Maternal exposure to the neurotoxin methylmercury (MeHg) has been shown to have adverse effects on neural development of the offspring in man. Little is known about the underlying mechanisms by which MeHg affects the developing brain. To explore the neurodevelopmental defects and the underlying mechanism associated with MeHg exposure, the cerebellum and cerebrum of Wistar rat pups were analyzed by [18F]FDG PET functional imaging, field potential analysis, and microarray gene expression profiling. Female rat pups were exposed to MeHg via maternal diet during intrauterinal and lactational period (from gestational day 6 to postnatal day (PND)10), and their brain tissues were sampled for the analysis at weaning (PND18–21) and adulthood (PND61–70). The [18F]FDG PET imaging and field potential analysis suggested a delay in brain activity and impaired neural function by MeHg. Genome-wide transcriptome analysis substantiated these findings by showing (1) a delay in the onset of gene expression related to neural development, and (2) alterations in pathways related to both structural and functional aspects of nervous system development. The latter included changes in gene expression of developmental regulators, developmental phase-associated genes, small GTPase signaling molecules, and representatives of all processes required for synaptic transmission. These findings were observed at dose levels at which only marginal changes in conventional developmental toxicity endpoints were detected. Therefore, the approaches applied in this study are promising in terms of yielding increased sensitivity compared with classical developmental toxicity tests.

Keywords: neurodevelopment; methylmercury; [18F]FDG PET functional imaging; field potential analysis; microarrays; neurotoxicity.

The development of the brain is a highly complex and precisely timed process, which starts at gestation and continues throughout juvenile stages to adolescence. The early exposure of fetal and juvenile brain to environmental hazards may have deleterious effect on its development. Methylmercury (MeHg), which is found in some fish and shellfish, has harmful effects on the developing human nervous system. MeHg is the most stable organic form of mercury, and it has a high bioaccumulation potential (Clarkson and Magos, 2006; European Commission, 2006, 2010). The clinical findings in children exposed to MeHg poisonings in Japan (Harada, 1968; Takeuchi, 1985; Takizawa and Kitamura, 2001) and Iraq (Bakir et al., 1973) have revealed the extreme sensitivity of the developing brain to this compound and have triggered a series of animal studies aiming to determine the exact consequences of pre- and perinatal exposure to MeHg (Castoldi et al., 2008). Neurobehavioral effects reported include altered motoric function and learning and memory disabilities; besides, in vitro studies showed inhibition of neuronal differentiation of neural stem cells (Johansson et al., 2007). Nevertheless, the mechanism of action of MeHg is unknown, as are the differences in sensitivity of the various brain regions. Elucidation of these aspects would contribute to fine tuning of guidelines for developmental neurotoxicity testing and thus optimal protection of the offspring health.

The current guidelines for the assessment of MeHg developmental neurotoxicity focus on developmental landmarks and behavioral and extensive neuropathological/stereological surveys. The classical “No Observed Adverse Effect Level” (NOAEL) approach (Crump, 1984; Slob, 2002) aims to identify the highest dose level tested without an observed change in the (critical) endpoint. However, the fact that no change could be (statistically) observed at the NOAEL does not necessarily imply that there is no biologically relevant adverse effect present (European Food Safety Authority (EFSA), 2009). Previously, we have shown that by applying the advanced benchmark statistical approach, a significant dose-response effect of MeHg exposure can be identified in the conditions where classical NOAEL approach fails to detect these effects (Tonk et al., 2010).
In another related study with equivalent design, the relevance of MeHg effects was shown by neuron counting method, which detected statistically significant neuron loss at both juvenile and adult stage of MeHg-exposed rat pups. In the same study, the conventional neuropathological and developmental guideline tests for developmental neurotoxicity (U.S. Environmental Protection Agency (U.S. EPA), 1996, 1998; Organisation for Economic Co-operation and Development (OECD), 2007) showed no statistically significant results (de Groot, personal communication). These observations demonstrate that conventional animal-based developmental neurotoxicity testing methods need to be complemented with more sensitive assays in order to accurately predict hazard and ultimately risk in man.

In this study, we investigate the early (lactation and weaning) and the late (adulthood) effects of pre- and perinatal MeHg exposure on structural and functional parameters of developing rat brain (cerebrum and cerebellum) by [18F]FDG PET functional imaging, field potential analysis, and microarray gene expression profiling. Exposure equaled pre- and perinatal window proposed in U.S.-EPA Test Guideline for developmental neurotoxicity, i.e., from gestation day 6 (GD6) to postnatal day 10 (PND10) (U.S. Environmental Protection Agency, 1998). MeHg dose of 1.5 mg/kg was assessed in all assays and both tissues, and transcriptional profiling of cerebellum was also performed at lower MeHg doses (0.1, 0.4, and 1 mg/kg) to test the sensitivity of the method. We found a suggestive delay in onset of neural development and/or function and uncovered the molecular mechanisms underlying these defects. Importantly, we found that the early maternal dietary exposure to MeHg results in effects that persist to the adult stage of the exposed rats. In addition to the health relevance of these findings, our results show that methods for assessment of MeHg neurotoxicity used in this study provide an alternative method of superior sensitivity to classical toxicity testing protocols.

**MATERIALS AND METHODS**

**Test substance.** Methylmercury (MeHg), CAS 115-09-3, was obtained from Sigma-Aldrich, Zwijndrecht, The Netherlands.

**Animals and animal husbandry.** The in-life part of the study was carried out at the Animal Facilities of TNO Location Zeist, The Netherlands, as previously described (Tonk et al., 2010). Animal care and use were in accordance with Directive 86/609/EEC, which established the general principles governing the use of animals in experiments of the European Communities and with Dutch-specific legislation (The Experiments on Animals Act, 1977). Female and male Wistar rats (Crl-[WI]-WU BR), purchased from Charles-River Germany (Sulzfeld, Germany), were acclimatized for 12 days before mating at a ratio of 2 females:1 male. Animals were supplied with RM3 breeding diet (SDS, Watham, UK) and tap water, both ad libitum. Animals were housed in groups of four per sex in the animal facility with a 12:12-h light:dark cycle and maintained at 22 ± 3°C and 30–70% humidity.

**Study design and group selection.** A regulatory developmental neurotoxicity study was carried out according to test guidelines US EPA OPPTS 870.6300/8600 (U.S. EPA, 1998). F0 female Wistar rats were orally dosed with MeHg dissolved in corn oil (Sigma). The MeHg was administered to the dams by gavage between GD6 and lactation day 10 (LD10) in the following concentrations: 0, 0.1, 0.4, 0.7, 1.0, 1.5, or 2.0 mg/kg body weight (BW) per day. The effects of MeHg on F1 offspring were studied during lactation, weaning, and adulthood by a series of conventional and more advanced tests.

The study started with 15 F0 female rats per group and an additional number of 8 females in the control group and also in the 1.5-mg MeHg groups. Per group, at least 10 dams with at least 10 pups each were selected for the neurocohort. Litters were culled on PND8 to n = 10 pups/litter (5 male and 5 female pups). Two subsets (1 pup/sex/litter; 10 litters/dose group; all groups/subset) were selected for conventional behavioral testing and neuropathology as indicated in the test guideline. For PET imaging, five female F1 animals (four and a spare rat) from different litters (control group and 1.5-mg MeHg dose group) were selected and scanned at PND18, 22, 37, and 61. These time points were chosen—as near as possible—as proposed in the test guideline for conventional functional testing, i.e., 13, 17, 21, 61 ± 1 day (functional observational battery [FOB] and motor activity assessment [MAA]) but were limited by ethics—to PET scanning allowed below the age of PND17—and logistics—staged start of experimentation and litters not born on the same day—leading to inclusion of PND37 to have another time point during adolescence. Likewise, animals for gene expression analysis and field potentials were selected as near as possible to weaning (PND21) and young adulthood (PND61 ± 1 day) as proposed for neuropathology survey in the test guideline (see below).

During lactation, developmental parameters (physical/sensory landmarks) were measured in both subsets of the neuro cohort, i.e., 2 male and 2 female pups/litter; all litters/group; all dose groups including control group. All behavioral tests like FOB and MAA (PND13, 17, 21, 61 ± 1 day), auditory startle response (PND23 ± 1 day), passive avoidance, and active avoidance tests (PND30 and 37 and PND60 and 67 ± 1 day, respectively) were carried out with 1 male and 1 female F1 animal/litter; 10 litters per group; all dose groups including the control group. Upto PND21, FOB and MAA were carried out in both subsets of the neuro cohort.

Subset 1 was sacrificed for neuropathology at PND21; subset 2 at PND70; the latter time point was needed to include active avoidance test for cognitive functioning (PND60 and 67 ± 1 day). Brains were dissected along neuroanatomical landmarks in such a way that left and right hemispheres could be used for different purposes (see below section “Brain samples preparation”). As such, still 10 animals/sex/group—all from different litters—were sampled for neuropathology (at PND21 and PND70); brain tissues (cerebrum and cerebellum separately) from at least five female F1 animals from different litters (control group and 1.5-mg MeHg group) were sampled for gene expression analysis (“genomics”) during sacrifice (PND21 and PND70). Five female F1 animals from five different litters were selected for field potential measurements (control group and 1.5-mg MeHg dose group, at PND28 ± 3 days and at PND65 ± 3 days).

Here we report on the assessment of advanced testing technologies, i.e., in vivo [18F]FDG PET imaging, ex vivo/din vitro field potential recording in brain slabs (hippocampus), and microarray gene expression/pathway analysis (cerebrum, cerebellum). For comparison of relative sensitivity, effects of conventional guideline testing is briefly touched upon (Supplementary material).

The study was accomplished in the spirit of Good Laboratory Practice.

**BW and health.** BW of the F1 animals was measured at different time points during experimentation: twice a week during lactation, starting on PND1 until PND21 (PND1, 4, 7, 10, 14, 17, and 21); weekly from PND21 onwards. Animals were checked daily for clinical signs of adverse effects. In the article, only the final outcome of effect of MeHg on BW is given in a brief summarizing table (Supplementary material).

**Brain sample preparation.** Brains were collected from the female F1 offspring immediately after sacrifice. Different brain parts were further dissected using neuroanatomical landmarks visible at the outer surface of the brain (de Groot et al., 2005a, b). Briefly, one coronal separation was made in between the cerebrum and olfactory bulb, and one separation was made in between the cerebellum and medulla oblongata/spinal cord at the dorsal end. Subsequently, the brain halves were separated along the midline. Then, the cerebrum was separated from the cerebellum by a coronal separation perpendicular to the midline. All brain parts were measured for size and weighed. Immediately thereafter, one brain half—alternating between the left and the right one (the first one was...
chosen randomly)—was collected in formalin for neuropathology; the other was frozen for microarray analysis and toxicokinetic analysis of brain mercury levels. Left and right cerebellar and cerebral regions were also randomly assigned to either microarray analysis or toxicokinetic analysis. Frozen samples were stored at −80°C until further use. In this article, we only present the microarray analysis procedures and results (cerebrum and cerebellum separately).

**Conventional neurodevelopmental toxicity testing.** The effects on F1 offspring were studied assessing conventional guideline endpoints (BW, clinical signs, developmental landmarks, neuropathology, and behavior); cerebellar volume and neuron numbers were assessed with stereology as previously described (de Groot et al., 2005a, b). This part of the study is not included in this article and will be published elsewhere. However, for comparison of the sensitivity of the advanced technologies assessed and described here, the final outcome of the conventional tests is given in a brief summarizing table (Supplementary material).

**[^8F]FDG PET imaging.** Female rats exposed to 0 (control group, n = 4, and a spare animal) or 1.5 mg/kg MeHg daily (MeHg group, n = 4, and a spare animal) from GD6 until LD10 were subjected to repeated PET imaging. Brain glucose metabolism—a surrogate marker for brain activity—was assessed by static[^8F]FDG PET imaging on PND18, 28 (± 3) and 65 (± 3) days old (Fig. 1) exposed to 0 (control group) or 1.5 mg/kg MeHg for cerebrum. Prior to isolation of total RNA, cerebral and cerebellar brain regions were homogenized with a mortar and pestle under liquid nitrogen. High-quality total RNA was used with the Affymetrix Eukaryotic One-Cycle Target Labeling and Control reagents to generate Biotin-labeled antisense cRNA. The quality of the cRNA was checked using the Agilent 2100 bioanalyzer. The labeled cRNA was further used for the hybridization to Affymetrix Rat230-2.0 Genome Genechips, harboring 31099 probe sets. After an automated process of washing and staining, absolute values of expression were determined by absorbency at 260 nm with the Nanodrop ND-1000, and quality and integrity were verified using the RNA 6000 Nano assay on the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA). Next, 2 μg of high-quality total RNA was used with the Affymetrix Eukaryotic One-Cycle Target Labeling and Control reagents to generate Biotin-labeled antisense cRNA. The quality of the cRNA was checked using the Agilent 2100 bioanalyzer. The labeled cRNA was further used for the hybridization to Affymetrix Rat230-2.0 Genome Genechips, harboring 31099 probe sets. After an automated process of washing and staining, absolute values of expression were calculated from the scanned array using the Affymetrix Command Console v1 software.

^{[^8F]FDG PET imaging.} Female rats exposed to 0 (control group, n = 4, and a spare animal) or 1.5 mg/kg MeHg daily (MeHg group, n = 4, and a spare animal) from GD6 until LD10 were subjected to repeated PET imaging. Brain glucose metabolism—a surrogate marker for brain activity—was assessed by static[^8F]FDG PET imaging on PND18, 28 (± 3) and 65 (± 3) days old (Fig. 1) exposed to 0 (control group) or 1.5 mg/kg MeHg for cerebrum. Prior to isolation of total RNA, cerebral and cerebellar brain regions were homogenized with a mortar and pestle under liquid nitrogen. High-quality total RNA was used with the Affymetrix Eukaryotic One-Cycle Target Labeling and Control reagents to generate Biotin-labeled antisense cRNA. The quality of the cRNA was checked using the Agilent 2100 bioanalyzer. The labeled cRNA was further used for the hybridization to Affymetrix Rat230-2.0 Genome Genechips, harboring 31099 probe sets. After an automated process of washing and staining, absolute values of expression were calculated from the scanned array using the Affymetrix Command Console v1 software.
Microarray data preprocessing and quality control. Quality control microarray data were performed using simplyaffy and affyplm packages from the R/Biocductor project through the Management and Analysis Database for MicroArray eXperiments (MADMAX) analysis pipeline, as previously described (Radonicj et al., 2009). Normalization of microarray data per tissue was performed through the same analysis pipeline using the library GC-RMA and employing the empirical Bayes approach for background correction followed by quantile normalization. The custom MBNI CDF-file (CustomCDF, rn230nontreg_v10.0.0), available at http://brainarray.mbi.med.umich.edu/Brainarray/Database/CustomCDF/CDF_download_v10.asp and http://nugo-r.bioinformatics.nl/NoGO_R.html was used to reannotate the probes to new probe sets, remove poor quality probes, and derive unique signal values for different probe sets representing the same gene. This resulted in gene expression values for 11,498 genes with unique identifiers. Data were additionally filtered based on expression signals. To pass filtering criteria, gene expression was required to have a value above 5 in at least one of the experiments, resulting in 10,422 genes in cerebellum and 10,229 genes in cerebrum.

Statistical analysis of microarray data, pathway analysis, and visualization. Differentially expressed genes were identified using the limma package, applying linear models and moderated t-statistics that implement empirical Bayes regularization of standard errors (Smyth, 2004). The statistical analyses were performed through the Remote Analysis Computation for gene Expression data (RACE) suite at http://race.unil.ch (Psarros et al., 2005). Doses of 0.1, 0.4, 1.0, and 1.5 mg/kg BW/day (GD6 to PND10) were tested on cerebellar gene expression. Gene expression under each MeHg dose treatment was compared with the control treatment (dose zero) per tissue and developmental stage (PND21 or PND70). To be statistically significant, fold change of gene expression was required to be either > 1.5 or < -1.5 and to have p value of < 0.01. The exception of the increasing dose effect (more differentially expressed genes with the increasing MeHg dose) at dose 1.5 mg/kg at PND70 may be due to the maternal cannibalism that we observed in this particular treatment group, indicating that this dose was too high for optimal viability. The surviving animals within this group showed large heterogeneity (resulting in relatively poor statistical power) of their gene expression response.

Hierarchical clustering and visualization of gene expression changes were performed in GeneSpring GX 7.3.1 software (Agilent Technologies). The expression value of each gene was normalized to the mean value of that gene across all conditions. The average expression per treatment group is plotted. The analysis of up- or downregulated Gene Ontology categories (GO, www.geneontology.org) in cerebrum was performed using Toxprofiler based upon the T-profiler algorithm (Boorsma et al., 2005). As input values, average log, ratio values of gene expression levels (MeHg treatment vs. control group) of all 10,229 genes were used. T scores were considered significant if E value (Bonferroni corrected) was smaller than 0.05. This analysis results in T scores representing over- and underrepresentation of pathway-specific gene sets. Identification of overrepresented functional categories among differentially expressed genes in cerebellum was performed using DAVID Functional Annotation Clustering tool (Dennis et al., 2003). The analysis was performed using regulated Gene Ontology, Protein domains, Pathways, and Functional categories according to the default settings. Representative statistically significant GO functional categories and genes belonging to these categories are manually selected and reported in Figure 3B.

RESULTS

Female Wistar rat pups were exposed to MeHg via maternal diet during intrauterine and lactational period from GD6 to PND10. The entire tested dose range was 0 (control treatment), 0.1, 0.4, 0.7, 1.5, and 2 mg/kg of MeHg. During weaning and adulthood, cerebellum and cerebrum were sampled for the analysis by [18F]FDG PET functional imaging, field potential analysis, and microarray gene expression profiling (Fig. 1). As a reference for sensitivity assessment of these alternative assays, conventional guideline tests for developmental neurotoxicity were also performed. In this article, a brief summary of the effects of MeHg found in the different conventional tests is given in Supplementary material. With exception of one parameter (i.e., sexual landmark “delayed vaginal opening”), none of the tests showed significant effect with NOAEL approach and a benchmark-advanced statistical method (Supplementary material).

Functional Imaging of Cerebellum and Hippocampus Suggests a Delay and Decrement in Brain Activity upon MeHg Exposure

As a surrogate biomarker for brain activity, glucose metabolism was assessed in a longitudinal manner by [18F]FDG PET imaging at PND18, 22, 37, and 61. Cerebellum and hippocampus of the control group and the rats exposed to MeHg at dose 1.5 mg/kg were included in the analysis. Group comparison of [18F]FDG uptake in cerebellum and hippocampus between MeHg-treated and control rats did not reveal significant differences at PND61. At PND18, however, [18F]FDG uptake in cerebellum (0.05 > p < 0.1) and hippocampus (0.05 > p < 0.1) tended to be lower in MeHg-treated animals than in controls. On day 22, however, [18F]FDG uptake in cerebellum (p < 0.05) and hippocampus (0.05 > p < 0.1) was (significantly) higher in MeHg-treated animals. On day 37, on the other hand, [18F]FDG uptake was again significantly lower in the MeHg group than in controls both in cerebellum (p < 0.05) and hippocampus (p < 0.05). Strikingly, the pattern of [18F]FDG uptake over time was markedly different between both experimental groups, whereas within each group, cerebellum and hippocampus showed similar uptake patterns (Fig. 2). As is illustrated in Figure 2, the FDG uptake apparently did not follow a gradual linear increase with age. In control animals, the average [18F]FDG uptake in both hippocampus and cerebellum decreased between PND18 and 22 although not significantly. From PND22 to PND61, [18F]FDG uptake in both brain regions increased, which resulted in [18F]FDG uptake in both brain regions being significantly higher on PND61 than on either PND18 or PND22 (p < 0.05). In contrast, [18F]FDG uptake in both hippocampus and cerebellum of MeHg-treated animals increased between day 18 and 22, then decreased between day 22 and 37, and increased again between day 37 and 61. None of these differences in tracer uptake between different days were statistically significant, except for the difference in [18F]FDG uptake in hippocampus between PND18 and 22 (p < 0.05). At PND22 and PND37, the [18F]FDG uptake levels of MeHg-exposed animals were similar to the ones of control animals at PND18 and PND22, respectively. These results might be suggestive for a possible delayed phase-shift pattern as depicted in Figure 2 by the artificial “15 days shift” graph, resulting from shifting the “dip” in [18F]FDG uptake in the MeHg curve (PND37) toward the “dip” in the curve of the control group (PND22). It should be borne in mind, however, that [18F]FDG uptake was measured only at four test ages. Brain activity in between the four measured time points is not known.
MeHg Exposure Modifies Neurotransmission in the Hippocampus Assessed In Vitro Using Field Potentials

Basic neurotransmission was assessed in the pyramidal cell layer of the hippocampal CA1 region using field potential recordings in acute brain slices. The slices were obtained from control and MeHg-exposed rats (dose 1.5 mg/kg) at time points PND28 and PND68. In each group, a total of five rats were tested, coming from separate litters. From each rat, the field potentials were recorded in two brain slices, one from the left and one from the right hemisphere. The field potential amplitudes were defined per slice, and the data were averaged over hemispheres and rats. Stimulation of the afferent Schaffer collaterals (Fig. 3A1) induces a field potential in stratum pyramidale that consists of a representation of the synaptic currents (fEPSP) and a superimposed synchronized action potential (the PS, Fig. 3A2) evoked in the pyramidal neurons (Fig. 3A1). Stronger stimulation leads to a PS of larger amplitude; Figure 3B gives a typical result for the PND28. The threshold and the maximum stimulation intensity were set for each slice. The currents required to reach a threshold and to evoke a maximum field potential were not significantly different between the control and MeHg-exposed group at 28 and 68 days. The relation between PS amplitude and stimulus intensity is also observed in the MeHg-exposed group. Comparable stimulus response relations were obtained for the PND68 (data not shown). However, the maximum PS was significantly smaller at PND68 than at PND28 ($p < 0.01$).

Applying a second stimulus shortly after the first one reveals the short-term dynamics of the activated synapses. The PS2/PS1 ratio was determined for each stimulus pair given (Fig. 3A2). A ratio < 1 indicates paired pulse depression, and a ratio > 1 indicates paired pulse facilitation. Although the mean amplitudes of the PS1 and PS2 are not different (Fig. 3B), the short-term dynamics of the network do show effects of age and maternal MeHg exposure (Fig. 3C). The PND68 control group shows facilitation, primarily at the lower stimulus intensities, which was

![Diagram](https://example.com/diagram.png)
not observed in the PND28 control group (ANOVA, main effect of age: $F = 145.5; p < 0.01$; interaction age $\times$ stimulus intensity: $F = 5.62; p < 0.01$). In the MeHg-exposed group, at PND28, the PS2/PS1 ratio was changed into a small paired pulse depression, whereas at PND68, the group showed an enhanced paired pulse facilitation (ANOVA: main effect of MeHg exposure: $F = 4.43; p < 0.05$; interaction age $\times$ MeHg exposure: $F = 17.1; p < 0.01$).

The interval between the two stimuli is an important parameter that elucidates the underlying mechanisms. We systematically varied the interpulse interval between 20 and 500 ms and kept the stimulus intensity fixed at 80% to ensure action potential firing in response to the first pulse. In the control and the MeHg-exposed groups, only a very small facilitation was observed at PND28, which gradually vanished for
longer intervals and was not different between the two groups (Fig. 3C). At PND68, the facilitation in controls is larger than at PND28, and in the MeHg-exposed group, it is even larger (Fig. 3D) than in controls. A gradual decline of the facilitation was observed as a function of the time interval between P2 and P1 (Fig. 3D). (ANOVA main effect MeHg: $F = 5.13$; $p < 0.05$; main effect age: $F = 21.98$; $p < 0.01$; interaction MeHg × age: $F = 6.76$; $p < 0.01$). The same interpulse interval experiment was repeated at a stimulus intensity of 10%. In this case, there will be no action potential firing in response to the first pulse, and no feedback inhibitory interneurons will be recruited (Fig. 3A1). The facilitation of the iEPSP in the PND68 MeHg was higher compared with the facilitation in the PND68 control group (data not shown), similar to the 80% interpulse interval experiment.

Transcriptional Profiling Reveals a Phase Shift in Gene Expression of MeHg-Exposed Rats Compared with the Control Animals

To identify molecular mechanisms underlying effects of MeHg on rat brain development, cerebellar and cerebral RNA extracts at weaning (PND21) and adulthood (PND70) of the control and MeHg-exposed rat pups were subjected to microarray gene expression profiling using Affymetrix Rat 230-2.0 Chips. Cerebellar effects were investigated at MeHg dose range of 0 (control), 0.1, 0.4, 1, and 1.5 mg/kg. The investigated dose for cerebrum was limited to 0 and 1.5 mg/kg. In total, 10,422 and 10,229 genes were identified as expressed in cerebellum and cerebrum, respectively.

The analysis of differentially expressed genes ($p$ value < 0.01 and absolute fold change > 1.5) reveals that MeHg affects larger number of genes at PND70 than at PND21 (Table 1). The annotated list of cerebellar and cerebral differentially expressed genes and their expression ratios compared with the control treatment is provided in Supplementary material. With the exception of the highest MeHg dose (1.5 mg/kg), the number of genes called significant in cerebellum increases with the exposure dose. To compare intensities of the gene expression changes across all conditions, differentially expressed genes in cerebellum and cerebrum were normalized to the mean value per gene and subjected to hierarchical clustering (Figs. 4A and B, respectively). This shows that in the control condition, there are many genes that are differentially expressed between the two developmental time points (PND21 and PND70). In animals exposed to MeHg at doses 1 and 1.5 mg/kg, cerebellar genes that are highly expressed at PND21 and lowly expressed at PND70 in the control condition are lowly expressed at PND21 and highy expressed at PND70 in MeHg-treated groups and vice versa. Such expression profiles of these genes thus appear phase shifted compared with the control groups. This suggested deregulation of appropriate timing of the neural gene expression program upon MeHg exposure resembles the suggestive MeHg-induced phase-shift pattern of the glucose uptake rate observed by [18F]FDG PET imaging.

Molecular Mechanisms Underlying the MeHg Effects on Neurodevelopment

To identify molecular processes that are possibly affected by MeHg exposure in developing rat brains, differentially expressed genes in cerebrum and cerebellum were subjected to pathway analyses. The results reveal that many of MeHg affected genes are involved in nervous system development, including both structural and functional aspects (Figs. 5A and B). In cerebellum, all GO categories related to neurodevelopmental processes are downregulated (Fig. 5A). Specifically, pathways related to structural aspects of brain development (e.g., nervous system development, ensheathment of neurons, myelination, cytoskeleton organization, and biogenesis) are significantly repressed at PND21, whereas PND70 is predominantly characterized by significant repression of pathways related to synaptic transmission and brain function (synaptic vesicle, transmission of nerve impulse, behavior). The analysis of overrepresented GO categories in cerebellum revealed that also in this brain part, MeHg significantly affects processes related to neural function and development, such as synaptic transmission, neuron projection, transmission of nerve impulse, dorsal/ventral pattern formation, and nervous system development (Fig. 5B).

Detailed examination of genes affected by MeHg cerebellum reveals expression changes in many developmental regulators (Foxg1, Ctxn [cortexin]), Gda, Pims, Akt, Basp, Lhx2, Arsb), developmental phase–associated genes (Cxxc4, St18, Atrx, Bmpr1c, Fti9, Kif1b, Map2, and PPARGC1b) and genes involved in small GTPase signaling pathways regulating cell growth and proliferation (Supplementary material). Apart from the structural aspects, representatives of all processes required for synaptic transmission are identified as significantly affected by MeHg. This includes neurotransmitters (Cck [chol-cystokinin], Pmch, Pcsk1n), neurotransmitter synthesis gene (Gad2), neurotransmitter receptors (Cnr1 [cannabinoid receptor 1], Gabrb3 [GABA$_{\alpha}$ receptor], and LOC289606 [GABA$_{\alpha}$ receptor homolog]), synaptic vesicle docking/transport/neurotransmitter secretion genes (Spt5, Syn1a, Cpxl2, Myo5a, Slc6a6, Lin7c, Lin7a, Exoc8), voltage-gated Ca$^{2+}$ channels (Cacnb4, Ryr3, LOC689560), Ca$^{2+}$/calmodulin binding proteins and kinases (Camkk2, Camk2n1, Camk4, Markcs1), and regulators of synaptic plasticity (Nrgn [neurogranin], Ddn [dendrin], and Ryf39). Particularly marked repression of several genes regulating brain development (Foxg1, Gda) and

<table>
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<tr>
<th>Number of Significantly Differentially Expressed Genes upon MeHg Exposure at PND 21 and 70</th>
<th>Cerebellum</th>
<th>Cerebrum</th>
</tr>
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<tr>
<td>MeHg (mg/kg)</td>
<td>0.1</td>
<td>0.4</td>
</tr>
<tr>
<td>PND21</td>
<td>6</td>
<td>7</td>
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<tr>
<td>PND70</td>
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function (Cck and Ngr, long-term potentiation and learning regulator) is observed at PND70, showing that pre-/perinatal MeHg exposure has distinct long-term effects on brain structure and function. In addition to effects on neural structure and function, a number of differentially expressed genes point to effects of MeHg on the brain immune system (Nrgn, Akt1, Adam10, Myo5a).

Together, microarray gene expression profiling corroborates findings regarding delay and decrement in brain function and compromised functionality of neurotransmission discovered by \[^{18}F\]FDG PET imaging and field potential analysis and identifies key regulators of these processes.

**DISCUSSION**

In the study presented here, maternal exposure to MeHg was studied in rat offspring using \[^{18}F\]FDG PET functional imaging, field potential analysis, and microarray gene expression profiling. For PET and field potential analyses, a dosage of 1.5 mg MeHg/kg BW/day (GD6-LD10) was used; for gene expression profiling, low dosages of 0.1, 0.4, and 1.0 mg MeHg/kg were studied in addition.

MeHg is a well established neurotoxin both in humans and animals. The developing brain appears more vulnerable to the toxic effects of MeHg than the adult, and much lower dosages are required to generate deleterious effects (Costa et al., 2004; Franco et al., 2006; Grandjean and Landrigan, 2006; Kjellstrom et al., 1989; Manfroi et al., 2004). Humans are exposed to MeHg, for example, through the consumption of fish and shellfish. After absorption through the digestive tract, MeHg can penetrate the blood-brain barrier and the placenta (Choi, 1989; Clarkson and Magos, 2006). Because of its long half life in the human body, it accumulates in the brain where it causes damage to the central nervous system (Coccini, 2000; Spyker, 1972). MeHg has been studied extensively, and adverse effects on brain development and animal behavior (functional) have been found (Weiss, 2005). Structural damage to the developing brain is diffuse, whereas damage is restricted
FIG. 5. (A) The selected GO functional categories significantly downregulated (negative $T$ values) in cerebrums of MeHg-exposed rats at PND21 and PND70. Pathways related to brain structure are mostly affected at PND21, whereas pathways related to brain function are affected at PND70. The Bonferroni corrected $E$ value < 0.05 is at $|T| > 4$. (B) The selected GO functional categories significantly overrepresented among 159 genes differentially expressed in cerebellum under at least one of the doses of MeHg compared with the control condition.
to cerebellum and visual cortex in the adult brain (Burbacher et al., 1990). Prenatal exposure is related to abnormal neuronal migration and deranged cerebral cortical organization. Children exposed to MeHg may be mentally retarded and show decreased IQ, impaired movements, visuospatial perception, and speech (Castoldi et al., 2008; Harada, 1995; Grandjean et al., 1997; Kjellström et al., 1989). Effects on animal behavior include, among others, reduced motor activity (Björklund, 2007), a decrease in memory ability (Carratu et al., 2006; Daré et al., 2003; Sakamoto, 2002) and learning (Paletz et al., 2006).

Mechanisms underlying mercury-induced neurotoxicity have been focused on for many years. To mention, disruption of calcium homeostasis or induction of oxidative stress via overproduction of reactive oxygen species or reduction of antioxidative defenses is likely to be critical factors in MeHg-induced cell damage, as are interactions with sulfhydryl groups (Ceccatelli et al., 2010; Farina et al., 2011a, b; Giordano and Costa, 2012). Yet, the molecular mechanisms mediating MeHg-induced neurotoxicity are not completely understood.

In this study, we investigated mechanisms underlying neurodevelopmental defects associated with maternal exposure to MeHg. $[^1^8$F$] $FDG PET functional imaging of cerebellum and hippocampus, the analysis of functional neurotransmission in the hippocampus, and microarray gene expression profiling of cerebrum and cerebellum were employed to assess the effects of MeHg exposure on structure and function of rat brains in juvenile and adult stages of development. The rat has been reported to be a good model to study developmental neurotoxicity of MeHg (Costa et al., 2011; Giordano and Costa, 2012).

We find that MeHg causes structural defects and delay and decrement in (onset of) neural activity in both cerebrum and cerebellum of Wistar rat pups. Importantly, although the pups were exposed to MeHg early in developmental stage (from GD6 to PND10, i.e., lactation) and the mercury levels in the brain already returned to control level on PND21 (data not shown), the significant effect on neural structure and function persisted into adulthood (PND70) on a functional and molecular level.

The development of the brain is a highly complex process in which timing of events is crucial to ensure that development proceeds normally (Mai and Ashwell, 2004). One of the main observations in this study is that this timing is disrupted in animals exposed to MeHg in both cerebrum and cerebellum. This is evident from the gene expression profiling, which shows that the specific timing of transcriptional programs associated with early and late developmental stage is disturbed in MeHg-treated groups. Genes that are required to be highly expressed at early stage and lowly expressed at the late stage in the control condition show an opposite pattern of expression in MeHg-treated groups. Indeed, many of such genes with phase shift in timing of expression are described as developmental phase-associated genes. $[^1^8$F$] $FDG PET imaging data appear to be in agreement with gene expression findings, as PET imaging results also seem to concur with a delayed glucose consumption pattern in hippocampus and cerebellum of MeHg-exposed animals. The peak in $[^1^8$F$] $FDG uptake observed in the control group around day 18 can be explained by the fact that rats of this Wistar strain are very active at this time point as is generally seen during MAA where activity at PND17 is larger than that measured at PND21. In the hippocampus of the MeHg group, $[^1^8$F$] $FDG uptake significantly increased between PND18 and PND22. The fact that this peak in brain activity—$[^1^8$F$] $FDG uptake—is found at a later time point in the MeHg group (PND22) where the activity in the control group is already going down (as in MAA) supports the suggestive neurodevelopmental delay depicted in the “15 days shift” in Figure 2. Clearly, a neurodevelopmental delay of 15 days early in life does not seem realistic. Most likely, MeHg interfered with neurodevelopmental processes at a critical time window of brain development inducing a small delay, which may even go unrecognized. Yet, neurodevelopment may increasingly lag behind with age, becoming apparent later in life during adulthood or senescence (Grandjean and Herz, 2011). Together, these results and gene expression findings suggest that MeHg induces a delay in onset of brain development and function both in cerebellum and cerebrum.

The assessment of MeHg effects at two time points allows us to discriminate between early (weaning) and late (adult) neurodevelopmental defects caused by pre-/perinatal exposure to MeHg. Surprisingly, the effect of MeHg is amplified and persisting at the adult stage, despite the fact that MeHg has been eliminated from the system long time ago. This is manifested by a higher number of differentially expressed genes at PND70 compared with PND21, persisting lower glucose uptake rate (also) at PND61 and increase in potentiation of hippocampal neurons specifically at PND68. In the cerebrum, phase-specific MeHg effects are evident from pathway analyses of differentially expressed genes. Pathways related to structural aspects of brain development are significantly repressed at PND21, whereas PND70 is predominantly characterized by significant repression of pathways related to synaptic transmission. This suggests that pre- and perinatal MeHg exposure at first instance causes impaired development of morphological features of the brain, which is in line with a previous report on significant neuron loss at PND21 (de Groot, personal communication), whereas at the adult stage, MeHg-caused impairment in cerebrum is mostly apparent in brain function disorders.

Functional changes at the adult stage by MeHg are also shown by the analysis of neurotransmission in hippocampus. The extracellular field potential recordings in the hippocampus provide a marker for synaptic transmission, and double pulse stimulation can elucidate some characteristics of the underlying mechanisms. MeHg exposure causes increased paired pulse facilitation at PND68, which is generally explained by an increase in neurotransmitter vesicle release. This increase could have several underlying causes, but one of the most common explanations at lower stimulus intensities (Fig. 3C) and one that is expected to gradually decline with stimulus interval...
Fig. 3D) is the residual calcium hypothesis (Katz and Miledi, 1968; Miledi and Thies, 1971; Parnas et al., 1982; Zucker, 1989). Additionally, network properties could also contribute to the change in vesicle release because activation of pyramidal cells leads to activation of feedback inhibition of the GABA-ergic interneurons (Fig. 3A1), which could in turn inhibit the second PS in the double pulse protocol (Stanford et al., 1995). However, at PND68, there is a strong paired pulse enhancement with an interval dependence that strongly suggests that the residual calcium is underlying it.

One of the most prominently differentially expressed genes under MeHg treatment is Neurogranin (Nrgn), regulator of synaptic plasticity (Díez-Guerra, 2010; Prichard et al., 1999). Nrgn is significantly repressed in cerebellum at both PND21 and PND70, even at doses as low as 0.4 and 0.1 mg/kg MeHg, suggesting that this factor may be responsible for regulating MeHg-induced functional impairment. Another severely repressed gene in cerebellum is Foxg1 (−8.3-fold downregulation at dose 1 mg/kg at PND70). FOXG1, also known as Brain factor 1, has been found to play an important role in the establishment of the regional subdivision of the developing brain and in the development of the telencephalon (Tao and Lai, 1992). In addition, Foxg1 mutations are associated with the neurodevelopmental disease Rett syndrome. Considering its severe repression upon MeHg exposure, it is plausible that this factor may be important for regulating MeHg-mediated structural defects.

Finally, in our study, the effects of MeHg observed by [18F]FDG microPET functional imaging, functional neurotransmission analysis, and microarray gene expression profiling were not identified by classical methods included in current guidelines for neurotoxicity testing. Such improved sensitivity of detection of relevant neurotoxic effects implies that the current testing protocols for neurotoxicity could be enhanced by employment of innovative methods in addition (or as an alternative) to conventional guideline endpoints. This may have important implications on juvenile health care but also on improvement of procedures for animal testing, such as increased efficiency and sensitivity and decrease of number of animals used, time, and costs of testing.

SUPPLEMENTARY DATA

Supplementary data are available online at http://toxsci.oxfordjournals.org/.

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