

BRIEF COMMUNICATION

The responses of germinating seedlings of green peas to copper oxide nanoparticles

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Abstract

The effects of copper oxide nanoparticles (CuONPs) on germinating seedlings of green pea (*Pisum sativum* L.) were studied. The seedlings were grown in a half-strength Murashige and Skoog semisolid medium containing 0, 50, 100, 200, 400, and 500 mg dm⁻³ CuONPs for 14 d under controlled growth chamber conditions. Exposures to 100, 200, 400, and 500 mg dm⁻³ CuONPs significantly reduced plant growth (shoot and root lengths) and increased reactive oxygen species (ROS) generation and lipid peroxidation. Gene expression study using real-time polymerase chain reaction showed no significant change in the expression of genes coding CuZn-superoxide dismutase (*CuZnSOD*), catalase (*CAT*), and ascorbate peroxidase (*APX*) in shoots. However in roots, a significant increase in the expression of the *CuZnSOD* gene was observed under the exposures to 100, 200, 400, and 500 mg dm⁻³ CuONPs, in the expression of the *CAT* gene under 100 and 200 mg dm⁻³ CuONPs, and in the expression of *APX* under 200 and 400 mg dm⁻³ CuONPs.

Additional key words: chlorophyll, gene expression, lipid peroxidation, oxidative stress, *Pisum sativum*.

Copper oxide nanoparticles (CuONPs) are widely used in several products, such as antimicrobial and antifouling paints, bioactive coatings, air and liquid filtration, textiles, and lubricant oils and super conducting materials (www.nanotechproject.org). The phytotoxic effects of CuONPs, e.g., an inhibition of seed germination, reduction in plant growth and biomass, and induction of oxidative stress, have been reported in various plants (Lin and Xing 2007, Stampoulis *et al.* 2009). However, only limited studies has been undertaken on the toxic effect of CuONPs in food crops (Shaw and Hossain 2013). In the present investigation, the toxic effects of CuONPs were studied in a green pea (*Pisum sativum* L.). The effects of CuONPs on seedling development (shoot and root lengths), total chlorophyll content, ROS generation, and lipid peroxidation were studied. Further, the modulation of expression of genes involved in antioxidative responses, such as those coding CuZn-superoxide dismutase (*CuZnSOD*), catalase (*CAT*), and ascorbate

peroxidase (*APX*), were evaluated. Since Cu ions released from CuONPs to the exposure medium may cause toxic responses, the toxic effect of CuONPs was compared with the effect of Cu²⁺ ions, and a medium devoid of CuONPs was used as negative control.

A semi solid half-strength Murashige and Skoog (MS) medium (pH 5.7) with 20 g dm⁻³ sucrose and 5 g dm⁻³ agar (*Duchefa Biochemie*, Haarlem, The Netherlands) was used. CuONPs were purchased from *Sigma-Aldrich* (St. Louis, MO, USA). The characterization of CuONPs and the amount of Cu²⁺ ions released to deionized water from the highest concentration of CuONPs tested (*i.e.*, 500 mg dm⁻³) was measured based on our earlier study (Nair and Chung 2014). As described by Lee *et al.* (2008), CuCl₂·2 H₂O (*Sigma-Aldrich*) was used for the preparation of a Cu²⁺ solution. After autoclaving, different concentrations of CuONPs and CuCl₂ were vortexed with 100 cm³ of a growth medium to reach final concentrations of 0, 50, 100, 200, 400, and 500 mg dm⁻³

Submitted 22 August 2014, last revision 9 December 2014, accepted 5 January 2015.

Abbreviations: APX - ascorbate peroxidase; CAT - catalase; CuONPs - copper oxide nanoparticles; CuZnSOD - CuZn-superoxide dismutase; HPF - 3'-hydroxyphenyl fluorescein; ICP-AES - inductively coupled plasma-atomic emission spectrophotometry; MS - Murashige and Skoog; NBT - nitroblue tetrazolium; PCR - polymerase chain reaction; ROS - reactive oxygen species.

Acknowledgements: This paper was supported by the KU Research Professor Program of the Konkuk University, Seoul, South Korea, and by the Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Science, ICT and Future Planning (2014R1A2A2A01002202).

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CuONPs and $0.2 \text{ mg dm}^{-3} \text{ Cu}^{2+}$, and distributed to plant growth vessels ($120 \times 80 \text{ mm}$; *Phytohealth, SPL Life Sciences*, Gyeonggi-do, South Korea). The medium was solidified immediately by keeping in a refrigerator at $4 \text{ }^{\circ}\text{C}$ for preventing precipitation of CuONPs.

Seeds were surface sterilized with a sodium hypochlorite solution (10 %, m/v) for 15 min and rinsed with sterilized deionized water five times. The seeds were germinated in the dark on wet *Whatman #1* filter paper in disposable plastic Petri dishes (*SPL Life Sciences*). Ten germinated seeds with 1 mm root length were transferred to each culture vessel and incubated in a growth chamber (*Hanbaek Scientific Co.*, Gyeonggi-do, South Korea) under a 16-h photoperiod, an irradiance of $80 \mu\text{mol m}^{-2} \text{ s}^{-1}$, and a temperature of $26 \pm 1 \text{ }^{\circ}\text{C}$ for 14 d. Four replications were maintained for the control and all treatments and the experiment was repeated twice.

For analysis of Cu content in plants, root and shoot tissues from the control and CuONPs exposed plants were thoroughly washed with deionized water and dried at $75 \text{ }^{\circ}\text{C}$ for 24 h in a dry air oven. The dried plant samples (100 mg) were digested with concentrated HNO_3 at $115 \text{ }^{\circ}\text{C}$ for 1 h, diluted to 25 cm^3 with deionized water, and filtered through $0.2 \mu\text{m}$ nylon filters (*Chromedisc*® syringe filter, Seoul, South Korea). The Cu content was determined by inductively coupled plasma-atomic emission spectrophotometry (ICP-AES; *Ultrace*, Jobin Yvon, France) using samples collected from three biological replications.

Shoot and root lengths were measured using a ruler, and fresh mass (FM) of shoots and roots were determined by weighing them on a digital balance (*Mettler Toledo*, Greifensee, Switzerland). Total chlorophyll content was determined according to Lichtenthaler (1987). Hydrogen peroxide content in shoots and roots was measured using the method described by Rao *et al.* (1997), and lipid peroxidation determined as per the method of Heath and Packer (1968). *In vivo* detection of superoxide and hydrogen peroxide formation in roots was done by treating them with nitroblue tetrazolium (NBT) (Fryer *et al.* 2002) and 3'-hydroxyphenyl fluorescein (HPF; *Invitrogen*, Carlsbad, USA) (Kwasniewski *et al.* 2013). The NBT and HPF treated root samples were mounted on $26 \times 76 \text{ mm}$ microscope slides (*Citoglas*®, Jiangsu, China) and photographed using a digital camera (*Canon*, Tokyo, Japan) and a fluorescence microscope equipped with digital camera (*BX61-32 FDIC, Olympus*, Tokyo, Japan), respectively.

Total RNA was isolated from roots and shoots using an RNA isolation kit and cleaned up using an RNA-clean up kit (*Qiagen*, Valencia, CA, USA). The quality and quantity of the RNA preparation was verified by absorbance spectrophotometry ($A_{260}/A_{280} > 1.8$) (a UV/Vis spectrophotometer, *Optizen*, Daejeon, South Korea) and agarose gel electrophoresis. One microgram of total RNA was used for cDNA synthesis using a *QuantiTect*® reverse transcription kit (*Qiagen*) integrated with a genomic DNA contamination removal step as per the manufacturer's instructions. Primers for the *CuZnSOD*

[forward (F): 5'-TTCAGTCAGGAGGGAAATGG-3'; reverse (R): 5'-TCCAAGATCACCAGCATGTC-3'], *CAT* (F: 5'-CTAGGGGAGCAAGTGCAAAG-3'; 5'-GACGGGAAAGTTGTTTCCAA-3'), *APX* (F: 5'-GGAAGGCTATGGGGCTTAG-3'; R: 5'-TCAACAAGAGGGCGGAATAC-3'), and *ACT* (F: 5'-GTTTGGATCTTGCTGGTCGT-3'; R: 5'-GAACCTCTCAGCTCCGATTG-3') genes were designed with publically available sequences in *NCBI Genbank* (<http://www.ncbi.nlm.nih.gov>) using the online *Primer3* program (<http://frodo.wi.mit.edu/primer3/>). The *P. sativum ACT* gene was used as internal control to normalize the gene expressions.

The mRNA expression analysis was done using a *Chromo-4 Opticon* real-time PCR system (*Bio-Rad*, Hercules, USA) according to the manufacturer's instructions. A reaction mixture included 1 mm^3 of cDNA, $0.2 \mu\text{M}$ corresponding forward and reverse primers, and 10 mm^3 of $2 \times \text{IQ SYBR Green Super Mix}$ (*Bio-Rad*) and made up to 20 mm^3 using sterilized deionized water. Reactions were run with an initial template denaturing step at $95 \text{ }^{\circ}\text{C}$ for 7 min, followed by 40 cycles of $95 \text{ }^{\circ}\text{C}$ for 15 s, $56 \text{ }^{\circ}\text{C}$ for 30 s, and $72 \text{ }^{\circ}\text{C}$ for 30 s, and a melting curve analysis was done. The relative expression of different genes under different exposure conditions were compared with the internal control using the gene expression analysis software (*Bio-Rad*). Data obtained from different experiments were analyzed using the one-way analysis of variance (*ANOVA*) with the *SPSS 12.0 KO* (*SPSS Inc.*, Chicago, IL, USA) programme. The Dunnett's post-doc test was done to determine the effect of different exposures on various parameters. Differences at a probability of $P < 0.05$ were considered as significant and at probabilities of $P < 0.01$ and $P < 0.001$ as highly significant.

The morphological analysis of CuONPs in the exposure medium using transmission electron microscopy shows that particles remained as single or in an agglomerated form (Fig. 1 Suppl.). The analysis of dissolution of CuONPs using ICP-AES in deionized water after 24 h showed the presence of $0.025 \pm 0.002 \mu\text{g dm}^{-3} \text{ Cu}$ ions.

No significant changes in the shoot and root lengths and FM were observed after the exposure to $0.2 \text{ mg dm}^{-3} \text{ Cu}^{2+}$ ions and $50 \text{ mg dm}^{-3} \text{ CuONPs}$ as compared to the controls (Fig. 1A,B). However, significant reductions in the shoot and root lengths and FM were observed upon the exposures to 100, 200, 400, and $500 \text{ mg dm}^{-3} \text{ CuONPs}$ (Fig. 1A,B). Except in the case of $500 \text{ mg dm}^{-3} \text{ CuONPs}$, no significant change in the total chlorophyll content was observed (Fig. 1C). The analysis of Cu content showed an average of $3.2 \pm 1.0 \text{ mg(Cu) g}^{-1}(\text{DM})$ in the control seedlings. However, increases in the Cu content to 5.1 ± 0.8 , 7.3 ± 0.9 , and $17.6 \pm 1.1 \text{ mg g}^{-1}(\text{DM})$ were observed upon the exposures to 50, 200, and $500 \text{ mg dm}^{-3} \text{ CuONPs}$, respectively.

The exposures to $0.2 \text{ mg dm}^{-3} \text{ Cu}^{2+}$ and to different concentrations of CuONPs did not change the H_2O_2 content and lipid peroxidation in shoots as compared to

the controls (Fig. 1D,E). Similarly, no significant changes in the H_2O_2 content and lipid peroxidation were observed in roots upon the exposures to 0.2 mg dm^{-3} Cu^{2+} and 50 mg dm^{-3} CuONPs (Fig. 1D,E). However, the exposures to 100, 200, 400, and 500 mg dm^{-3} CuONPs significantly increased the H_2O_2 content and lipid peroxidation in roots (Fig. 1D,E). The *in vivo* detection of

superoxide generation using NBT staining showed no change in roots of the control and Cu^{2+} exposed plants (Fig. 2A Suppl.). However, a gradual increase in superoxide generation was observed in roots after the treatment with different concentrations of CuONPs (Fig. 2A Suppl.). The detection of H_2O_2 generation using the HPF treatment showed no increase in ROS generation

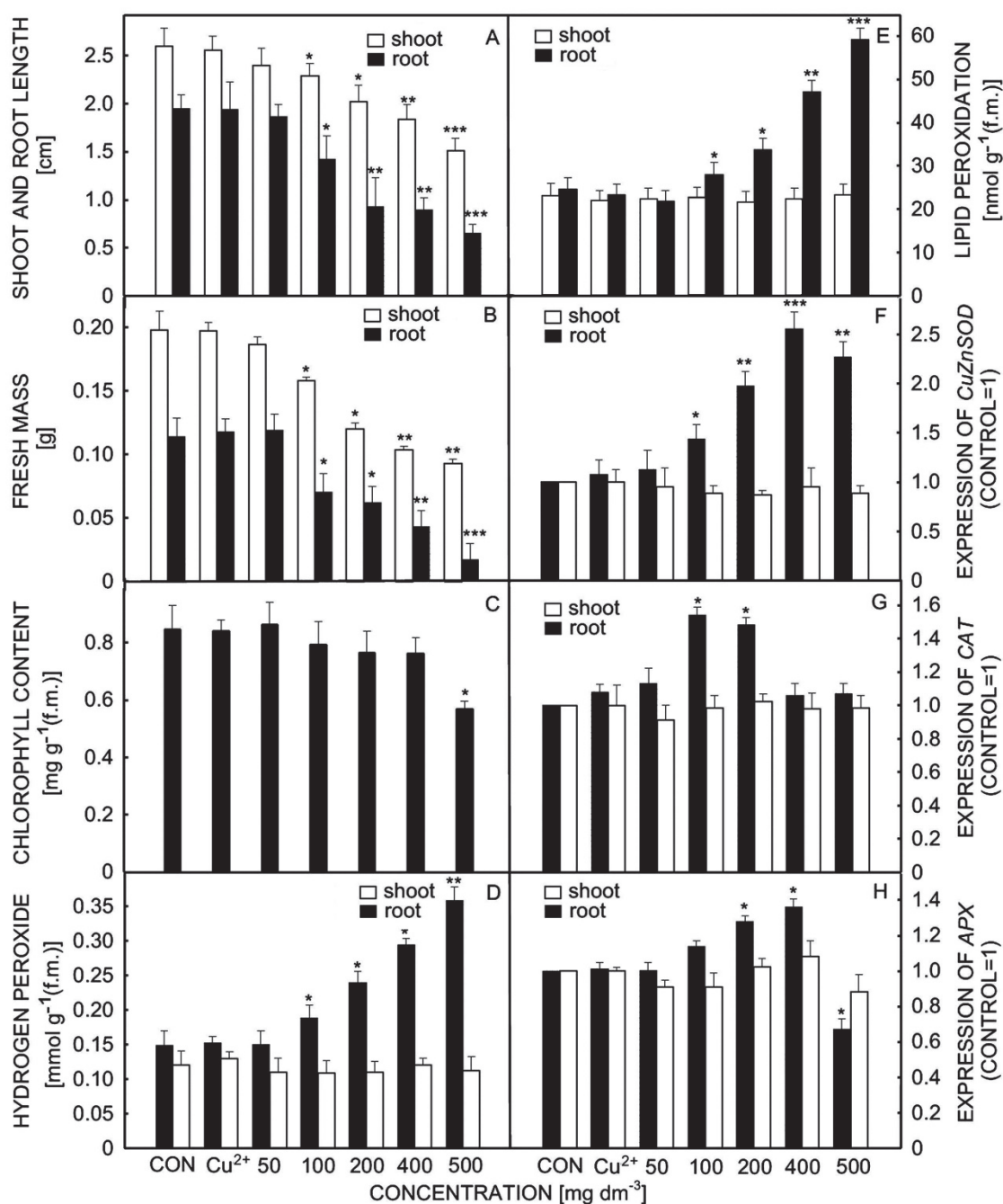


Fig. 1. Average shoot and root lengths (A), shoot and root fresh mass (B), total chlorophyll content (C), hydrogen peroxide content (D), lipid peroxidation (E), *CuZnSOD* expression (F), *CAT* expression (G), and *APX* expression (H) in green pea seedlings exposed to 0.2 mg dm^{-3} Cu^{2+} and $50, 100, 200, 400,$ and 500 mg dm^{-3} CuONPs. Data are means \pm SE of four replicates. The asterisks indicate significant differences at $P < 0.05^*$, $P < 0.01^{**}$, and $P < 0.001^{***}$.

in roots exposed to Cu^{2+} as compared to the control. However, in roots, the ROS generation increased upon the exposures to increasing concentrations of CuONPs (Fig. 2B Suppl.).

The expression of *CuZnSOD* did not change significantly in shoots after the treatment with Cu^{2+} and different concentrations of CuONPs (Fig. 1F). No significant changes in the expression of the *CuZnSOD* gene were also observed in roots upon the exposures to Cu^{2+} and 50 mg dm^{-3} CuONPs (Fig. 1F). However, a significant increase in the expression of *CuZnSOD* was observed in roots after the exposures to 100 - 500 mg dm^{-3} CuONPs (Fig. 1F). The expression of the *CAT* gene did not change significantly in shoots under any of the exposures as compared to the controls. In roots, the expression of *CAT* showed no significant changes after the exposures to Cu^{2+} ions and 50, 400, and 500 mg dm^{-3} CuONPs. However, a significant increase in the *CAT* expression was observed in roots upon the exposures to 100 and 200 mg dm^{-3} CuONPs (Fig. 1G). The analysis of the expression of the *APX* gene did not show any significant changes in shoots upon the exposures to Cu^{2+} and different concentrations of CuONPs. In roots, no changes in the *APX* gene expression were observed after the exposures to Cu^{2+} and 50 and 100 mg dm^{-3} CuONPs. However, the *APX* expression in roots significantly increased upon the exposures to 200 and 400 mg dm^{-3} CuONPs but decreased upon the exposure to 500 mg dm^{-3} CuONPs (Fig. 1H).

The phytotoxic dose of CuONPs varies between different plant species. For example, according to Wu *et al.* (2012), the phytotoxic doses of CuONPs in lettuce, radish, and cucumber are 12.9, 397.6, and 175.4 mg dm^{-3} , respectively. Since there is not specific regulations for studying the effect of engineered nanoparticles in plants, the guidelines established by the US Environmental Protection Agency (USEPA 1996) is generally followed. Therefore, in this study, the selection of the phytotoxic doses of CuONPs was done based on their effect on inhibition of root growth. It was observed that more than a 50 % reduction in root growth was observed after the exposure to 200 mg dm^{-3} CuONPs. Moreover, the exposure to CuONPs strongly inhibited seedling development, and the inhibition was positively correlated with the concentration of CuONPs. In accordance with our results, Shaw and Hossain (2013) has also reported that shoot and root growth of rice seedlings is significantly reduced under CuONPs stress. However, in this study, it was observed that the exposure to 0.2 mg dm^{-3} Cu^{2+} ions has not affected shoot as well as root development of the green pea seedlings. It is well known that trace amount of Cu is required for normal plant growth and development since it is an essential micronutrient. Therefore, low concentrations of Cu might support seedling development as observed in this study

and elsewhere (Lee *et al.* 2008). In a recent study, Shi *et al.* (2014) also reported that phytotoxicity in a copper tolerant plant *Elshotzia spendens* is due to CuONPs exposure and not as result of exposure to soluble Cu ions or bulk CuONPs. In this study, it was observed that the exposure to the highest concentration of CuONPs significantly reduced the total chlorophyll content in the green pea seedlings, and this might be due to the presence of excess Cu as result of the CuONPs exposure. It has been known from earlier studies that the presence of excess Cu can interfere with enzymes associated with chlorophyll biosynthesis (Maksymiec *et al.* 1994) or can lead to Fe deficiency as result of antagonism between Cu and Fe uptake (Pätsikkä *et al.* 2002). In accordance with our hypothesis, Hong *et al.* (2015) reported that except for CuCl_2 , all Cu treatments including CuONPs significantly reduce Fe content in shoots and roots of alfalfa and lettuce.

In this study, both qualitative and quantitative measurements indicate that the exposure to CuONPs increased ROS generation and lipid peroxidation in roots of the green pea seedlings. Based on the Cu content analysis, it can be assumed that the increase in the Cu content in the CuONPs exposed plants might have enhanced the production of ROS in the green pea seedlings. Since Cu is redox active element, the presence of excess Cu could lead to an increased ROS generation in plants either through Fenton or Haber-Weiss reactions (Takeshi *et al.* 1997), or through interaction with the photosynthetic electron transport system (Sandmann and Boger 1980). It has been known from previous studies that exposure to CuONPs can result in their uptake to the plants (Wang *et al.* 2012) and also lead to their dissolution as result of a reduced pH and interaction with organic acids and proteins inside the plant tissues (Shi *et al.* 2014). Moreover, the up-regulation of the *SOD* gene in roots indicates an excess ROS generation and the conversion of superoxide to H_2O_2 in roots under CuONPs stress (Bowler *et al.* 1992). It is known that cells are protected from the excess accumulation of H_2O_2 either by the action of *CAT* or through the ascorbate-glutathione cycle by the action of *APX* which reduces H_2O_2 to H_2O . However, though the expression of the *CAT* and *APX* genes were up-regulated, incomplete scavenging H_2O_2 might lead to an increased ROS generation and a subsequent increase in lipid peroxidation levels in roots. In recent studies, Shaw and Hossain (2013) and Shaw *et al.* (2014) also reported that though the activity of *APX* increases, the H_2O_2 content in leaves of rice and barley seedlings does not decrease when they are subjected to CuONPs. Enhanced ROS generation as well as lipid peroxidation has also been reported from different biological models and plants under CuONPs stress (Wang *et al.* 2012, Melegari *et al.* 2013, Shaw and Hossain 2013, Nair and Chung 2014, Shaw *et al.* 2014).

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