



The discrepancy between absence of copper deposition and presence of neuronal damage in brain of Atp7b^{-/-} mice

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Title Page**Title**

The discrepancy between absence of copper deposition and presence of neuronal damage in brain of *Atp7b*^{-/-} mice

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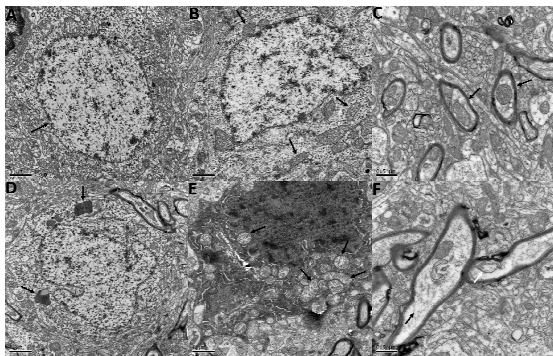
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Table of contents entry



The neuronal damages were identified in the basal ganglia despite the absence of copper accumulation in the region.

Abstract

Wilson's disease (WD) is caused by mutations within the copper-transporting ATPase (ATP7B), characterized by copper deposition in various organs, principally the liver and brain. With the availability of *Atp7b*^{-/-} mice, the valid animal model of WD, the mechanism underlying copper-induced hepatocyte necrosis has been well understood. Nonetheless, little is known about adverse impact of copper accumulation on the brain in WD. Therefore, the aim of this study was to identify copper disturbances according to various brain compartments and further dissect the causal relationship between copper storage and neuronal damage using *Atp7b*^{-/-} mice. Copper levels in the liver, whole brain, brain compartments and basal ganglia mitochondria of *Atp7b*^{-/-} mice and age-matched controls were measured by atomic absorption spectroscopy. Delicate electron microscopic studies on hepatocyte and neurons in the basal ganglia were performed. Here we further confirmed the remarkably elevated copper content and abnormal ultrastructure findings in livers of *Atp7b*^{-/-} mice. Interestingly, we found the ultrastructure abnormalities on neurons of the basal ganglia of *Atp7b*^{-/-} mice, whereas copper deposition was not detected in the whole brain, even within the basal ganglia and its mitochondria. The disparity provided the new understanding of neuronal dysfunction in WD, and strongly indicated that copper might not be the solely causative player and other unidentified pathogenic factors could enhance copper toxic effect on neurons in WD.

Keywords: Wilson's disease · *Atp7b*^{-/-} mice · Copper homeostasis · Ultrastructure feature

Introduction

Wilson's disease (WD) is a severe copper metabolism disorder caused by mutations within *ATP7B*, which encodes the copper-transporting ATPase. The protein is mainly expressed in the liver,¹ where it performs two vital physiologic functions, including biliary copper excretion and synthesis of holoceruloplasmin. Accordingly, when *ATP7B* function is disrupted, copper gradually accumulates in the liver and other organs thereby causing complex symptoms. It principally encompasses hepatic, neurological and psychiatric disturbance or complicated combinations of these malfunctions.

Currently, several animal models for WD have been successfully established, including the Long-Evans Cinnamon (LEC) rats and Toxic milk mice (*tx* mice) have also been characterized in details.^{2,3} Although they share some similarities with WD patients, there are still some limitations residing in these models, such as the incomplete loss-of-function of *Atp7b* in *tx* mice⁴ and various liver pathologies exist between LEC rats lineages due to involvement of other likely candidate genes.⁵ Consequently, the genetically engineered *Atp7b*^{-/-} mice eluding from the above shortcomings were generated and reckoned as an excellent rodent model for probing into the consequence of copper overload in the liver.^{6,7}

Apart from hepatic insufficiency, the nervous system is usually implicated in WD patients as well. Some neuroimaging findings show that the most common lesion in the brain is observed in the basal ganglia.⁸⁻¹⁰ Thus, copper disturbance in the brain is postulated to be not ubiquitous over the course of WD. Therefore, it is necessary to re-analysis copper concentrations on the basis of various brain regions of *Atp7b*^{-/-} mice.

Additionally, the accumulating evidences indicated that other trace elements,

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3 other than copper, could overload in the brain and disrupt neuronal homeostasis in
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5 WD.^{11, 12} Thus, the definite correlation between copper overload and brain lesions
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7 deserves further investigation. To better verify this perspective, we specially
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9 adopted the mutant mice, displaying no significant difference in the copper levels
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11 of the basal ganglia, to investigate whether their neuron homeostasis is disturbed.
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13 Altogether, the aim of this study was to evaluate whether there are significant
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15 differences in copper content of various brain regions between the two genotyped
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17 mice, and obtain some novel understandings of causative factors responsible for
18
19 neuronal dysfunction in WD.
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22 **Experimental details**

23 **Animal husbandry and preparation of samples**

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25 The *Atp7b*^{-/-} mice were kindly donated by Prof. Svetlana Lutsenko from Johns
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27 Hopkins University, and generation procedure has been explicitly depicted in the
28
29 previous literature.⁶ The mice were housed at Animal Care Facility of Shanghai
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31 Medical College and kept under standard conditions. *Atp7b*^{+/+} mice, being a sibling
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33 line of *ATP7b*^{-/-} mice, were used as normal controls. The liver and brain were
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35 immediately separated after being euthanized. The brain samples were divided
36
37 into three discrete areas consisting of cerebral cortex (CX), basal ganglia (BG) and
38
39 cerebellum (CB). CX encompasses frontal, temporal and parietal cortices; BG
40
41 consists of caudate nucleus, putamen and globus pallidus. These studies were
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43 approved by the Institutional Animal Care and Use Committee of China and in
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45 accordance with the Guidelines on Animal Experiments of Shanghai Medical
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47 College.
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54 **Qualification of copper in the liver , whole brain and diverse brain** 55 **compartments** 56 57 58 59 60

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3 The samples were dried in a vacuum oven at 56°C until water was thoroughly
4 evaporated. After the acquisition of dried tissues weight, the samples were burned
5 into ashes in the electric furnace of 500°C and then dissolved in concentrated
6 HNO₃ in an induction cooker at 150°C until the solution became transparent.
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8 Copper content in the solution was determined by polarized atomic absorption
9 spectrophotometry (AAS) using a Hitachi Z-5000 spectrophotometer. Finally,
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11 copper levels were presented as µg/g tissue (dry weight).
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18 **Copper content determination in mitochondrial isolation from the liver and** 19 **brain homogenates**

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22 The Mitochondria Isolation Kit for Tissue (Pierce, America) was applied to
23 isolate mitochondria from the liver tissues and basal ganglia. Copper levels in
24 diverse mitochondrial preparations were analyzed via AAS after wet washing of
25 mitochondria fraction with concentrated HNO₃.
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32 **Electron microscopy examinations on hepatocyte and neuron of basal** 33 **ganglia**

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36 Electron microscopy was performed in 7 Atp7b^{-/-} mice and 7 Atp7b^{+/+} mice
37 aged 10 months. The tissues were rinsed by the pre-cooling (4°C) normal saline
38 and carved to the blocks (≤ 3mm³). The blocks were in turn immersed in 2.5%
39 glutaraldehyde for fixing (≥ 2 hours), for rinsing 3 times, 1% OsO₄ for post-fixing
40 and 3 times again rinsing. After the completion of fixation, they were transferred to
41 the ethanol and acetone for dehydrating and Epon for embedding. For thoroughly
42 curing, the tissues were successively put in oven at 37°C for 24 hours, 45°C for 12
43 hours and 60°C for 48 hours. With the availability of Leica ultramicrotome, the
44 ultrathin sections were double-obtained and then were stained with uranyl acetate
45 and chromatic acid lead. Ultimately, the section were viewed and photographed by
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3 the means of JOEL transmission electron microscope.
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5 **Statistical analyses**

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7 Copper levels were expressed as mean \pm SD. Student's t-test was used to
8 assess whether statistically significant variations of copper concentrations existed
9 between the two genotyped mice in liver and three main brain compartments.
10 Significant differences were considered when the p value < 0.05 . In order to avert
11 the measurement error, each sample was determined two times.
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18 **Results**

19 **The significantly increased copper levels in the liver is in agreement with the** 20 **abnormal electron microscopic findings on the hepatocyte**

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22 In order to assure that our bred animal model were successful, we analyzed
23 hepatic copper concentrations of Atp7b^{-/-} and Atp7b^{+/+} mice at aged 1, 3, and 10
24 months. The hepatic copper data demonstrated the statistically significant copper
25 elevations in Atp7b^{-/-} mice compared with age-matched controls (**Table 1**), being in
26 accordance with the previous report.⁷ Comparison of hepatic copper content of
27 Atp7b^{-/-} mice at different ages revealed the discontinuous trend in copper
28 accumulation. The magnitude of copper deposition correlated with the
29 copper-induced hepatic necrosis other than the length of exposure time. The
30 highest copper level was detected at 3 months of age and the concentration values
31 of Atp7b^{-/-} mice were over 36 times higher than those of age-matched Atp7b^{+/+}
32 mice. Then the elevated trend of copper decreased to 34-fold at 10-month mice.
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50 As shown in **Figure 1**, the typical hepatic ultrastructure alterations of WD
51 patients were well-preserved in our mice model. Some cell compartments,
52 including mitochondria and lysosome, were responsive to elevated copper.
53 Specifically, noted mitochondrial alterations and high electron-dense granulation
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3 accumulations in lysosomes were comprehensively observed in the livers of all the
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5 7 $Atp7b^{-/-}$ mice (**Figure 1: C, D**). Meanwhile, the extensive ultrastructure
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7 alternations were not observed in the controls (**Figure 1: A, B**).

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10 **Ultrastructure abnormalities on neurons of $ATP7b^{-/-}$ mice exist prior to the**
11
12 **abnormal copper metabolism**

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14 In order to specifically dissect whether copper homeostasis in the whole brain
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16 and several brain compartments of $Atp7b^{-/-}$ mice were affected by the abnormal
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18 ATP7B protein function, we determined copper levels between the two genotyped
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20 mice. At variance with copper disturbance in the liver, the obvious difference was
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22 not observed between $Atp7b^{-/-}$ and $Atp7b^{+/+}$ mice at 1 and 3 months of age. Taking
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24 the gradual deposition trend of copper into account, we further compared two
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26 groups of mice up to 10 months for the sake of eliminating the possibility of the
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28 inadequate observation time, and there were after all not statistically significant
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30 changes between the two genotyped mice (**Table 2**).

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33 Given that the previous report showing basal ganglia was the most vulnerable
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35 brain region in WD,¹³ the delicate electron microscopy studies were employed to
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37 explore whether changes in the neuronal ultrastructure resembled those of liver.
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39 Strikingly, the dramatic changes in neurons were observed (**Figure 2: D, E, F**)
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41 whereas the electron microscopy remained normal in 7 age-matched $Atp7b^{+/+}$ mice
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43 (**Figure 2: A, B, C**). Except for the clear similarities in some ways, microtubule and
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45 microfilament also exhibited the loose conformation.

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49 **The preliminary mitochondria abnormalities in the basal ganglia neuron are**
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51 **not correlated to copper deposition**

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53 Although copper concentrations were normal in the basal ganglia of $Atp7b^{-/-}$
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55 mice, several cellular compartments in neuron, especially mitochondria, displayed
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3 structural peculiarities. These gross mitochondrial impairments were similar to the
4 findings in livers of WD patients and $ATP7b^{-/-}$ mice, which were thought to be
5 specific and an early hallmark. Moreover, massive studies demonstrated that
6 mitochondria could be the first responder under an imbalanced copper condition,
7 and these specific structure changes are among the earliest detectable
8 pathological features in WD. Thus, we further determined copper concentrations in
9 mitochondria of livers and basal ganglia regions between two genotyped mice.
10 Being paralleled to copper abnormalities in livers, the intra-mitochondrial copper
11 levels were significantly high in $Atp7b^{-/-}$ mice aged 10 months (**Figure 3**).
12 Unexpectedly, the mitochondrial copper concentrations in the basal ganglia still
13 displayed no significant difference (**Figure 3**).
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27 Discussion

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30 The disrupted copper metabolism and resultant depositions in some organs
31 are clinical hallmark in WD due to the inactivation of copper transporter ATP7B
32 protein. Liver dominates the unique position in understanding the overview of WD
33 since it is the earliest affected organ. Thus we determined the copper levels and
34 ultrastructure features of liver in our bred mice so as to ensure the accuracy of
35 subsequent research on brain sections. Definitely, our study is in agreement with
36 the previous result.⁷ Moreover, copper levels in the liver at three distinct stages
37 further clued that it might be released from necrotic hepatocytes as disease
38 progressed.
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50 The clinical picture of WD is wide, and understanding of various disease
51 presentations is important. In WD patients, the neurological manifestations
52 generally appear later than the hepatic abnormalities¹⁴ and are thought to be
53 secondary to hepatic insufficiency. The neurological profile mainly encompasses
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3 cerebral-related, cerebellar and pyramidal manifestations.¹⁵ The impaired brain
4 regions in WD are always closely associated with excess copper deposition.¹⁶
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7 Apart from the basal ganglia, known as the most susceptible region in WD patients,
8 the cerebellum and cortical cortex are also implicated in the advanced course.¹⁷ In
9
10 view of the scarce brain samples of patients, *Atp7b*^{-/-} mice became the essential
11
12 tool for helping to unveil copper imbalance in the brain sections. In order to
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14 facilitate the development of animal models, we analyzed and compared the
15
16 copper levels between *Atp7b*^{-/-} and *Atp7b*^{+/+} mice according to three distinct brain
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18 regions. In the present study, copper concentrations of various brain regions in
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20 *Atp7b*^{-/-} mice were not significantly different from those in *Atp7b*^{+/+} mice till 10
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22 months aged. This result appeared to be at variance with findings in the livers.
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28 To preclude whether there were the elementary interspecies differences in
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30 brain copper metabolism, it is necessary to compare *Atp7b*^{-/-} mice with the two
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32 other models, LEC rats and *tx* mice. Although there are clear similarities in hepatic
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34 phenotype among them, brain abnormalities in *Atp7b*^{-/-} mice are less prominent
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36 than the two latters.^{2,3} LEC rats not only show significant copper accumulation in
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38 the brain compared to LEA rats, but occasionally present with neurological
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40 symptoms at aged between 8 and 12 months.² Contrarily, there is the only report
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42 roughly suggesting that copper content in the whole brain of *Atp7b*^{-/-} mice
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44 significantly increase so far.⁶ The following reasons might explain the diversity.
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48 Firstly, in rats, Borjigin and colleagues discovered a splice variant,¹⁸ pineal
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50 night-specific ATPase (PINA), being selectively produced from the promoter
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52 downstream of exon 8. Therefore, this variant, if also existing in *Atp7b*^{-/-} mice,
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54 might be insusceptible to abnormal splice within exon 2. Presumably, the presence
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56 of the similarly alternative ATP7B variant could partially function in exporting
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3 copper. Secondly, more and more studies demonstrated that ATP7A protein, one
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5 homologous copper-transporting ATPase, could compensate for the complete loss
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7 of ATP7B function in *Atp7b*^{-/-} mice.¹⁹⁻²¹ Overall, the above modifiers might be, at
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9 least in part, involved in the regulatory process of copper metabolism in *Atp7b*^{-/-}
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11 mice.
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14 It is widely thought that excess copper storage play essential role in the
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16 pathogenesis of WD. Because of the exhausted capacity to sequester copper in
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18 the liver, massive copper are released from copper-loaded hepatocytes and
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20 overload in the brain and other organs in succession. Copper is the dominating
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22 source of free-radical production and causes cell necrosis in liver.²² Thus the
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24 complicated neurological picture of WD is probably closely associated with copper
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26 accumulations in diverse brain regions. Nonetheless, some conflicting findings
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28 cast doubts on the theory that copper is the solely causative factor bringing about
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30 the pathologic lesions of brain. Through investigating the copper distribution in the
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32 various brain compartments of patient died for WD, Faa and colleagues have
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34 demonstrated that the abnormal copper distribution is inconsistent with the
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36 symptom-related brain lesions, and the basal ganglia seems relatively normal,
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38 which determines the common neurologic symptoms in WD.¹² This discrepancy
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40 strongly stressed the existence of other players aggravating the copper toxicity in
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42 the brain. The paucity of brain autopsy specimens of WD patients further hinders
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44 the dissection into definite relation between copper deposition and neuronal
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46 impairment. Thus, an available *Atp7b*^{-/-} model helps to determine the complex
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48 mechanism responsible for neuronal dysfunction or death in WD. Despite some
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50 studies have yielded supportive evidences for copper accumulation in some brain
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52 regions, they could not yet exclude the hypothesis that other factors also affect the
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3 neurological profile of WD. In order to explicitly elucidate the correlation, we
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5 especially selected the 10-month aged mice to observe neuronal ultrastructure
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7 changes. The interesting finding that the abnormal microscopy alternations existed
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9 in neuron with the absence of copper overload was identified. This result further
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11 supports the aforementioned hypothesis.
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14 The healthy ATP7B protein has dual play, except for excreting the excessive
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16 copper into bile, biosynthesis of holoceruloplasmin is another importantly
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18 physiological process. Copper overload in WD merely refers to the disrupted
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20 copper excretion. However, whether the drastic reduction of holoceruloplasmin
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22 could be involved in the pathogenesis of WD remained unclear. Holoceruloplasmin
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24 is a multicopper oxidase being tightly associated with iron metabolism, and on the
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26 molecular level iron and copper metabolism are closely interacted.²³ Therefore,
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28 some reports on the disrupted iron metabolism in livers of WD patients have been
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30 released.^{11, 24} Moreover, researchers have detected that some WD patients
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32 manifested as the eccentric hypointensity on T2-weighted images and reckoned
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34 that this rare appearance could be due to the existence of paramagnetic effects of
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36 some trace elements, for instance iron and manganese.⁸ These findings further
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38 demonstrated that other causative factors might participate in the pathogenesis of
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40 WD except for copper. Besides, patients with WD at the later stage often
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42 presented with the severe portal-systemic encephalopathy, thus chronic liver
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44 disease could enhance copper toxic role as well. Certainly, we only discovered the
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46 disparity at present and intensive study need to be performed to identify other
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48 exact players being involved in WD pathogenesis.
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53 54 **Conclusions**

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56 This study firstly identified the causal relationship between copper and
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3 neuronal lesions in the *Atp7b*^{-/-} mice in detail. The discrepancy that abnormal
4 neuronal alternations occurred in the basal ganglia with the absence of copper
5 deposition was detected. This disparity strongly indicated that copper might not be
6 the solely causative player and other unidentified morbidic factors could enhance
7 copper toxic effect on neurons in WD. In addition, compared with copper
8 metabolism in brain of *Atp7b*^{-/-} mice, the noted copper metabolism profile in the
9 liver suggested that the rodent model is the valid and excellent model to uncover
10 the liver pathogenesis of WD.
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20 **Disclosure**

21 The authors report no conflicts of interest.
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Legends of Figures

Figure 1. Ultrastructure features of livers in 10-month $Atp7b^{+/+}$ and $Atp7b^{-/-}$ mice. A: normal morphology of mitochondria (solid arrows) and nucleus (hollow arrow) in $Atp7b^{+/+}$ hepatocyte; B: abnormal electron-dense granulation in lysosome being not observed in $Atp7b^{+/+}$ hepatocyte; C: vacuolization of massive mitochondria in $Atp7b^{-/-}$ mutant hepatocyte (solid arrows); D: extensive electron-dense granulation existing in abnormal lysosome of $Atp7b^{-/-}$ mutant hepatocyte (solid arrows). Original magnifications: 5000 (A, C); 20000 (B, D).

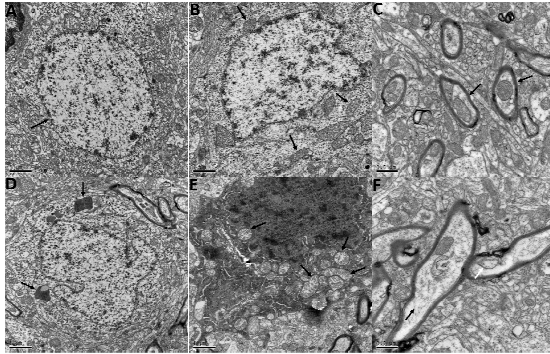
Figure 2. Ultrastructure features of neurons in the basal ganglia region of 10-month $Atp7b^{+/+}$ and $Atp7b^{-/-}$ mice. A: normal nucleus inside $Atp7b^{+/+}$ neuron (solid arrow); B: normal mitochondria inside $Atp7b^{+/+}$ neuron (solid arrows); C: normal ultrastructure of $Atp7b^{+/+}$ axons (solid arrows); D: lipofuscin accumulation in the perinuclear area of $Atp7b^{-/-}$ mutant neuron (solid arrows); E: vacuolization of massive mitochondria in $Atp7b^{-/-}$ mutant neuron (solid arrows); F: the occurrence of loose conformation of microtubule and microfilament (solid arrow), and swollen mitochondria (hollow arrow) in the malformed axons (much larger in diameter and irregular shape) of $Atp7b^{-/-}$ mutant neurons. Original magnifications: 10000 (A, B, D, E); 20000 (C, F).

Figure 3. Copper content in mitochondria of the liver and basal ganglia of 10-month $Atp7b^{+/+}$ and $Atp7b^{-/-}$ mice. There is significantly difference of copper content in mitochondria of the liver of $Atp7b^{-/-}$ mice in comparison to aged-matched controls. However, in mitochondria of the basal ganglia, the significant difference was not detected between two genotyped mice. Significant difference is indicated

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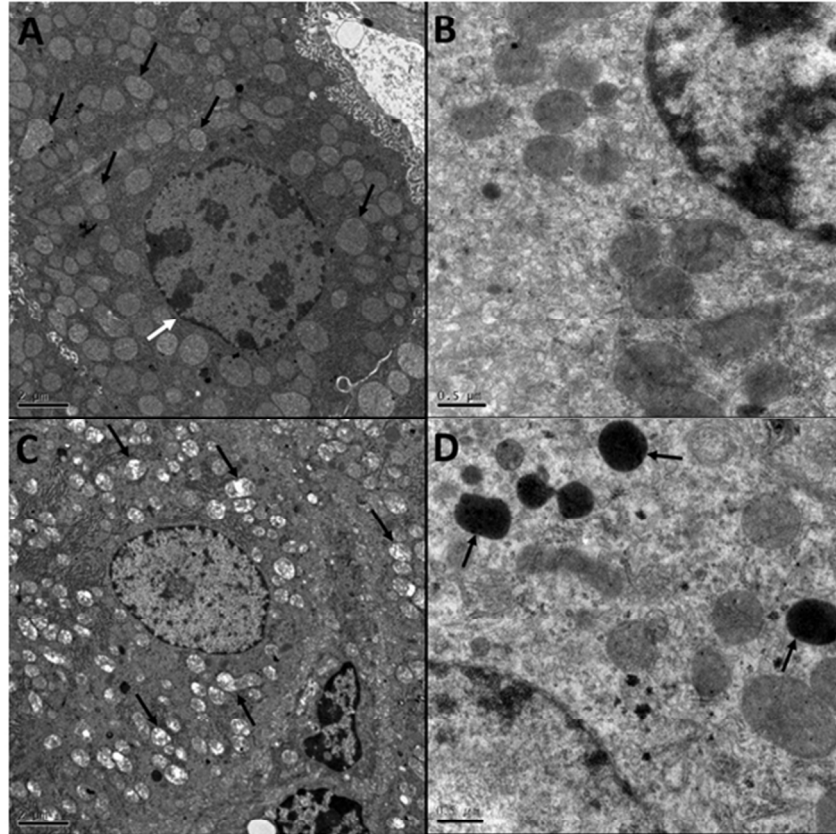
by asterisk (***) $p < 0.001$).

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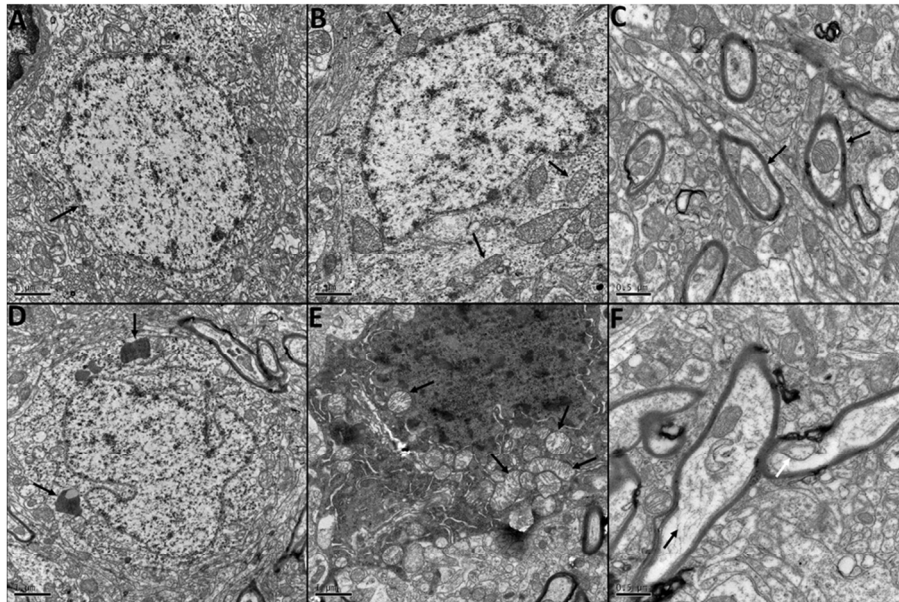


The neuronal damages were identified in the basal ganglia despite the absence of copper accumulation in the region.

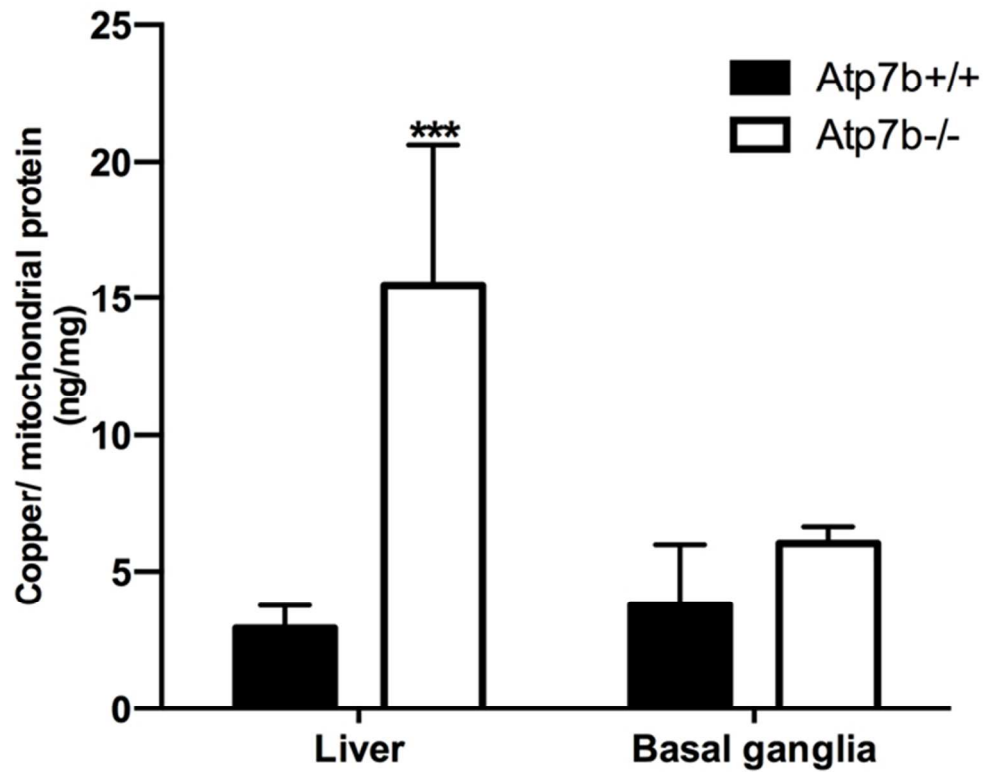
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Ultrastructure features of livers in 10-month *Atp7b*^{+/+} and *Atp7b*^{-/-} mice. A: normal morphology of mitochondria (solid arrows) and nucleus (hollow arrow) in *Atp7b*^{+/+} hepatocyte; B: abnormal electron-dense granulation in lysosome being not observed in *Atp7b*^{+/+} hepatocyte; C: vacuolization of massive mitochondria in *Atp7b*^{-/-} mutant hepatocyte (solid arrows); D: extensive electron-dense granulation existing in abnormal lysosome of *Atp7b*^{-/-} mutant hepatocyte (solid arrows). Original magnifications: 5000 (A, C); 20000 (B, D).
60x60mm (300 x 300 DPI)



Ultrastructure features of neurons in the basal ganglia region of 10-month *Atp7b*^{+/+} and *Atp7b*^{-/-} mice. A: normal nucleus inside *Atp7b*^{+/+} neuron (solid arrow); B: normal mitochondria inside *Atp7b*^{+/+} neuron (solid arrows); C: normal ultrastructure of *Atp7b*^{+/+} axons (solid arrows); D: lipofuscin accumulation in the perinuclear area of *Atp7b*^{-/-} mutant neuron (solid arrows); E: vacuolization of massive mitochondria in *Atp7b*^{-/-} mutant neuron (solid arrows); F: the occurrence of loose conformation of microtubule and microfilament (solid arrow), and swollen mitochondria (hollow arrow) in the malformed axons (much larger in diameter and irregular shape) of *Atp7b*^{-/-} mutant neurons. Original magnifications: 10000 (A, B, D, E); 20000 (C, F).
99x70mm (300 x 300 DPI)



Copper content in mitochondria of the liver and basal ganglia of 10-month Atp7b+/+ and Atp7b-/- mice. There is significantly difference of copper content in mitochondria of the liver of Atp7b-/- mice in comparison to aged-matched controls. However, in mitochondria of the basal ganglia, the significant difference was not detected between two genotyped mice. Significant difference is indicated by asterisk (***) $p < 0.001$.
60x49mm (300 x 300 DPI)

Table 1 Copper levels in livers of *Atp7b*^{-/-} mice and controls

	One month	Three months	Ten months
Atp7b ^{+/+}	21.2±2.0 (n=3)	24.1±3.7 (n=3)	18.4±1.4 (n=12)
Atp7b ^{-/-}	575.5±27.9* (n=3)	874.5±9.4* (n=3)	627.0±48.4* (n=10)
Copper ratio (<i>Atp7b</i> ^{-/-} / <i>Atp7b</i> ^{+/+})	21	36	34

Copper levels are expressed as the mean concentration (µg/g dry weight) ± SD with number of animals in each group in parenthesis. The copper concentrations in *Atp7b*^{-/-} mice were significantly different from controls during three distinct stages (* $p < 0.005$).

Table 2 Comparisons of copper levels in whole brain and distinct brain regions between the two-genotyped mice

Age(months)	Basal ganglia copper		Cerebellum copper		Cerebellum copper		Brain copper	
	Atp7b ^{-/-}	Atp7b ^{+/+}	Atp7b ^{-/-}	Atp7b ^{+/+}	Atp7b ^{-/-}	Atp7b ^{+/+}	Atp7b ^{-/-}	Atp7b ^{+/+}
1	35.1±5.7 (n=3)	30.4±7.4 (n=3)	20.8±7.2 (n=3)	20.1±2.0 (n=3)	45.3±14.3 (n=3)	40.0±12.0 (n=3)		
3	35.5±9.5 (n=3)	25.2±2.3 (n=3)	17.1±1.7 (n=3)	17.4±1.8 (n=3)	26.8±0.7 (n=3)	41.4±7.8 (n=3)		
10	30.7±2.7 (n=10)	39.8±4.1 (n=11)	27.5±2.8 (n=10)	22.5±3.0 (n=11)	49.9±7.0 (n=10)	33.7±4.8 (n=11)	32.9±3.0 (n=6)	29.9±2.6 (n=4)

Copper levels are expressed as the mean concentration ($\mu\text{g/g}$ dry weight) \pm SD with number of animals in each group in parenthesis. The mean copper concentrations of three brain compartments and total brain were not significantly different between mutant mice and controls.