MeCP2 Dependent Heterochromatin Reorganization during Neural Differentiation of a Novel Mecp2-Deficient Embryonic Stem Cell Reporter Line

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Abstract
The X-linked Mecp2 is a known interpreter of epigenetic information and mutated in Rett syndrome, a complex neurological disease. MeCP2 recruits HDAC complexes to chromatin thereby modulating gene expression and, importantly regulates higher order heterochromatin structure. To address the effects of MeCP2 deficiency on heterochromatin organization during neural differentiation, we developed a versatile model for stem cell in vitro differentiation. Therefore, we modified murine Mecp2 deficient (Mecp2-/-) embryonic stem cells to generate cells exhibiting green fluorescent protein expression upon neural differentiation. Subsequently, we quantitatively analyzed heterochromatin organization during neural differentiation in wild type and in Mecp2 deficient cells. We found that MeCP2 protein levels increase significantly during neural differentiation and accumulate at constitutive heterochromatin. Statistical analysis of Mecp2 wild type neurons revealed a significant clustering of heterochromatin per nuclei with progressing differentiation. In contrast we found Mecp2 deficient neurons and astroglia cells to be significantly impaired in heterochromatin reorganization. Our results (i) introduce a new and manageable cellular model to study the molecular effects of Mecp2 deficiency, and (ii) support the view of MeCP2 as a central protein in heterochromatin architecture in maturating cells, possibly involved in stabilizing their differentiated state.

Introduction
Heterochromatin is defined as chromatin that stays densely packed during interphase. Cytologically, heterochromatin can be further subdivided into constitutive and facultative heterochromatin [1,2], with facultative heterochromatin usually differing between cell types [3–6]. Hence, heterochromatin is amongst the key features of cellular differentiation and transdifferentiation [7,8].

Heterochromatin is commonly associated with transcriptional silencing and characteristic epigenetic marks on the level of histone [9] and nucleotide modifications [10]. Together both kinds of marks act on the degree of compaction and accessibility of DNA, thereby creating sub-nuclear compartments of less dense euchromatin and more compacted heterochromatin. In mouse cells the majority of constitutive heterochromatin is constituted by AT rich tandem repeats (major satellites) adjacent to the centric region of the chromosomes [11]. It is well known that pericentric heterochromatin domains of different chromosomes are organized in so called chromocenters [12,13] during interphase which reorganize during cellular differentiation [5,6,14].

One characteristic epigenetic mark of chromocenters is the covalent methylation at the carbon 5 position of cytosine (5 mC) in CpG dinucleotides. This epigenetic mark is read and interpreted by the methyl cytosine binding protein 2 (MeCP2) [15–18]. The Mecp2 gene is encoded on the X chromosome [19] and its product was initially identified as a selective 5-methyl cytosine binding protein [20–22]. Meanwhile it is one of the best-studied members of the methyl cytosine binding protein (MDB) family [23–27] and was found to be mutated in the neurological disorder Rett syndrome (RTT, OMIM #312750) occurring with a frequency of 1 in 10,000 female birth [28–31]. Children affected by RTT show an apparently normal development up to 6–18 months. Thereafter they start to lose acquired hand skills and spoken language and instead of further progress most RTT patients develop repetitive
hand movements, autistic features, seizures and abnormalities in growth, breathing and sleep [29].

The devastating effects of RTT were originally considered to be the consequence of MeCP2 deficiency in adult neurons resulting in gene deregulation [32]. This hypothesis was supported by deleting MeCP2 only in neurons, which resulted in RTT-like symptoms in mice [33,34]. A variety of studies suggested that MeCP2 acts as a transcriptional repressor [22,35–39] exhibiting increasing protein levels with progressive in vitro and in vivo differentiation [3,40,41]. Surprisingly, analysis of gene expression profiles in the hypothalamic and cerebellar regions of MeCP2-null and overexpressing mice [42,43] suggested that MeCP2 acts as a transcriptional activator for several thousand of genes. Although the differences in gene expression were subtle, the notion of MeCP2 as an activator of transcription was supported by its biochemical interaction with the transcriptional activator CREB [42]. As MeCP2 was recently reported to be expressed in neurons at near nucleosome levels tracking methylated CpG dinucleotides and replacing histone H1 [41], it might function as a global chromatin architect. MeCP2 deficiency seems also to affect glial cells with not yet fully understood consequences for neural cell survival [44–47]. Several lines of evidence show that not only the lack of functional MeCP2 but also MeCP2 protein oversupply results in severe symptoms [48–50]. Overall, the accumulating evidence argues for a multifunctional role of MeCP2 acting as a modulator of gene expression levels [35,37,42,43,51,52] and, together with several other proteins [14,37,53], as a global heterochromatin organizer [5,41,54,55] thereby stabilizing a cell’s differentiated state.

Here we focus on heterochromatin reorganization, which is a common feature of cellular differentiation in a variety of eukaryotic cells [3–5,55–58]. Previously it has been shown that MeCP2 protein is necessary and sufficient for chromatin clustering and that ectopic MeCP2 is able to mimic heterochromatin reorganization [5,54]. Given that lack or malfunction of MeCP2 severely affects brain function we were interested in MeCP2 dependent heterochromatin reorganization during neural differentiation. Hence, we established a new murine MeCP2 deficient (MeCP2<sup>–/–</sup>) embryonic stem (ES) cell line as a part of a versatile and easy to handle in vitro cellular differentiation system. A feeder free, one-step differentiation protocol [59] allowed us to follow specifically neural differentiation of MeCP2 wild type (MeCP2<sup>wt</sup>) and deficient (MeCP2<sup>–/–</sup>) cell cultures. We analyzed and quantified heterochromatin organization in MeCP2<sup>wt</sup> cells during neural differentiation and compared the results to MeCP2<sup>–/–</sup> deficient cells. Although the latter were able to differentiate, the absence of MeCP2 led to significant differences in their chromatin higher order organization.

**Materials and Methods**

**Generation and Characterization of MeCP2<sup>–/–</sup> tau::EGFP (MeCP2<sup>–/–</sup>) tEG Cells**

MeCP2<sup>–/–</sup> deficient (MeCP2<sup>–/–</sup>) ES cells were made by Cre-mediated deletion of a conditional MeCP2 allele in the ES cell line described in Guy et al. [34]. An EGFP knock-in into the Mapt/tau locus was created using a vector kindly provided by Yves-Alain Barde (Basel, Switzerland) as described [60] (Figure S1A). Properly targeted clones were identified by PCR with primers surrounding Mapt/tau exon 1 (forward: 5’ AGGACGTACAAGCTTGAC; reverse: 5’ GAACTTCAGGGTCAGCTG). To verify properly targeted clones an inverse PCR approach was performed [61]. Specifically, 1 µg genomic DNA was treated with 10 U BamHI I (New England Biolabs, USA), purified, and subjected to a DNA ligation reaction. Inverse PCR was subsequently performed with purified ligated products using the following primers: forward 5’ CTCAGCGCA-ACTTAAACTG; reverse 5’ TCAAGTACTAAGCTAGCT (Figure S1B). For the following experiments one verified clone has been used and checked for genomic stability by karyotyping (Figure S1C).

**Stem Cell Culture and Differentiation**

Murine wild type MeCP2<sup>TK2 1K</sup> 2<sup>tau::EGFP</sup> embryonic stem cells were kindly provided by the Austin Smith lab (Cambridge, UK) [60,62,63]. Both, MeCP2<sup>TK2 TK23</sup> 2<sup>tau::EGFP</sup> wild type and MeCP2<sup>–/–</sup> deficient cells, hereafter referred to as MeCP2<sup>wt</sup> tEG and MeCP2<sup>–/–</sup> tEG, were originally derived from the murine strain E14 [34] and cultured feeder-free at 37°C and 5% CO2 either on gelatin coated culture vessels or poly-D-lysine/laminin coated glass slides. Standard gelatin coating was performed using a filter sterilized 0.1% (v/v) gelatin solution (Sigma-Aldrich, Germany) in sterile PBS for at least 30 min at room temperature. Glass slides were coated by incubation in 0.01 mg/ml poly-D-lysine (Sigma Aldrich, USA) for 30 min at 37°C, followed by two brief washing steps in 1× PBS. Subsequently, slides were incubated over night in 2 µg/ml laminin (Sigma-Aldrich, Germany) in PBS at room temperature.

Undifferentiated stem cells were maintained in expansion medium consisting of: Glasgow minimal essential medium (GMEM, Sigma-Aldrich, Germany) supplemented with 2 mM glutamine (Life technologies, Germany), 1 mM sodium pyruvate (Sigma-Aldrich or Life Technology, both Germany), 100 µM non essential amino acids (Sigma-Aldrich, Germany), 10% (v/v) FCS (PAA, Germany), 0.05 mM 2-mercaptoethanol (Carl Roth or Sigma-Aldrich, both Germany), 100 U/ml penicillin/streptomycin (Life Technology, Germany), and 1,000 U/ml leukemia inhibitory factor (LIF, Millipore, USA) or Esgro LIF (Sigma-Aldrich, Germany) respectively. Expansion medium was exchanged in 24 hour intervals and cultures were passaged every second day.

For differentiation according to Fico et al. [59] 10<sup>3</sup> to 2.9×10<sup>5</sup> cells/cm<sup>2</sup> were seeded on either gelatin or poly-D-lysine/laminin coated glass slides (see above) and maintained 24 hours in expansion medium. To compensate for the slower growth of MeCP2<sup>–/–</sup> tEG, the cell number seeded was doubled compared to MeCP2<sup>wt</sup> tEG cultures. Differentiation was induced by LIF deprivation in LIF-free Knockout Dulbecco’s minimal essential medium (Life technology, Germany) supplemented with 15% knockout serum replacement (Invitrogen, Germany), 2 mM glutamine (Life technologies, Germany), 100 U/ml penicillin/streptomycin or 50 µg/ml gentamicin (Sigma-Aldrich, Germany), and 0.1 mM 2-mercaptoethanol (Carl Roth or Sigma-Aldrich, both Germany). During differentiation, medium was changed every day and cells were fixed for immunostaining at day 0, 7, 13, 21, and 23 (whereas day 0 refers to undifferentiated cells before LIF deprivation).

**Immunoblotting**

Proteins were detected using the following primary antibodies: anti-beta actin (as loading control) 1:2,500 (A2066, Sigma Aldrich, Germany) and anti-MeCP2 1:2,000 (M9317, Sigma Aldrich, Germany). Signals were visualized using a goat anti-rabbit IgG-HRP secondary antibody (sc-2004, Santa Cruz, USA) in a 1:10,000 dilution.

**Immunofluorescence**

For immunofluorescence cells were cultured on gelatin or poly-D-lysine/laminin coated glass slides. If not stated otherwise all incubation and washing steps were performed at room temper-
ature for 5 min. Neuronal cells were identified by tau promoter driven EGFP reporter signals and further characterized with specific marker antibodies for neurons and astroglia. DNA and chromocenters were visualized with 4’,6-diamidino-2-phenylindole (DAPI, 1 μg/ml, Sigma-Aldrich, Germany) and the presence or absence of MeCP2 was shown with the monoclonal rat anti-MeCP2 clone 4H7 [64]. For all immunofluorescence experiments in combination with the anti-MeCP2, cells were fixed in 4% PFA in PBS (EM grade, Electron Microscopy Science, USA) for 10 min at 4°C or 30 min at room temperature. After fixation, samples were washed once in PBS and permeabilized for 10 min in PBS/0.25% TritonX-100 (Sigma-Aldrich, Germany). Following permeabilization and two to three washing steps in PBS/0.02% Triton X-100/0.02% Tween 20 (Sigma-Aldrich, Germany) samples were incubated for 15–30 min in blocking solution (4% BSA in PBS/0.02% Tween 20 or PBS/0.1% Triton X-100/10% normal goat serum). Primary antibody incubation was done over night at 4°C or one hour at room temperature. Antibodies used are listed in Table 1.

After three washing steps in PBS, samples were DAPI stained (333 ng/ml, Sigma-Aldrich, Germany) for 10 min. Prior to mounting in 90% glycerol in 20 mM Tris·HCl pH 7.4 supplemented with 1,4-diazobicyclo [2,2,2]-octane (DABCO, Sigma-Aldrich, Germany), slides were washed in PBS and briefly dipped into distilled water to remove excess salts.

**Microscopy**

Epifluorescence and phase contrast images were obtained on a Zeiss Axiovert 200 microscope equipped with Plan-Apochromat 63×/NA 1.4 (pixel size XY = 104 nm) and Plan-Neofluar 40×/NA 1.3 (pixel size XY = 168 nm) oil immersion objectives and a Zeiss AxioCam mRM camera.

For acquisition of 3D and multicolor confocal images we used a Perkin Elmer UltraVIEW VoX spinning disk confocal system mounted on an inverted Nikon Ti-E microscope. Images were taken with a Hamamatsu C9100-50 EMCCD camera and Nikon CFI Apochromat TIRF 60 x/NA 1.49 (pixel size XY = 120.478 nm) or CFI Plan Fluor 40 x/NA 1.3 (pixel size XY = 163.2 nm) oil immersion objectives.

**Statistical Evaluation**

After chromocenter counting, data were analyzed using the software numbers (Apple, iWork, USA) and GraphPad Prism version 5.0. (GraphPad Software, USA, ‘www.graphpad.com’). Calculations and plots were done with Prism, if not stated otherwise. Whisker-box plots show the 5–95% confidence interval as whiskers, median values as horizontal lines, and indicate mean values as crosses and outliers as dots. P-values for significant differences of means (p<0.05) were calculated using an unpaired t-test (two-tailed) with Welch’s correction.

**Table 1. List of antibodies used.**

| Antibody | Host | Dilution | (Catalog no.) Company/Reference |
|----------|------|----------|---------------------------------|
| anti-Tyrosine Hydroxylase (TH) | mouse | 1:100 | MAB 1637, Merck Millipore, Germany |
| anti-Serotonin (Sero) | rabbit | 1:200 | AB152, Merck Millipore, Germany |
| anti-Glial Fibrillary Acidic Protein (GFAP) | rabbit | 1:500 | AB 5804 Merck Millipore, Germany |
| anti-beta Tubulin III (βTubIII) | mouse | 1:100 | MAB 1637, Merck Millipore, Germany |
| anti-MeCP2 | rat | undiluted | Jost et al. [64] |
| anti-mouse IgG-Cy3 | donkey | 1:100 | 715-165-151, Jackson Immuno Research, USA |
| anti-mouse IgG-Cy5 | donkey | 1:100 | 715-175-450, Jackson Immuno Research, USA |
| anti-rat IgG-Cy5 | donkey | 1:100 | 712-175-153, Jackson Immuno Research, USA |
| anti-rat IgG-Cy3 | donkey | 1:100 | 712-165-153, Jackson Immuno Research, USA |
| anti-rabbit IgG-Cy3 | donkey | 1:100 | 711-165-152, Jackson Immuno Research, USA |

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Concerning the unbiased counting approach the mean values of three independent biological replica sets were calculated and the effects of the variables ‘type’ (referring either to Mecp2+/y or Mecp2−/−) and ‘time’ (referring to differentiation time in days in LIF-free differentiation medium) on the dependent variables (i.e. chromocenter numbers) were analyzed using mixed linear models (SAS 9.2 PROC GLIMMIX; SAS Institute Inc., Cary, NC, USA) [65,66]. We compared 13 covariance structures and selected a banded Toeplitz matrix (one band) according to the corrected Akaike criterion (AICC; [67]). For the calculation of degrees of freedom, we selected the Kenward-Roger approximation [65,68]. The studentized residuals and conditional studentized residuals were examined for normality by means of graphical display (histograms and quantile residuum plots); nearly Gaussian distributions could be ascertained. For post hoc multiple comparisons we used Tukey adjusted tests.

Results and Discussion

Large Scale Heterochromatin Reorganization Takes Place during Embryonic Stem Cell Differentiation

To investigate the role of MeCP2 as a heterochromatin reorganizer we studied heterochromatin structure during neural differentiation (Figure 1) in Mecp2 wild type ES cells (Mecp2+/y ES) using the established mouse TK23 embryonic stem cell line [60,62,63]. In parallel, we generated a novel Mecp2 deficient ES cell line (Mecp2−/− tES) by knocking in EGFP under the neuronal tau promoter control (Figure S1A) to ascertain possible effects of Mecp2 deficiency on heterochromatin reorganization. The Mecp2−/− tEG ES cell clones obtained were checked for correct targeting and genomic stability (Figure S1). Mecp2−/− tEG and Mecp2+/y tEG stem cells were differentiated (Figure 1; Figure S2–S3) using a single step protocol in LIF-free differentiation medium (Figure S3) and we did not observe obvious differences between Mecp2 wild type and Mecp2 deficient cultures concerning cellular morphology and onset of differentiation. Multiple independent differentiation experiments yielded similar results, indicating that this system is a robust and simplified in vitro model for neural differentiation. Importantly, this system allowed us to follow differentiation of Mecp2 wild type and Mecp2 deficient ES cells into astroglia and neuronal cells, that are easy to discriminate by intrinsic or extrinsic markers and accessible for microscopic evaluation (Figure 1B).

Different studies have shown that the MeCP2 protein level increases with progressive differentiation in both neural [40,71–74] and myogenic [5,14] context. Moreover increasing MeCP2 protein level was linked to large-scale heterochromatin reorganization [5]. In different studies this reorganization was monitored by quantitative analysis of chromocenters [5,6,75] and its role in heterochromatin organization [54] we proceeded to quantitatively address effects of MeCP2 on heterochromatin architecture during neural in vitro differentiation. We performed at least three independent differentiation experiments with both Mecp2+/y and Mecp2−/− tEG cultures. To cover different differentiation stages we acquired three-dimensional confocal images of nuclei at day 0 (undifferentiated cells), day 7 (early differentiation), day 13 (differentiated cell) and after day 20 (late differentiation). Since neither MeCP2 nor EGFP was detectable in IF experiments of early stages, we decided for experimental consistency to quantify heterochromatin organization data in biological replicas of 100 DAPI stained nuclei per nucleus within the first two weeks of differentiation. Thereafter, the chromocenter number did not change significantly (p = 0.177). Statistical significance was tested with individual unpaired t-tests following Welch’s correction.

Figure 1. In vitro differentiation of Mecp2 wild type ES cells is accompanied by large scale heterochromatin reorganization. A. Shown are representative low and high (insets) magnification images of phase contrast (Ph) and DAPI DNA staining. Cells were kept in an undifferentiated state (day 0) in LIF containing medium. Differentiation of ES cells was induced by LIF withdrawal and plating into differentiation medium. Rosettes (arrow heads) indicated regions of neural differentiation, clearly visible as of day 7. Shortly thereafter EGFP positive neurons could be detected around and within rosettes and mark differentiating neural cells. At day 13 cells exhibit a tissue like growth. Bar: 10 μm. B. The neural identity of rosettes could be demonstrated by EGFP reporter expression driven by the neural tau promoter as of day 5 to 7 and most prominent after 13 days. Most EGFP positive cells are located within rosette structures, often surrounded by GFAP positive astroglia. Bar: 10 μm. C. Replicas of 100 DAPI stained nuclei were statistically analyzed and shown combined in a whisker box plot. Whiskers depict the 5–95 percentile of the confidence interval; the median is shown as a horizontal line within the box, and mean values are highlighted as white crosses. We noticed a highly significant (p < 0.0001) decrease of mean chromocenter number per nucleus within the first two weeks of differentiation. Thereafter, the chromocenter number did not change significantly (p = 0.177). Statistical significance was tested with individual unpaired t-tests following Welch's correction.

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Figure 2. MeCP2 becomes detectable in heterochromatic chromocenters at late differentiation stages. A. MeCP2wt and Mecp2\textsuperscript{2}/y tEG cells were differentiated, fixed, and immunostained with antibodies to MeCP2. Tau promoter driven EGFP expression highlights neuronal cells. Additional markers as beta tubulin III (neuronal cell) and GFAP (astroglia) allow discrimination of different cell populations. In immunofluorescence experiments MeCP2 protein is detected as of day 13 (left) and remains constant thereafter (middle) in EGFP\textsuperscript{+} cells. Line profiles across chromocenters highlight MeCP2 protein accumulation at these structures (black line) as well as their intense DAPI signal (blue line). Some GFAP\textsuperscript{+} astroglia revealed a relative weaker MeCP2 signal (black line) compared to neurons. Mecp2 deficient cells (right) were used as control. Bar: 10 \textmu{}m. B. Immunoblot experiments demonstrate the increase of MeCP2 protein over time in wild type cells (wt) while Mecp2 deficient cells (\textasciitilde/y) show no signal. Beta actin was used as a control for equal loading. 

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Figure 3. MeCP2 absence does not prevent neuronal and astroglia differentiation. Confocal microscopy optical sections of Mecep wild type (left) and Mecp2 deficient cells (right) at differentiation day 13 revealed astroglia (GFAP+) and different neuronal subtypes (EGFP+, TH+, Sero+). Bar: 10 μm. A. Differentiated Mecp2 wild type and Mecp2 deficient cells exhibit GFAP positive astroglia (red) and EGFP positive neurons (green). Both labels marked mutually exclusive cell populations. B. The population of EGFP positive cells could be further subdivided into tyrosine hydroxylase (TH+) positive neurons (red). Those cells were found to be present in both Mecp2 wild type and Mecp2 deficient cells. While not all EGFP+ neurons (green) are TH+, all TH+ are positive for EGFP (yellow color in overlay). C. In addition to a TH+/EGFP+ subpopulation neurons, another serotonin positive (Sero+) subpopulation was detected in both cell lines. Similar to the situation described above, Sero+ cells (red) were always EGFP+ (green) while a considerable amount of EGFP− cells were Sero−.

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day 13 (Figure 2), we consider both signals to be equivalent markers for quantification of heterochromatin organization [22].

By manual data evaluation and subsequent statistical analysis we found the chromocenter number in undifferentiated Mecp2 wild type stem cells to scatter around 11±3.3 chromocenters per nucleus (Figure 1C, Figure S4, S5). One week after LIF withdrawal the chromocenter average decreased significantly to 7.3±2.2 while the overall scatter got slightly reduced (Figure S5). This trend continues and after two weeks the average chromocenters number per nucleus was 5.3±1.7. These data also agree with recent results reported by Singleton et al. [55] for Mecp2 wild type primary cortical mouse neurons. We also prolonged our differentiation studies up to day 23 but did not detect further decrease and found both average and standard deviation to remain constant (5.3±1.7). Testing the mean values of the early and late differentiated data sets for significant differences yielded a p-value of 0.177, confirming that both sets were not significantly different.

These findings agree with previous reports on neural [6,70] and myogenic [5] in vitro differentiation. Although the MeCP2 protein level in muscle is not as high as in brain tissue where the levels are the highest [40,41,71], we previously observed MeCP2 increase during myoblast differentiation, which was sufficient to reorganize heterochromatin [5]. This suggests that heterochromatin reorganization is a shared feature of multiple differentiation pathways and correlated with MeCP2 protein level whose threshold is thought cell lineage specific. It would be interesting to compare MeCP2 thresholds during differentiation of controlled and simplified in vitro systems such as the one presented here and their more complex in vivo counterparts, which not only respond to spatial and temporal cues but also to environmental stimuli.

MeCP2 becomes Detectable in Late Differentiation Stages and is Associated with Chromocenters

Previous studies linked heterochromatin organization to MeCP2 protein level in different cell lines [5,6]. Accordingly, we found a significant increase of MeCP2 signal in differentiated cells (Figure 2B) as we compared undifferentiated (day 0) to differentiated Mecp2 wild type ES cells (day 13) in immunoblots and immunofluorescence experiments. In both assays, Mecp2+/− tEG controls revealed no detectable MeCP2 signals (Figure 2). With a rat monoclonal antibody [64] we were able to show a maximum of MeCP2 signals in differentiated EGFP+ neurons as of day 13 (Figure 2A). Additional line scan profiles in optical sections further showed a co-localization of MeCP2 and DAPI signal as reported by Nan et al. [22] at chromocenters sites in all EGFP+ cells. In contrast, MeCP2+ line scans of EGFP+ cells in Mecp2+/− tEG cultures remained within background noise.

Interestingly, our rat monoclonal antibody against MeCP2 also detected a relatively weak but positive MeCP2 signal in GFAP+ astroglia as of day 13 compared to the signal intensity in neurons (Figure 2A). As MeCP2 was initially reported to be absent in glial cells [40,41,71] our data contribute to the increasing evidence arguing for MeCP2’s engagement in glia [44,46,47,79,80].

Moreover, we did not find all GFAP+ cells to be positive for MeCP2. This observation suggests a temporally restricted presence and function of MeCP2 in the astroglia lineage, which could also explain the contradicting data on presence or absence of MeCP2 in this lineage.

The Absence of MeCP2 during Neural in vitro Differentiation does not Interfere with Differentiation into a Variety of Neural Subtypes and Astroglia

It has been shown that MeCP2 is able to cluster [54] and to reorganize heterochromatin in a dose-dependent manner and that an increase in MeCP2 protein results in a decrease of average chromocenter numbers [5]. It is also known that during neural differentiation MeCP2 protein level increases to reach a maximum in differentiated neurons [32]. Therefore, we wanted to know how the lack of MeCP2 might interfere with differentiation of ES cells. Would Mecp2 deficiency preserve an undifferentiated chromatin organization state and perhaps interfere with the capability to differentiate? To address this question we differentiated Mecp2−/− tEG stem cells by LIF deprivation for 13 days and checked for the presence of astroglia and neural differentiation markers as a control for general differentiation capability (Figure 3). We found both Mecp2 wild type and Mecp2 deficient stem cells positive for the astroglia marker GFAP (glial acidic fibrillary protein) and the neural markers tyrosine hydroxylase (TH) and serotonin (Sero). Therefore, we conclude that the lack of MeCP2 in Mecp2−/− tEG does not interfere with differentiation capacity per se. Moreover, we did not observe obvious differences concerning the amount of marker positive cells nor the timing of marker expression.

While GFAP and EGFP signals were mutually exclusive and positive cells constitute separate populations, we could subdivide EGFP+ neurons into EGFP+ only and EGFP+/marker+ populations. However, it remains to be answered if the EGFP+ only population could be further subdivided or resembles an earlier differentiation state before the onset of both tyrosine hydroxylase or serotonin marker expression.

After showing that both cell lines were able to produce differentiated neurons and astroglia, our next step was a quantitative analysis of heterochromatin reorganization in differentiated cells. If heterochromatin reorganization would be truly MeCP2 dependent, Mecp2 deficiency would prevent a decrease of average chromocenters number per nucleus during differentiation.

MeCP2 Deficiency Causes Structural Changes in Heterochromatin Organization of Neurons and Astroglia

As we analyzed differentiated Mecp2 wild type stem cells at day 13 we found the average chromocenter number in EGFP+ cells to be significantly decreased compared to undifferentiated cells (Figure 4). In EGFP+/TH+ wild type neurons we observed an average number of 5.9±2.3 chromocenter per nucleus compared to 10.4±2.3 chromocenter in Mecp2 deficient cells (Figure 4B). These numbers were quite similar in the corresponding EGFP+ only population showing 5.4±2.3 chromocenters in wild type and 10.1±2.2 chromocenters in Mecp2 deficient cells. Also EGFP+/
Sero+ neurons revealed a significant decrease of chromocenters in differentiated cells: while \textit{Mecp2} wild type cells showed 4.9±1.4 chromocenters at day 13, \textit{Mecp2} deficient cells exhibit at the corresponding time point 9.3±2.0 chromocenters. In addition to neuronal cells we also analyzed the GFAP+ astroglia population. Here we found 5.8±2.4 chromocenters in \textit{Mecp2} wild type cells compared to 10.2±2.3 chromocenters in \textit{Mecp2} deficient cells.

Figure 4. \textit{Mecp2} deficient neurons and astroglia cells have significantly more chromocenters than wild type cells. A. Representative confocal microscopy optical sections of differentiated \textit{Mecp2} wild type and \textit{Mecp2} deficient nuclei revealed characteristic differences in heterochromatin organization. Positive immunostaining for the astroglial marker GFAP (upper left) or for neuronal markers TH (lower left) and serotonin (lower right) indicated a differentiated cell state. In addition, the population of EGFP-only positive neurons was analyzed (upper right). Bar: 10 μm. B. Compared to wild type cells \textit{Mecp2}+/y tEG nuclei (n = 100 each) revealed significantly more chromocenters, here visualized in whisker-box plots. Median values are shown as horizontal lines within the box, whiskers represent the 5–95 percentile, mean values are indicated as crosses, and outliers are visualized as dots. All analyzed samples show a highly significant (p<0.0001) difference of mean values. GFAP+/EGFP+ wild type cells revealed an average chromocenter number of 5.8±2.4 compared to 10.2±2.3 chromocenters in \textit{Mecp2}+/- tEG cells. The mean chromocenter number per nucleus in TH+/EGFP+ \textit{Mecp2} wild type cells was 5.9±2.0 versus 10.4±2.3 chromocenters in \textit{Mecp2} deficient cells. In Sero+/EGFP+ wild type cells we found on average 4.9±1.4 chromocenter versus 9.3±2.0 chromocenters per nucleus in \textit{Mecp2} deficient cells. The EGFP+ only population, showing 5.4±2.0 chromocenters in \textit{Mecp2} wild type cells and 10.1±2.2 chromocenters in \textit{Mecp2}+/- tEG cells, mirrored these tendencies. C. Unbiased analysis of data from three biological replicates (n = 100 per data set) for \textit{Mecp2} wild type (solid line) and \textit{Mecp2} deficient (dashed line) cells at different time points revealed significant decrease of chromocenters within the first two weeks of differentiation whereas extended differentiation time to 21 days did not result in further large scale heterochromatin remodeling. Error bars: 95% confidence intervals according to the mixed linear model.

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It is noteworthy that although MeCP2 protein levels do differ in neurons (EGFP) and astroglia (GFAP), we found similar tendencies concerning chromocenter numbers for both lineages, i.e., an increase in the absence of MeCP2 (Figure 4). As we have previously reported a concentration dependent effect of MeCP2 on heterochromatin reorganization [5], it is tempting to speculate that the threshold level of MeCP2 needed for chromatin remodelling varies for different lineages. Furthermore, recent evidence hints to distinct requirements for MeCP2 at different differentiation systems will be required to clarify this issue. In addition, it would be very interesting to investigate chromatin reorganization in differentiating ES cells derived from heterozygous MeCP2+/− mice. The latter would allow direct comparison within the same culture of MeCP2 positive and negative cells, thus reducing any potential differences related to cellular heterogeneity.

We conclude that the differences in chromocenter clustering observed between MeCP2 wild type and MeCP2−/− tEG cells were not due to a lack of differentiation capability of MeCP2 deficient cells. Hence, we assume that MeCP2 is necessary for heterochromatin reorganization and responsible for chromocenter clustering in astroglia and neuronal lineages. We could confirm our hypothesis in an unbiased approach as we compared MeCP2 wild type and deficient cells at different differentiation time points in biological replicas of 100 nuclei each. A mixed linear model analysis confirmed a highly significant influence of the parameters “type” (i.e. MeCP2 protein presence) and “time” (i.e. differentiation in days) on the mean chromocenter number as well as an interaction effect of both parameters within a data set (Figure 4C).

Although undifferentiated MeCP2 wild type and deficient cells were quite similar (wt: 11.8 in astroglia and neuronal lineages. We could confirm our matin reorganization and responsible for chromocenter clustering although undifferentiated interaction effect of both parameters within a data set (Figure 4C).

“type” (i.e. MeCP2 protein presence) and “time” (i.e. differentiation at different time points in biological replicas of 100 nuclei each). A mixed linear model analysis confirmed a highly significant influence of the parameters “type” (i.e. MeCP2 protein presence) and “time” (i.e. differentiation in days) on the mean chromocenter number as well as an interaction effect of both parameters within a data set (Figure 4C).

Although undifferentiated MeCP2 wild type and MeCP2−/− tEG cells were not due to a lack of differentiation capability of MeCP2 deficient cells. Hence, we assume that MeCP2 is necessary for heterochromatin reorganization and responsible for chromocenter clustering in astroglia and neuronal lineages. We could confirm our hypothesis in an unbiased approach as we compared MeCP2 wild type and deficient cells at different differentiation time points in biological replicas of 100 nuclei each. A mixed linear model analysis confirmed a highly significant influence of the parameters “type” (i.e. MeCP2 protein presence) and “time” (i.e. differentiation in days) on the mean chromocenter number as well as an interaction effect of both parameters within a data set (Figure 4C).

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B. As in MeCP2wt cultures the majority of EGFP positive cells is found inside (arrow head) or in the vicinity of rosettes. Bar: 10 μm. (TIF)

Figure S4 Biological replicates demonstrate the robustness of the differentiation system. The whisker-box-plots show a comparison of three biological replica experiments based on DAPI signals (set A-C; n = 100 each) and revealed a quite robust data distribution. Results for MeCP2 wild type (MeCP2wt) cells are shown on the left; for MeCP2 deficient (MeCP2−/−) cells on the right. Horizontal lines depict median values, crosses indicate mean values, outliers are depicted as dots, and whiskers indicate the 5–95 percentile. (TIF)

Figure S5 Differences in heterochromatin organization of MeCP2 wild type and deficient cells during differentiation. A. Comparison of MeCP2 wild type (MeCP2wt; left) and MeCP2 deficient (MeCP2−/−; right) cells revealed significant differences in heterochromatin reorganization over differentiation. While in MeCP2 wild type cells the mean chromocenter number per nucleus (based on DAPI signal) halved from 11.8 (±0.3) to 5.1 (±0.3), it remained elevated in MeCP2 deficient cells and only slightly drops from 11.2 (±0.3) to 9.9 (±0.6). A Scatter plots mark the mean value as red lines within a 95% confidence interval (black whiskers) for each time point. B. Accompanying whisker-box-plots indicate highly significant differences (p<0.0001) between data sets (asterisks). For both MeCP2 wild type (right) and MeCP2 deficient cells (left) no significant differences of mean and median values were detected between late differentiation stages (day 13 and >20 days). (TIF)

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Author Contributions

Conceived and designed the experiments: BB BH FLB MMLDB. Contributed reagents/materials/analysis tools: BH. Wrote the paper: BB FDR MCC MD. 

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MeCP2 dependent heterochromatin reorganization during neural differentiation of a novel Mecp2-deficient embryonic stem cell reporter line.

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Suppl. Fig. 1 Targeting of EGFP in the tau locus produces ES cells stably expressing EGFP in postmitotic neurons.

A The schematic drawing modified according to Tucker et al. depicts the targeting strategy used to insert an EGFP cDNA into exon 1 of the Mapt/tau locus, resulting in the expression of EGFP protein under control of the neuronal Mapt/tau promoter. The integrated cassette consist of an EGFP cDNA sequence (green), located upstream of a Pgk-Neo resistance cassette (Neo<sup>R</sup>). Indicated are BamHI restriction sites, exon 1 integration site (black), and the 5′ and 3′ genomic arms for homologous recombination in light and dark grey, respectively. Blue and red arrows mark the position of the primers used for the amplification reactions shown in B (left and right panel, respectively). B Long-range amplification (left) shows some representative transfected clones (lanes 3-10). The 2.5 kb band indicates the correct insertion of EGFP in tau locus in clones B9, C3, C9, D1 and D11. A TK23 sample and a wild-type sample have been also included as a positive and negative control, respectively (lanes 1,2). Inverse PCR results (right) show amplification of some representative transfected clones (lanes 5-10). The strategy allows the amplification of the genomic region flanking the EGFP/Neo<sup>R</sup> cassette. Only clones carrying the cassette in tau locus will produce a band of expected size (1085 bp). A 46C sample (derived from a cell line where the same targeting vector has been used to knock in EGFP cDNA in Sox2 promoter) and a TK23 sample have been also included as a positive and negative control, respectively (lanes 3,4). C Representative image of a Giemsa-stained metaphase spread from one of the clones whose targeting has been positively verified. Karyotype analysis shows no obvious chromosomal aberrations.
Suppl. Fig. 2 The majority of neurons develop from rosettes and form interconnected clusters over time

A Shown is a typical multilayered rosette region in a differentiated Mecp2 wild type ES culture (upper right, see also Fig. 1). For the indicated region of interest (dashed box) inverted single channel images are shown (left) as well as merged channel images (lower right). Neurons are identified by tau promoter driven EGFP and astroglia are visualized by anti glial fibrillary acidic protein (GFAP) antibody. EGFP and GFAP signals are mutually exclusive and mark different cell populations. While the majority of EGFP+ cells reside inside rosettes some single EGFP+ neurons are located outside rosettes. GFAP+ cells are excluded from the center of rosette but often found adjacent to outer rosette regions. Bar: 10 μm. B After two weeks of LIF deprivation tissue-like regions (upper left corners) and multilayered islands (asterisks) appear throughout Mecp2 wild type and Mecp2 deficient cultures. Most of those islands consisted of EGFP+ cells. In addition single EGFP+ cells (arrow head) are found in less dense regions. Occasionally EGFP+ islands are connected by nerve like fibers, as shown in the live cell image. Bar: 50 μm.
Suppl. Fig. 3 Mecp2<sup>+/y</sup> tEG cells revealed no obvious morphological differences compared to Mecp2<sup>+/+</sup> tEG in vitro differentiation

A Shown are DAPI DNA stainings (blue) and phase contrast (Ph) images of undifferentiated (day 0), early differentiated (day 7), differentiated (day 13), and late differentiated (>20 days) Mecp2<sup>+/y</sup> tEG cells. In Mecp2<sup>+/+</sup> cultures first morphological signs of neural differentiation are rosette structures, clearly visible as of day 7. Neural fate could be verified by tau promoter driven EGFP reporter expression shortly thereafter. Bar: 10 μm. B As in Mecp2<sup>+/+</sup> cultures the majority of EGFP positive cells is found inside (arrow head) or in the vicinity of rosettes. Bar: 10 μm.
Suppl. Fig. 4 Biological replicates demonstrate the robustness of the differentiation system.

Comparison of three biological replica experiments with 100 measurements (based on DAPI signal) per time point (set A-C) revealed a quite robust data distribution visualized in a whisker-box plot. Mecp2 wild type (Mecp2\(^{wt}\)) cells are shown on the left; Mecp2 deficient (Mecp2\(^{-/}\)) cells are shown on the right. Median values are depicted as horizontal lines, mean values are indicated as crosses, outliers are depicted as dots, and whiskers indicate the 5-95 percentile.
Suppl. Fig. 5 Differences in heterochromatin organization of Mecp2 wild type and deficient cells during differentiation.

Comparison of Mecp2 wild type (Mecp2<sup>wt</sup>vTEG; left) and Mecp2 deficient (Mecp2<sup>-/y</sup>vTEG; right) cells revealed significant differences in heterochromatin reorganization over differentiation. While in Mecp2 wild type cells the mean chromocenter number per nucleus (based on DAPI signal) halves from 11.8 (± 0.8) to 5.1 (± 0.3), it remains elevated in Mecp2 deficient cells and only slightly drops from 11.2 (± 0.3) to 9.9 (±0.6). A Scatter plots mark the mean value as red lines within a 95 % confidence interval (black whiskers) for each time point. B Accompanying whisker-box-plots indicate highly significant differences (p< 0.0001) between data sets by asterisks. For both Mecp2 wild type and Mecp2 deficient cells no significant differences of mean and median values were detected between late differentiation stages (day 13 and > 20 days).