

Parasitemia and antimalarial-induced oxidative stress and histological alterations in infected mice

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Abstract: In lieu of the reports on re-emergence of chloroquine sensitive *Plasmodium falciparum*, the choice of the drug for the treatment of malaria especially in the endemic areas may not be ruled out. Here, we reported the anti-oxidative status and histology of some vital organs in mice infected with *P. berghei* and subsequently treated with chloroquine. The study was a 4 by 10 model design as follows: the control non-infected, the infected (IN) and chloroquine-treated infected (CqTI) / non-infected (CqTNI) mice. The challenged animals were subjected to five days treatment after parasitemia was established using Gemsa stain. Assays were conducted on the animals following standard procedures. The results showed that parasitemia and Chloroquine induced oxidative stress in (IN) and (CqTNI) groups. This was indicated by significant ($p < 0.05$) changes in the antioxidant defence indices viz superoxide dismutase (SOD), reduced glutathione (GSH), glutathione-S-transferase (GST), catalase (CAT), malondialdehyde (MDA) and protein concentration. There were also alterations in the architectures of some vital organs such as liver, kidney and heart of the experimental groups compared with control. The subsequent treatment of the infected group with Chloroquine (CqTI) restored some of the indices altered during the infection to a normal level. This study shows that malaria and its radical treatment in vivo can induce oxidative stress which in turn can cause injury to the host tissues particularly during chronic administration of Chloroquine-an implication for prolong intake of the drug.

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Key words: *Plasmodium berghei*, antimalaria, oxidative stress, organs, mice

1. Introduction

Plasmodium berghei bears similar characteristics with *P. falciparum*, a virulent human malaria parasite transmitted by *Anopheles* mosquitoes (Sherman, 2008). The parasite infects the liver after its injection into the bloodstream by a bite of an infected female *Anopheles* mosquito. After a short period (a few days) of development and multiplication (exoerythrocytic-stage infection), these parasites leave the liver and invade erythrocytes (erythrocytic-stage infection). This latter stage causes more liver apoptosis and hepatic pathological changes leading to liver dysfunction and other systemic complications (Kochar et al., 2003; Sand et al., 2005). Some of the pathological condition and systemic complications include anaemia and damage of essential organs of the host such as lungs, liver, spleen (Janse et al., 2006).

The World Health Organization has advocated the use of antimalarial drugs for chemoprophylaxis, prevention and treatment of

uncomplicated malaria (WHO, 1997). Chloroquine still remains a drug of choice for treatment of malaria in the endemic areas despite the reported plasmodia resistance. Presently, there are evidences for re-emergence of chloroquine sensitive *P. falciparum* strains in these areas and this may not be unconnected with years of reliance on antimalarials other than chloroquine (James et al., 2003; Kublin et al., 2003). For instance, in a study conducted in Nigeria, chloroquine efficacy in children under five years was rated 72% in terms of adequate clinical and parasitological response (Umar et al., 2008). Previous literatures had described the impact of the concentration of chloroquine in different organs of the body following its administration during the episode of disease (Kublin et al., 2003; Desai et al., 2010). Reports have also implicated chloroquine in the disruption of a wide range of biochemical processes which include the inhibition of major metabolic enzymes like alcohol dehydrogenase, succinate

dehydrogenase and glucose 6-phosphate dehydrogenase. Effect of chloroquine on antioxidant enzymes as well as its inhibitory tendency on cytochrome P-450-mediated mixed function oxidase activities both in vivo and in vitro have been demonstrated (Thabrew & Ioannides, 1984; Magwere et al., 1997).

Infectious diseases such as malaria are known to activate the body phagocytes causing release of reactive oxygen species (ROS). Oxidative stress occurs when the generation of ROS in a system, exceeds the system's ability to neutralize and eliminate them. The imbalance can result from a lack of antioxidant capacity caused by disturbance in production, distribution, or by an over-abundance of ROS from an environmental or behavioural stressor. If not properly regulated, the excess ROS can damage a cell's lipids, protein or DNA, inhibiting normal function while a more severe oxidation stress can cause all death (Jodah et al., 2008).

All cells have endogenous antioxidants (such as superoxide dismutase and glutathione) which are very important for protection from oxidative stress at all times. Glutathione (GSH) is very important as an intracellular antioxidant; GSH has been found to be low in many disease states indicating oxidative stress and inadequate antioxidant activity to "keep up" with the free radicals. This study aims at investigating the influence of *Plasmodium* infection and chloroquine individually and synergistically in the treatment regime on the histopathological and oxidative stress profile in mice.

2. Materials and Methods

2.1. Experimental Animals

Eight-week-old male albino mice bred at the animal house unit of College of Medicine, University of Lagos, Nigeria were used as experimental animals. The animals were kept in a protected and ventilated animal house, fed *ad libitum* with commercial pellet (from Ladokun Feeds Ltd. Ibadan, Oyo State, Nigeria) and water.

2.2. Experimental Design

The study was a 4 by 10 model design as follows: the mice were divided into four groups of ten mice each i.e. the control non-infected, the infected (IN), and chloroquine-treated infected (CqTI)/non-infected (CqTNI) mice.

2.3. Procurement and Administration of ANKA strain of *P. berghei*

ANKA strain of *P. berghei* was obtained from the Nigerian Institute for Medical Research (NIMR) Yaba, Lagos, Nigeria. Standard inoculums of 1×10^7 parasitized erythrocytes obtained from the infected

mouse in volume of 0.1ml was administered intraperitoneally to each experimental animal.

2.4. Drug Administration and Establishment of Parasitemia

The CqTI and CqTNI groups of mice were administered with daily oral doses of chloroquine phosphate (Sigma, USA) (10 mg/kg body weight) for five consecutive days after the establishment of *P. berghei* infection. This was confirmed using thin films of blood stained with Giemsa to ascertain parasitemia levels.

2.5. Histological Examination

Kidney, liver and heart tissues were obtained per animal in each group for routine histological procedures. The tissues were sectioned and stained to obtain permanent digital micrographs of the desired sections. The tissues were also prepared for the following assays as described by Iyawe and Onigbinde (2009).

2.6. Biochemical Assays

Lipid peroxidation was determined followed the method described by Gutteridge and Wilkins (1982). Malondialdehyde has been identified as a product of lipid peroxidation that reacts with thiobarbituric acid to give a red specie absorbing at 535nm. Plasma protein estimation was determined by means of Biuret method as described by Gornall et al. (1949) with some modifications. The levels of SOD activity in plasma by the method of Misra and Fridovich (1972). Sinha (1971) method was used to determine catalase activity. Glutathione S-transferase activity was determined by the method of Habig et al., (1974). The total sulphhydryl groups, protein bound sulphhydryl groups, free sulphhydryl groups (such as reduced glutathione) in biological samples was determined using Ellman's reagent (DTNB) as described by Sedlak and Lindsay (1968), and Jollow et al (1974).

2.7. Data collection and Statistical analysis

Statistical analysis was carried out using SPSS 15.0 for windows; SPSS Inc., Chicago, USA. The difference between mean was determined using One Way Analysis of Variance (ANOVA). Data were reported as Mean \pm Standard deviation and $P < 0.05$ was considered significant. Least Significant Difference (LSD) was used to determined differences in means at 95% confidence interval as post hoc analytical method.

3. Results and Discussion

Alteration in certain conditions and chemical application can lead to excessive production of reactive

oxygen species (ROS) (Farombi et al., 2003). These ROS are important mediators of tissue injury either during the infection or the application of the drug. The sensitivity of malaria parasites to oxidative damage has been proved by the efficacy of some antimalarial drugs that are known to act via generation of ROS. In the present study, malaria infection causes a significant increase in antioxidant defence indices viz., superoxide dismutase (SOD), reduced glutathione (GSH), Glutathione S-transferase (GST) and plasma lipid peroxidation (MDA) while catalase showed a significant decrease (Fig.1, 2, 3 and Table 1). The increase in SOD activity here is attributed to parasitemia and it could be due to mobilization of immune system in infection state whereby free radicals were generated against xenobiotics as been asserted in the earlier report (Iyawe and Onigbinde, 2012). Previous investigation has also reported decrease in catalase activity particularly in *Plasmodium berghei* and *P. vivax* infection (Erel et al., 1997; Seth et al., 1985). ROS such as superoxide anion has been shown to inhibit catalase by converting it to ferroxo and ferryl states, the inactive forms of enzyme (Areekul et al., 1986). This situation will lead to the accumulation of H₂O₂ and increase the burden of H₂O₂-induced oxidative stress (Aniya and Naito, 1983) in the *Plasmodium* infected erythrocytes. However, increased GSH will eliminate hydrogen peroxide and this may reduce the burden of H₂O₂-induced oxidative stress in the infected erythrocytes. Although, previous report has demonstrated the potential of glutathione peroxide to eliminates H₂O₂ at low concentration (Casado et al., 1995). Similar reports of raised GST levels have been documented (Farombi and Emerole, 1998) and this could be due to its induction in an attempt to counter the effect of increased oxidative stress (Status of lipid peroxidation, glutathione, ascorbic acid, vitamin E and antioxidant enzymes in patients with osteoarthritis (Surapaneni and Venkataramana 2007). During the schistosome parasite infection, GSTP_i was reported as one of the proteins upregulated (Harvie et al., 2007). Also, GSTP_i mRNA has been shown to be upregulated in blood of *P. vivax*-infected subjects as compared to healthy ones (Sohail et al., 2010). Earlier investigation showed MDA level as an index for lipid peroxidation and this increased during *P. berghei* infection in mice (Siddiqi et al., 1999). The elevation in lipid peroxidation in the plasma of infected mice may point to lipid peroxide level as a reflection of the severity of a disease process (Das et al., 1993).

Following administration of chloroquine to un-infected mice, we noticed increase in all the parameters considered in this study except reduced GSH. The increased SOD levels could be due to the response to an increased production of ROS as a result of exposure to chloroquine or its metabolites (Farombi

et al., 2003). The increase in the activity of SOD supports the earlier report which shows the effect of chloroquine on experimental animals (Magwera et al., 1997). In other investigation, amodiaquine, another 4-aminoquinoline was reported to have similar effect on rats (Farombi, 2000). The increased activity of GST may have resulted in response of GST to detoxify the chloroquine (Glatt et al., 1983, Anyasor et al., 2012). High level of MDA (Malondialdehyde) might be due to the formation of hydroxyl radicals that perturbed the membrane to increase the formation of malondialdehyde as reported by Iyawe & Onigbinde (2009). The low level of GSH may arise from chloroquine reaction with other molecules making it to inhibit these antioxidants with consequence reduction in their activities followed by the utilization of cellular reduced glutathione. Reduced Glutathione (GSH) serves as a sulfhydryl buffer which protects the -SH groups of proteins from the damaging effects of reactive oxygen species (Akkus, 1995; Kidd, 1997).

Treatment of infected mice with chloroquine resulted in decrease of parasitemia and restoration of all oxidative stress and antioxidant defence indices to normal levels. Decreased SOD activity may indicates less production of H₂O₂ while increased catalase activity may mean low level of ROS such as superoxide anion generated since this could not inhibit catalase. However, catalase could have catalyzed available hydrogen peroxide to molecule oxygen and water thereby mopping up the non radical hydrogen peroxides (Mishra et al., 1994, Ueda et al., 2005). This situation will lead to decrease in the burden of H₂O₂-induced oxidative stress. Previous report has also demonstrated the potential of GPX to eliminate H₂O₂ at low concentration (Casado et al., 1995). Increased MDA (Malondialdehyde) as reported here would trigger the induction of endogeneous antioxidant defense system to scavenge reactive species (Pham-Huy et al., 2008). Decrease in the level of GSH was observed, its alteration under conditions of oxidative stress (Stocker et al., 1986) in malaria infected subjects treated with chloroquine has been reported. Such decrease has been linked with an attempt to increase defense against oxidant damage.

Comparing sections of stained organs in the control groups (Fig. 4 a, b, c) with the experimental groups, the following were observed. The Plasmodia infection caused marked congestion, marked hepatocytes necrosis and mild vascular congestion in the heart, liver and kidney respectively (Fig. 4 d, e, f). The presence of the parasite might have induced the cells of these organs causing the observed damages. Heavy parasitemia have been implicated in the occurrence of tubulointerstitial damages as well as glomerulonephritis and renal failure in the kidney of the infected patients (Mahakur et al., 1983;

Rajapurkar, 1994; Saroj and Bhabani, 2008). In chloroquine-treated non-infected (CqTNI), liver showed binucleate with granular eosinophilic cytoplasm, severe vascular congestion and hepatocyte necrosis (Fig. 4 g, h, i).. Previous studies showed lisosomotropic properties of chloroquine where relatively loose arrangement of hepatocytes was observed in the liver (**Patel et al., 2005**). This was attributed to the activation of lysosome enzymes leading to cell damage and /or necrosis (**Maniam et al., 2012**). The chloroquine-treated infected (CqTI) mice showed normal conditions in all the organs tested with mild congestions in the heart and kidney(Fig. 4 j, k, l). In other studies, liver histology was found to be restored to normal after administration of chloroquine for four days following the infection (**Maniam et al., 2012**). Here, the ability of the parasite to digest the

haemoglobin was interrupted by chloroquine (**Sharrock et al. 2008**). Hence, the free haem monomers produced might have caused oxidative damage to *Plasmodium* parasite (**Patel et al., 2005**).

Conclusion

This study implicates the dual action of malaria parasite and antimalaria in altering antioxidant status *in vivo* leading to oxidative damage. The resulting injuries contribute to pathophysiological effects of the disease and administration of the antimalaria to un-infected animals. The administration of antimalaria to infected animals restored the oxidative stress and pathological conditions of the affected organs. However, caution should be taken in prolong administration of the drug.

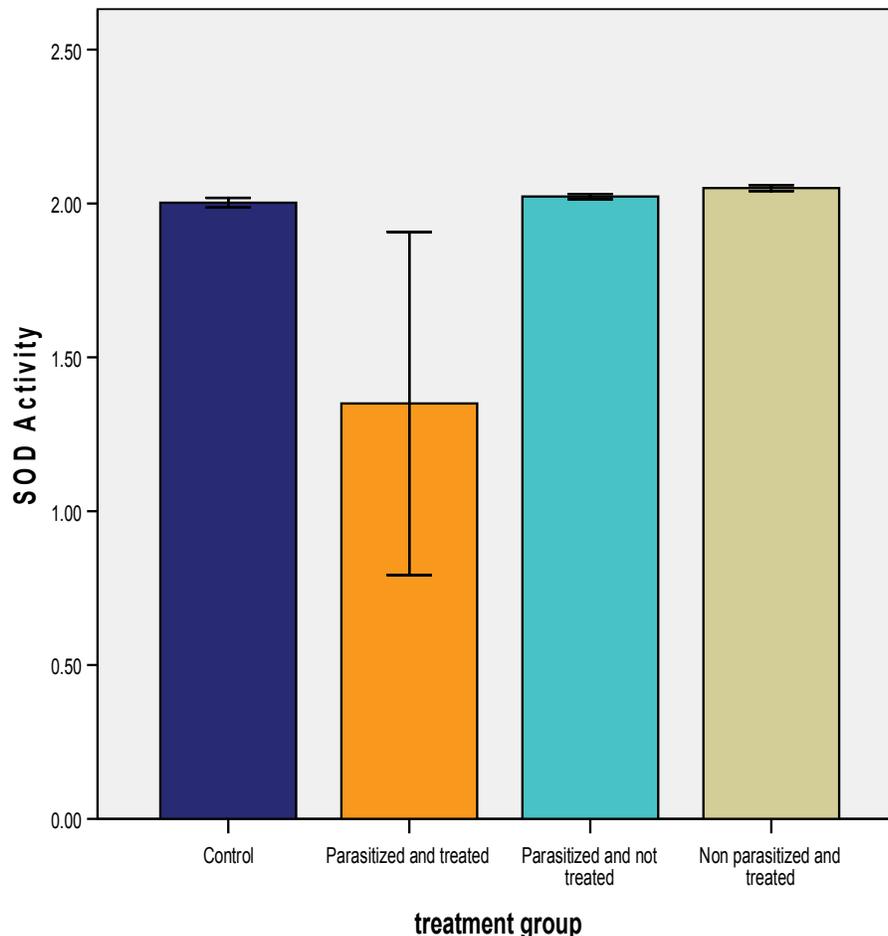


Fig. 1: Superoxide Dismutase activity in control and experimental groups: CqTI, IN and CqTNI.

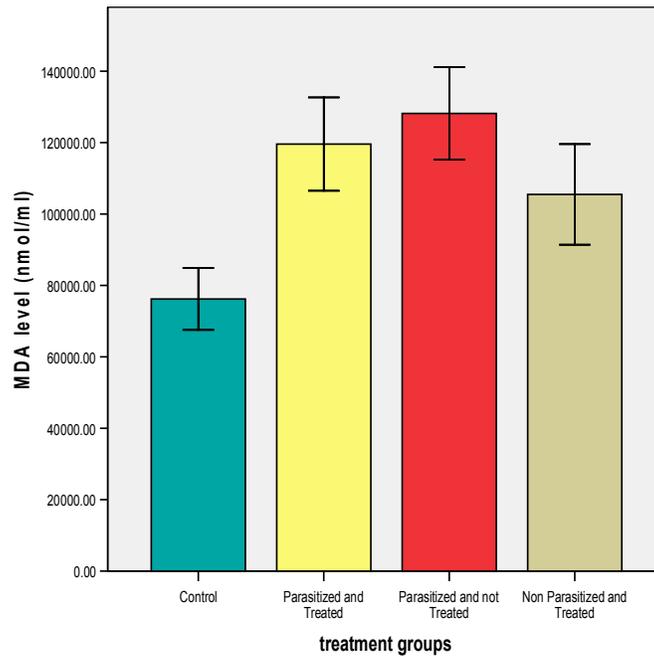


Fig. 2: MDA levels in control and experimental groups: CqTI, IN and CqTNI.

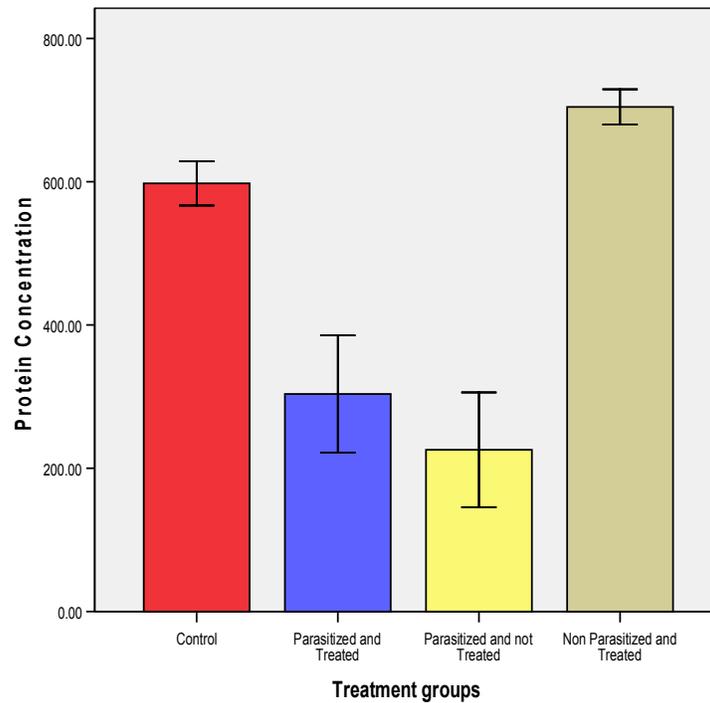
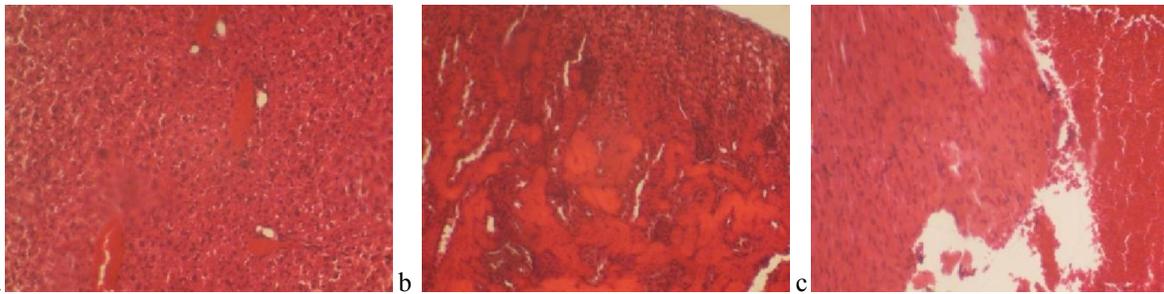
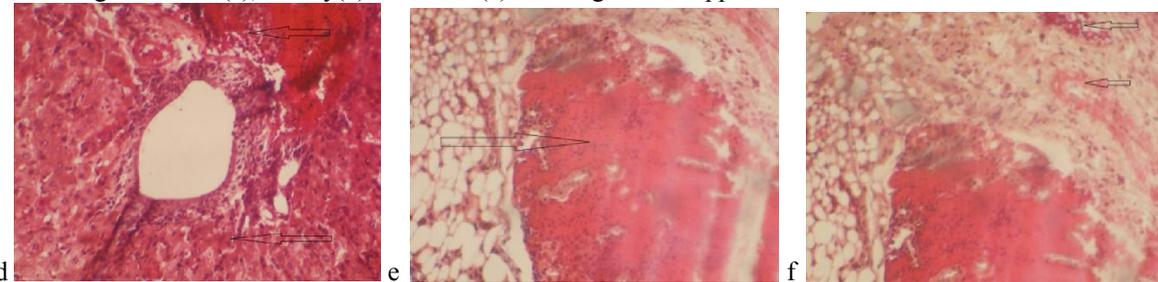


Figure 3: Protein concentration in control and experimental groups: CqTI, IN and CqTNI (Values were derived from unit/mg protein and expressed as Mean \pm S.D)



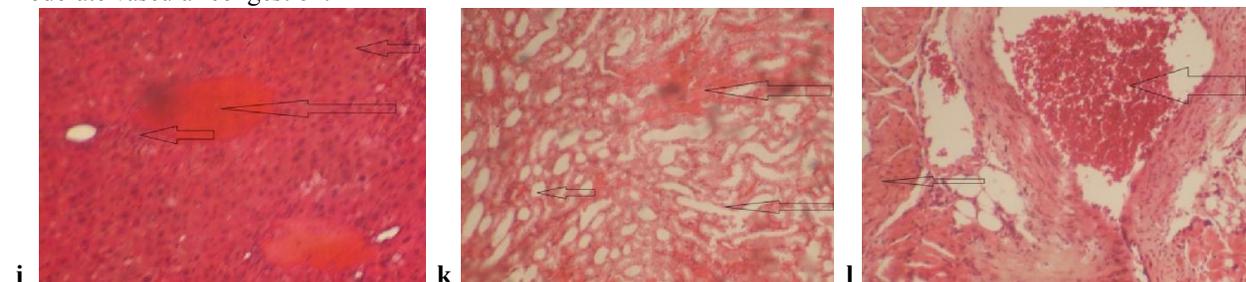
Sections through the liver (a), kidney(b) and heart (c) showing normal appearance in control non – infected mice.



Sections through the liver (d), kidney(e) and heart (f) in infected (IN) mice. The arrow (up, right) in (d) indicates interlobular neutrophilic infiltrate and marked vascular congestion. The arrow (down, right) indicates marked hepatocytes necrosis (interlobular) and piece meal necrosis. In (e), the arrow (left) indicates mild vascular congestion. In (f), the arrows (right) indicates marked congestion.



Sections through the liver (g), kidney(h) and heart (i) in chloroquine-treated non-infected (CqTNI) mice. The arrow (up, right) in (g) indicates binucleate hepatocytes with granular eosinophilic, arrow (middle) indicates severe vascular congestion in cytoplasm and arrow (down) indicates marked periportal and interlobular neutrophilic infiltrate with focal hepatocyte necrosis. The kidney (h) showed no abnormalities while the heart (i) showed moderate vascular congestion.



Section through the chloroquine-treated infected (CqTI) mice, liver (j) with normal hepatocyte tract and central vein. Kidney(k) with arrows (up, right) and (down, left and right) showing mild congestion respectively with normal glomerulus & tubules. The heart(l), arrow (up, right) showed mild portal congestion and arrow (down, left) showed normal myocytes.

Fig 4: Sections of stained organs (liver, kidney and heart) prepared from control mice (a, b & c), *P.berghei* infected mice (d, e & f), Chloroquine –treated non-infected (g,h & i) and treated infected mice (j, k & l),

Table 1: The activities of GSH, Catalase and GST in control and experimental groups. Values were expressed as Mean \pm S.D., CqTI, IN and CqTNI; n=10 in each group.*Significantly different from other groups at P<0.05.

Parameter	Control	CqTI	IN	CqTNI
GSH(ug/mg)	19.62 \pm 0.23	19.57 \pm 0.24	19.63 \pm 0.16	19.53 \pm 0.18
Catalase (U/L)	4.78 \pm 3.15	5.37 \pm 2.28	1.14 \pm 7.71 *	4.47 \pm 4.24
GST(ug/mg)	4.45 \pm 1.32*	3.13 \pm 2.37	3.23 \pm 2.42	3.56 \pm 1.27

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