463	Sec3l1	SEC3-like 1 (S. cerevisiae)
1391075_PM_at	-0.817	0.568	0.341	Rgs17	regulator of G-protein signaling 17
1392823 PM at	-0.818	0.567	0.419	Snhg11	small nucleolar RNA host gene 11 (non-protein coding)
1369418_PM_at	-0.828	0.563	0.419	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9
1369280_PM_at	-0.833	0.561	0.326	Kcnk9	potassium channel, subfamily K, member 9
1387291_PM_at	-0.861	0.551	0.123	Itih3	inter-alpha trypsin inhibitor, heavy chain 3
1379481_PM_at	-0.863	0.550	0.123	Pabpn1	poly(A) binding protein, nuclear 1
1370248_PM_at	-0.873	0.546	0.400	Fxyd6	FXYD domain-containing ion transport regulator 6
1371132_PM_a_at	-0.875	0.545	0.159	Ank3	ankyrin 3, node of Ranvier
	-0.875 -0.887	0.545	0.439	Slc39a7	
1389089_PM_at					solute carrier family 39 (zinc transporter), member 7
1386940_PM_at	-0.911 -0.920	0.532 0.528	0.419 0.479	Timp2 Mlec	TIMP metallopeptidase inhibitor 2 malectin
1379046_PM_at					
1398303_PM_s_at	-0.948	0.518	0.459	Tpm3	tropomyosin 3, gamma
1368883_PM_at	-0.969 0.073	0.511	0.184	Nov	nephroblastoma overexpressed gene
1376980_PM_at	-0.973 1.020	0.510	0.222	Htr2c	5-hydroxytryptamine (serotonin) receptor 2C
1392555_PM_at	-1.029 1.045	0.490	0.166	Etv1	ets variant 1
1397513_PM_at	-1.045 1.054	0.485	0.431	Ralyl lafbo4	RALY RNA binding protein-like
1371462_PM_at	-1.054 1.068	0.482	0.103	lgfbp4 Amp21	insulin-like growth factor binding protein 4
1373257_PM_at	-1.068 1.091	0.477	0.419	Arpp21	cAMP-regulated phosphoprotein 21
1389155_PM_at	-1.081 1.005	0.473	0.393	Dos Crtoo1	downstream of Stk11
1368381_PM_at	-1.095 1.110	0.468	0.439	Crtac1	cartilage acidic protein 1
1384809_PM_at	-1.119 1.121	0.460	0.026	Gpr123	G protein-coupled receptor 123
1390865_PM_at	-1.121	0.460	0.026	Cadps2	Ca++-dependent secretion activator 2
1385491_PM_at	-1.143	0.453	0.299	Pnmal2	PNMA-like 2
1370602_PM_at	-1.301	0.406	0.159	Atp2b4	ATPase, Ca++ transporting, plasma membrane 4
1385788_PM_at	-1.479	0.359	0.419	Ephb3	Eph receptor B3
1368564_PM_at	-1.482	0.358	0.133	Slc17a6	sodium-dependent inorganic phosphate cotransporter
1368892_PM_at	-1.654	0.318	0.026	Adcyap1	adenylate cyclase activating polypeptide 1
1368505_PM_at	-1.868	0.274	0.032	Rgs4	regulator of G-protein signaling 4

Expression profiling by Affymetrix oligonucleotide microarray revealed that long-term OVX intensely regulates the hippocampal transcriptome in middle-aged rats. Using the FC >1.7 selection criterion, the top list contains 24 up- and 32 downregulated genes.

Table 2. PCR results

Assay ID	Symbol	Target name	RQ	P value
Neurotransmitter	and neuropep	tide signaling/ Synaptic plasticity		
Rn01645174_m1	Cartpt	CART propeptide	2.598	0.003
Rn00562124_m1	Ttr	transthyretin	2.251	0.097
Rn00564688_m1	Slc18a2	vesicular monoamine transporter 2	1.645	0.001
Rn00578981_m1	Gnrhr	gonadotropin releasing hormone receptor	1.631	0.004
Rn01454304_m1	Dagla	diacylglycerol lipase alpha	1.387	0.013
Rn00582505_m1	Slc12a2	Na-K-Cl cotransporter	1.386	0.094
Rn03993699_s1	Cnr2	cannabinoid receptor 2	1.250	0.070
Rn01505088_m1	Enpp2	ectonucleotide phosphodiesterase 2	1.221	0.015
Rn01234233_m1	Kcnc2	voltage-gated potassium channel	0.861	0.058
Rn00563215_m1	Cck	cholecystokinin	0.821	0.007
Rn01512605_s1	Chrm4	cholinergic receptor, muscarinic 4	0.775	0.031
Rn00578611_m1	Crhr1	corticotropin releasing hormone receptor 1	0.766	0.063
Rn00565867_m1	Cckbr	cholecystokinin B receptor	0.748	0.111
Rn01430567_m1	Vip	vasoactive intestinal peptide	0.733	0.001
Rn00561699_m1	Oprd1	delta 1 opioid receptor	0.723	0.051
Rn00585276_m1	Hrh3	histamine receptor H3	0.686	0.000
Rn00575617_m1	Crhr2	corticotropin releasing hormone receptor 2	0.650	0.016
Rn00567566_m1	Penk	preproenkephalin	0.644	0.000
Rn01456072_m1	Cadps2	Ca-dependent activator protein for secretion	0.599	0.001
Rn02532012_s1	Sstr1	somatostatin receptor 1	0.382	0.001
Rn00562748_m1	Htr2c	5HT receptor 2C	0.363	0.000
Rn00573505_m1	Gm8	glutamate metabotropic receptor 8	0.357	0.001
Rn00584780_m1	Slc17a6	vesicular glutamate transporter 2	0.260	0.000
Rn00583820_m1	Chrna3	cholinergic receptor nicotinic alpha 3 subunit	0.214	0.001
Growth and tropl	n factor signali	ng/ Neurogenesis		
Rn01414596_m1	Otx2	orthodenticle homeobox 2	4.934	0.014
Rn00591759_m1	Folr1	folate receptor 1	2.360	0.004
Rn00580123_m1	KI	klotho	2.104	0.094
Rn00572130_m1	Ntrk1	neurotrophic receptor tyrosine kinase 1	1.870	0.069
Rn01754856_m1	Ucp2	uncoupling protein 2	1.548	0.002
Rn00561634_m1	Ngfr	nerve growth factor receptor	1.506	0.008
Rn00579280_m1	Ntf3	neurotrophin 3	1.491	0.003
Rn01640372_m1	Esr1	estrogen receptor alpha	1.422	0.030
Rn01427989_s1	Cdkn1a	cyclin-dependent kinase inhibitor 1A	1.404	0.002
Rn00675549_g1	Mdk	midkine	1.355	0.054
Rn01533872_m1	Ngf	nerve growth factor	1.306	0.023
Rn00689153_m1	Fgf1	fibroblast growth factor 1	1.278	0.039
Rn01537468_g1	Sgk1	serum- glucocorticoid-regulated kinase 1	1.257	0.018
Rn01454518_m1	lgf2	insulin-like growth factor 2	1.160	0.109
Rn00578713_m1	Adcy2	adenylate cyclase 2	0.881	0.004
Rn00575368_m1	Fkbp1b	FK506 binding protein 1B	0.863	0.017
Rn00441185_m1	Rxra	retinoid X receptor alpha	0.852	0.068
Rn00567957_m1	Map6	microtubule-associated protein 6	0.814	0.020
Rn99999125_m1	Bcl2	B-cell lymphoma 2	0.780	0.001
Rn00562044_m1	Thrb	thyroid hormone receptor beta	0.777	0.008
Rn00578390_m1	Nov	nephroblastoma overexpressed	0.732	0.001
Rn01464112_m1	lgfbp4	insulin-like growth factor binding protein 4	0.480	0.001
Rn00566438_m1	Adcyap1	adenylate cyclase activating polypeptide 1	0.411	0.001
Rn01483363_m1	Atp2b4	ATPase plasma membrane Ca transporting 4	0.361	0.000
Rn00566938_m1	Sod1	superoxide dismutase 1	0.284	0.001
Rn01490867_g1	Rgs4	regulator of G protein signaling 4	0.272	0.000
Immune modulat				
Rn03034964_u1	RT1-EC2	RT1-EC2	2.121	0.012
Rn00580555_m1	Ccl2	C-C motif chemokine ligand 2	1.930	0.010
Rn00566466_m1	C3	complement C3	1.750	0.001
Rn01488472_g1	TIr3	toll-like receptor 3	1.663	0.006
Rn00709342_m1	ltgam	Cd11b	1.639	0.005
Rn00580432_m1	II1b	interleukin 1beta	1.437	0.114
Rn00560589_m1	A2m	alpha-2-macroglobulin	1.330	0.001
Rn00564605_m1	Ptgds	prostaglandin D2 synthase	1.253	0.039
Rn01483598_m1	Fcgr3a	Fc gamma receptor 3a	1.245	0.058
Rn00574125_g1	Aif1	allograft inflammatory factor 1	1.207	0.036
D-00FC00404	TIr4	toll-like receptor 4	1.197	0.028
Rn00569848_m1	1117	ton like receptor 4	1.101	0.020

Real-time PCR study revealed transcriptional regulation of 62 genes. Thirty-three of them were upregulated. The OVX-regulated genes were grouped in three functional clusters: neurotransmitter and neuropeptide signaling/ synaptic plasticity, growth and troph factor signaling/ neurogenesis, immune modulation/ defense. RQ, relative quantity.

671 Table 3. Pathway analysis

KEGG Pathways				
Pathway ID	Pathway description	Count	FDR	
4080	Neuroactive ligand-receptor interaction	15	0.0007	
4723	Retrograde endocannabinoid signaling	9	0.0007	
5202	Transcriptional misregulation in cancer	10	0.0032	
4210	Apoptosis	7	0.0057	
5205	Proteoglycans in cancer	11	0.0072	
4915	Estrogen signaling pathway	7	0.0075	
4725	Cholinergic synapse	7	0.0111	
4750	Inflammatory mediator regulation of TRP channels	7	0.0111	
4724	Glutamatergic synapse	7	0.0134	
4919	Thyroid hormone signaling pathway	7	0.0170	
5200	Pathways in cancer	12	0.0204	
4810	Regulation of actin cytoskeleton	9	0.0328	
4261	Adrenergic signaling in cardiomyocytes	7	0.0379	
4921	Oxytocin signaling pathway	7	0.0419	
4726	Serotonergic synapse	6	0.0480	

Top gene ontology pathways affected by OVX in middle-aged rats. The analysis was performed on the web-based KEGG platform. Terms were ranked based on their FDR values. FDR, false discovery rate.

Table 4. Functional clusters of upregulated genes in OVX, middle-aged rats

	Functional gene clusters upregulated by OV	'X
Symbol	Gene name	FC
Growth/tro	oph factors/transcription regulation	
Esr1 Fgf1 Hif1a Igf2 Mdk Ngf Ngfr Ntrk1 Ntf3 Nr4a3 Otx2	estrogen receptor alpha fibroblast growth factor 1 hypoxia-inducible factor 1, alpha subunit insulin-like growth factor 2 midkine nerve growth factor nerve growth factor receptor neurotrophic tyrosine kinase, receptor, type 1 neurotrophin 3 nuclear receptor subfamily 4, group A, member 3 orthodenticle homeobox 2	1.422 1.278 1.802 1.160 1.355 1.306 1.506 1.520 1.491 1.522 4.934
Rerg	RAS-like, estrogen-regulated, growth-inhibitor	1.947
Peptides/f	ransmitters/ion channels/signaling	
Cartpt Gria4 Grm1 Gls Gnrhr Kcnj6 KI Slc12a2 Ttr Slc18a2	CART prepropeptide glutamate receptor, ionotrophic, AMPA 4 glutamate receptor, metabotropic 1 glutaminase gonadotropin releasing hormone receptor K inwardly-rectifying channel, subfamily J, 6 klotho Na-K-Cl cotransporter transthyretin vesicular monoamine transporter 2 esponse/defense	2.278 1.506 1.532 1.580 1.631 1.517 2.104 1.386 2.251 1.645
Aif1	allograft inflammatory factor 1	1.207
A2m Ccl2 C3 Itgam Cfh	alpha-2-macroglobulin C-C motif chemokine ligand 2 complement C3 Cd11b complement factor H	1.330 1.930 1.750 1.639 1.551
Fcgr3a	Fc gamma receptor 3a	1.245
II1b RT1-EC2 Sep7	interleukin 1beta RT1-EC2 septin 7	1.437 2.121 1.545
TIr3 TIr4	toll-like receptor 3 toll-like receptor 4	1.663 1.197

- Representative upregulated genes grouped in three functional clusters as growth/troph factors/
 transcriptional regulation, peptides/transmitters/ion channels/signaling and immune response/ defense.
- FC in italics refers to PCR results. FC, fold change.

Table 5. Functional clusters of downregulated genes in OVX, middle-aged rats

Symbol	Gene name	FC
-	nsmitters/receptors/ion channels/signaling	
Htr2c	5HT receptor 2C	0.363
Adcy2	adenylate cyclase 2	0.881
Adcyap1	adenylate cyclase activating polypeptide 1	0.411
Crebl2	cAMP responsive element binding protein-like 2	0.604
Cbln2	cerebellin 2 precursor	0.613
Cck	cholecystokinin	0.821
Cckbr	cholecystokinin B receptor	0.748
Chrna3	cholinergic receptor nicotinic alpha 3 subunit	0.214
Chrm4	cholinergic receptor, muscarinic 4	0.775
Crhr1	corticotropin releasing hormone receptor 1	0.766
Crhr2	corticotropin releasing hormone receptor 2	0.650
Oprd1	delta 1 opioid receptor	0.723
Grm8	glutamate metabotropic receptor 8	0.357
Hrh3	histamine receptor H3	0.686
Kcnk9	K channel, subfamily K, member 9	0.561
Kcnj9	K inwardly-rectifying channel, subfamily J, 9	0.563
Kcnma1	K large conductance Ca-activated channel, subfamily M	0.574
Nts	neurotensin	0.653
Penk	preproenkephalin	0.644
Rgs4	regulator of G protein signaling 4	0.272
Rgs17	regulator of G-protein signaling 17	0.568
Sstr1	somatostatin receptor 1	0.382
Vip	vasoactive intestinal peptide	0.733
Slc17a6	vesicular glutamate transporter 2	0.260
Vdac1	voltage-dependent anion channel 1	0.641
Kcnc2	voltage-gated potassium channel	0.861
Solute carri	ers	
Slc1a4	solute carrier family 1, member 4	0.657
Slc10a4	solute carrier family 10, member 4	0.638
Slc17a6	solute carrier family 17, member 6	0.358
Slc25a18	solute carrier family 25, member 18	0.646
Slc39a7	solute carrier family 39, member 7	0.541
Slc4a3	solute carrier family 4, member 3	0.653
Slc6a17	solute carrier family 6, member 17	0.623
Slc9a1	solute carrier family 9, member 1	0.631
Slc9a5	solute carrier family 9, member 5	0.648
Growth fact	or/transcription regulation	
Amt2	aryl hydrocarbon receptor nuclear translocator 2	0.657
Crabp1	cellular retinoic acid binding protein 1	0.572
Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	0.646
Igfbp4	insulin-like growth factor binding protein 4	0.480
Rxra	retinoid X receptor alpha	0.852
Thrb	thyroid hormone receptor beta	0.777
Immune res	ponse/defense	
Apitd1	apoptosis-inducing, TAF9-like domain 1	0.643
Bcl2	B-cell lymphoma 2	0.780
C1ql3	complement component 1, q subcomponent-like 3	0.766
01410 113ra	interleukin 3 receptor, alpha	0.661
Sod1	superoxide dismutase 1	0.284
Sncb	synuclein, beta	0.614

Representative downregulated genes assembled in four functional clusters as peptides/transmitters/receptors/ion channels/signaling, solute carriers, growth factor/transcription regulation and immune response/defense. FC in italics refers to PCR results. FC, fold change.

Figure legends

Predicted interactions among proteins encoded by upregulated genes in long-term ovariectomized, middle aged rats. The network is based on combined results of microarray and quantitative real-time PCR studies and was constructed by using the STRING 10 Known and Predicted Protein-Protein Interactions program (http://string-db.org/). Analysis was performed at confidence value 0.6 and non-interacting elements were excluded. Selected protein clusters of the network are shown by color frames. The red box marks growth factor signaling, blue identifies immune response, yellow indicates peptide and transmitter signaling, green marks regulation of transcription.

Figure 2. Predicted interactions among proteins encoded by downregulated genes in long-term ovariectomized, middle aged rats. The network is based on combined results of microarray and quantitative real-time PCR studies and was constructed by using the STRING 10 Known and Predicted Protein-Protein Interactions program (http://string-db.org/). Analysis was performed at confidence value 0.6 and non-interacting elements were excluded. Selected protein clusters of the network are shown by color frames. The red box marks peptide and transmitter signaling, blue indicates potassium channels, orange marks transcriptional regulation, green identifies heterogeneous nuclear ribonucleoproteins.



