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Copper Oxide nanomaterial fate in plant tissue: Nanoscale impacts on reproductive tissues

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1 **Copper Oxide nanomaterial fate in plant tissue: Nanoscale impacts on**
2 **reproductive tissues**

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19

20 **Abstract**

21 A thorough understanding of the implications of chronic low dose exposure to Engineered
22 Nanomaterials (ENMs) through the food chain is lacking. The present study aimed to characterize
23 such response in *Cucurbita pepo* L. (zucchini) upon exposure to a potential nanoscale fertilizer:
24 copper oxide (CuO) nanoparticles. Zucchini was grown in soil amended with nano-CuO, bulk CuO
25 (100 mg Kg⁻¹) and CuSO₄ (320 mg Kg⁻¹) from germination to flowering (60 days). Nano-CuO
26 treatment had no impact on plant morphology or growth, nor pollen formation and viability. The
27 uptake of Cu was comparable in the plant tissues under all treatments. RNA-seq analyses on

28 vegetative and reproductive tissues highlighted common and nanoscale-specific component of the
29 response. Mitochondrial and chloroplast functions were uniquely modulated in response to
30 nanomaterial exposure as compared with conventional bulk and salt forms. X-ray Absorption
31 Spectroscopy (XAS) showed that Cu local structure changed upon nano-CuO internalization,
32 suggesting potential nanoparticles biotransformation within the plant tissues. These findings
33 demonstrate the physiological, cellular, and molecular consequences related to nano-CuO application
34 as a plant fertilizer, highlighting the differential mechanisms involved in the exposure to nano-CuO,
35 bulk or salt and the pathways of plant response to minimize environmental and health risk, through
36 sustainable nano-enabled agricultural strategies.

37

38 Keywords: nanomaterials, nanofertilization, RNA-seq, pollen, biotransformation, *Cucurbita pepo*.

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40

41 **Synopsis**

42

43 Fertilization with nanoscale CuO affected zucchini at the physiological and molecular levels, from
44 roots to flowers, with significant internalization and particle biotransformation being evident.

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54 **Introduction**

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56 In recent years, interest in the utilization of nanotechnology to produce nano-enabled materials
57 and delivery platforms to address the progressive inefficiency of mineral fertilization has been rapidly
58 growing.^{1,2} However, these nanomaterials are by their very nature more reactive and bioavailable than
59 traditional forms utilized in agriculture,¹⁻³ and as such, have raised concerns over sustainability and
60 safety with regard to human and environmental health. For example, direct utilization in agriculture
61 raises the clear possibility of food chain contamination from staple plants to humans through the
62 direct consumption of contaminated plant products as could happen with rice, maize and peanuts.^{3,4}
63 In addition, the potential widespread use of engineered nanomaterials (ENMs) as part of “nano-
64 agricultural chemistry” has created concerns over damage to non-target organisms and to potential
65 trophic transfer through terrestrial food chains, through vegetables grazing by simple insects and then
66 spreading out to higher insects and predators.⁵⁻⁹ As such, safety assessment and sustainability
67 evaluation must be a core component in novel materials formulations for agri-food production
68 purposes (e.g. nanopesticides, nanofertilizers).^{1,10-13}

69 A number of recent studies have demonstrated the unique potential of Cu-based nanomaterials
70 in agriculture,^{11,14,15} including field studies demonstrating how materials such as $\text{Cu}_3(\text{PO}_4)_2$ based-
71 nanosheets and commercial CuO NPs can be foliar applied to young seedlings so as to increase plant
72 growth and suppress *Fusarium* spp. infections of tomato (*Solanum lycopersicum* L.) and watermelon
73 (*Citrullus lanatus* L.) in full life cycle studies. Furthermore, Ma *et al.* (2020)¹³ studied how
74 nanomaterial chemistry could be tuned to optimize the effects of pathogen suppression and nutrient
75 release from Cu-based ENMs on sudden death syndrome (SDS) in soybean (*Glycine max* L.),
76 developing a thermodynamic model to describe how morphology and matrix effects are implicated
77 in Cu release and plant response. In addition, Cu-based nanoformulations are known to interact with
78 organic acids in plant root exudates. These interactions significantly influence ENM stability,
79 biotransformation and bioavailability,¹⁶ as well as induce modifications in the plant metabolome.¹⁷

80 The role of Cu nanomaterial bioavailability has also been investigated through trophic transfer
81 experiments, including an assessment of how initial chemical form is impacted by relevant
82 weathering conditions and subsequent material transformation.¹⁸ These findings highlight the
83 importance of controlling ENMs physico-chemical properties (e.g. morphology, composition and
84 dissolution) so as to develop safer and more sustainable nanoscale formulations for agriculture,
85 simultaneously enhancing the targeting and delivery efficiency to optimize utilization of resources
86 while minimizing negative impacts on the environment.¹

87 The current study investigated the potential effects of CuO NPs on zucchini (*Cucurbita pepo*
88 L.) from a morphological, physiological, molecular, and atomic perspective, with a particular focus
89 on gametogenesis and pollen development. Conventional CuO bulk material and CuSO₄ salts were
90 used as controls to clarify nanoscale-specific effects of CuO NPs with regard to its fate within the
91 plant tissues. Particular attention was focused on the function and regulation of chloroplast and
92 mitochondrion activity, which play a critical role in pollen development. The coupling of a global
93 transcriptomic approach (by RNA-seq) with synchrotron-based analyses, such as μ -X-ray
94 Fluorescence (μ -XRF) mapping and Extended X-ray absorption fine structure (EXAFS) spectroscopy
95 of Cu states, enabled a thorough understanding of the connection between the observed biological
96 response and the physico-chemical condition of CuO NPs at a molecular and sub-molecular level in
97 different plant tissues.

98

99 **Methods**

100 *Nanomaterial characterization*

101 Copper oxide nanoparticles (CuO NPs) (99% purity; 40 nm average sized) were purchased
102 from U.S. Research Nanomaterials, Inc. (Houston, TX). Cu represents 79.8% of the total molecular
103 weight of the molecule. CuO NPs were characterized by electron microscopy (TEM, Talos F200S
104 G2, SEM FEG Thermo Fisher Scientific, Waltham, MA, USA) as reported in Figure S1. The average
105 particle size (dh) and zeta (ζ) potential in ddH₂O were 533.9 ± 47.2 nm and of -24.7 ± 1.4 mV as

106 determined by Zetasizer Nano Series ZS90 (Malvern Instruments, Malvern, UK), after sonication by
107 a Fisher Scientific Model 505 Sonic Dismembrator (Fisher Scientific, Waltham, MA) at 40%
108 amplitude for 60s. CuO bulk material and CuSO₄·5H₂O were purchased from Sigma Aldrich (St.
109 Louis, MO, US).

110 For particle dissolution analysis, CuO NPs and CuO bulk solutions (1000 mg L⁻¹) were
111 prepared in ddH₂O, avoiding shaking and light, and portions were collected after 1, 2, 3, 7, and 14d.
112 Aliquots of 1 ml for each sample were precipitated by ultracentrifugation at 30000 rpm, for 10 min,
113 at 20°C (Optima Max-XP Ultracentrifuge, Beckman-Coulter Inc., Brea, CA, USA). The liquid phase
114 was collected and digested in 4 mL of 1M HNO₃ (purity: 67% w/w) for 40 min at 200°C using a
115 VELP DK20 digester (VELP Scientifica, Usmate, Italy). The digests were analysed by flame atomic
116 absorption spectroscopy (FA-AAS; AA240FS, Agilent Technologies, Santa Clara, CA, USA) for the
117 presence of Cu (lamp current: 4 mA; fuel: acetylene; support: air; wavelength 324.7 nm; slit with: 0.5
118 nm; linearity of calibration, R²: 0.9982), in three replicates. The average dissolution for CuO bulk
119 and CuO NPs were between 0.1% and 0.15%, respectively, considering the theoretical value of 100%
120 dissolution of ionic copper in CuSO₄.

121

122 *Plant exposure*

123 *Cucurbita pepo* L. (cv. Costata Romanesco) seeds were pre-germinated in vermiculite
124 amended with Hoagland's Solution (10%) for 10 days prior to transplanting to soil. The Cu
125 concentration administered in pre-germination was about 2 µg Kg⁻¹. Zucchini seeds were purchased
126 from Johnny's Selected Seeds (Albion, ME, USA). The experimental soil was collected from the
127 Connecticut Agricultural Experiment Station (CAES) Lockwood Farm in Hamden, CT, USA.
128 Individual solutions of CuO NPs and CuO bulk material in water (30% water capacity of
129 soil/vermiculite mixture) were probe sonicated by a Fisher Scientific Model 505 Sonic Dismembrator
130 (Fisher Scientific, Waltham, MA) at 40% amplitude for 60–120s to maximize dispersion. Solutions

131 of CuO NPs, CuO (bulk) or (copper sulfate) CuSO₄ were slowly added to pots containing 500g of
132 soil and manually mixed. The final concentration of NPs and bulk CuO in pots was 100 mg kg⁻¹ while
133 for CuSO₄·5H₂O (copper sulfate pentahydrate), the amount was 320 mg kg⁻¹. Considering the
134 molecular weight of the single molecules taken into account, this represented a total concentration of
135 approximately 80 mg kg⁻¹ for all the treatments. Additional data related to the Cu release in treated
136 soils are reported in Supporting Information (SI). The concentrations utilized were chosen to be below
137 the limit considered as potential Cu contamination in soil, and yet still able to provide information on
138 chronic plant exposure.¹⁹⁻²⁰ Furthermore, the low dose utilized and the long growth period (60 days)
139 are indicative of a chronic exposure scenario that is not common in the literature.²¹ Zucchini seedlings
140 were planted (one each pot) and grown indoor under supplemental fluorescent lighting (60 μE m²
141 sec) under a photoperiod of 16h light at approximately 22–28 °C until flowering. Plants were top
142 watered during a 60-d growth period. For all the conditions, ten biological replicates were included.

143

144 *Pollen morphology and pollen viability*

145 Alexander's staining protocol was used to test pollen viability. Free anthers were collected
146 when pollen was mature but anthers were still non-dehiscent (stage 12-13), and were fixed in
147 Carnoy's fixative (6 ethanol: 3 chloroform: 1 acetic acid) for 2h. Mature pollen was collected and
148 stained as described in Peterson *et al.* (2010).²² After staining, all aborted and non-aborted pollen
149 grains were counted using a Zeiss Apotome 2 microscope at 20x magnification (Zeiss, Oberkochen,
150 Germany). Pollen grains were analysed fresh with no fixation or staining; they were collected from
151 mature flowers and positioned on 2 cm diameter stainless-steel sample holder (stub) covered with
152 adhesive carbon tape. An environmental scanning electron microscope (ESEM) FEG2500 FEI (FEI
153 Europe, Eindhoven, The Netherlands) operating in low-vacuum (60 Pa) with LFD (Large Field
154 Detector) was used to enable optimal Secondary Electron (SE) imaging. The cone PLA (Pressure
155 Limiting Aperture) of 500 μm improved the signal available to the Bruker X-ray detector,

156 QUANTAX XFlash. SE imaging was performed at 10 KeV with a beam size of 2.5 μm , EDX analysis
157 at 20 KeV acceleration voltage, final lens aperture of 40 μm , and beam size of 4 μm . SE images and
158 EDX spectra were collected from samples treated with CuO NPs, CuO bulk and untreated controls.

159

160 *Metal uptake measurement*

161 Flowers harvested for elemental analyses were sampled and thoroughly rinsed with tap water,
162 MilliQ water (resistivity: 18.2 M Ω cm) and 2% HNO₃ (0.01 M) to remove soil and surface-attached
163 NPs. To determine Cu content in the tissues, fresh samples were dried at 100 °C for 72 h and digested
164 in HNO₃ (purity: 67% w/w) at 115 °C, 25 min. After 30 min, 1 mL of H₂O₂ (purity: 30 % w/w) was
165 added to each digestion tube and the samples treated for an additional 30 min prior dilution to 50 mL
166 with ddH₂O. The digested samples from the 10 biological replicates per treatment were analysed by
167 inductively coupled plasma mass spectrometry (ICP-MS) Agilent 7500ce (Agilent Technologies,
168 Santa Clara, CA) for Cu presence (63 amu). The digests Cu content were quantified against a five-
169 point calibration curve based on certified reference material (SPEX CertiPrep, Metuchen, NJ, USA),
170 and that had been previously evaluated for linearity (R²: 0.9999) and accuracy. Analytical blanks,
171 matrix blanks, and calibration verification samples were included in each sequence.

172 Roots, stems, leaves and flower biomass samples were collected after 60-d for elemental analysis.
173 Samples (10 replicates for each tissue) were digested as in the case of ICP-MS analyses and analysed
174 by Atomic Absorption Spectroscopy (AAS) (AA240FS device, Agilent Technologies, Santa Clara,
175 CA; lamp current: 4 mA; fuel: acetylene; support: air; wavelength 324.7 nm; slit with: 0.5 nm;
176 linearity of calibration, R²: 0.9993). AAS analyses were conducted with a four-point calibration curve
177 based on standard reference material (SPEX CertiPrep, Metuchen, NJ). Biomass and Cu content in
178 all tissues were evaluated by a one-way ANOVA with a pairwise Tukey's multiple comparison test
179 (IBM SPSS v. 26.0).

180

181 *RNA extraction and whole transcriptome analysis*

182 RNA samples were extracted from 0.1 g (fresh weight) of pollen, leaves or roots samples from
183 unamended control, CuO NP, CuO bulk and CuSO₄ treatments. Total RNA was extracted from 0.1 g
184 of fresh plant material using a Sigma-Aldrich Spectrum Plant Total RNA Kit (Sigma-Aldrich, St.
185 Louis, MO). Three biological replicates per treatment were used. Total RNA quality was assessed by
186 gel electrophoresis and RNA quantity was determined using a Thermo Scientific Nanodrop Lite
187 Spectrophotometer (Thermo Fisher Scientific, Wilmington, DE). Samples were sent to IGA
188 Technologies Srl (Udine, IT) for RNA sequencing service. TruSeq Stranded mRNA kit (Illumina,
189 San Diego, CA) was used for library preparation following the manufacturer's instructions. RNA
190 samples were quantified and quality tested by Agilent 2100 Bioanalyzer RNA assay (Agilent
191 Technologies, Santa Clara, CA). Final libraries were checked Agilent Bioanalyzer DNA assay
192 (Agilent Technologies, Santa Clara, CA). Libraries were prepared for sequencing and sequenced on
193 single-end 75 bp mode on NextSeq 500 (Illumina, San Diego, CA). Alignment of reads to the
194 reference transcriptome available on Cucurbitgenomics database (<http://cucurbitgenomics.org/>)²³
195 was performed using STAR software with default parameters. The resulting raw data have been
196 normalized and the differentially expressed genes were identified using a 2.3 threshold of FPKM data
197 (in log₂). Data have been deposited in the NCBI GEO database (accession number GSE173716).

198 A student *t* test was applied for analysis of homogeneity of variance, statistical analysis for
199 scatter plots, box and whiskers graphs. A principal component analysis (PCA) was performed with R
200 statistical software (www.r-project.org). Venny bioinformatics tool
201 (<http://bioinfogp.cnb.csic.es/tools/venny/>) was used for the generation of Venn diagrams. Gene
202 Ontology (GO) analysis and *A. thaliana* ortholog gene identification was performed by the
203 Cucurbitgenomics database. The GO term enrichment analysis was conducted using a cut-off p-value
204 of 0.05 for cellular components and biological processes, and 0.03 for relevant pathways,

205 respectively. Network analysis was performed using the GeneMANIA data service
206 (<http://www.genemania.org/>) using *A. thaliana* orthologues genes.

207

208 *Samples preparation for synchrotron-based analyses*

209 μ -XRF and XANES analyses were performed at ELETTRA, Sincrotrone Trieste, in order to
210 analyse Cu presence and distribution in tissues; root, leaf and flower samples (0.1 g, fresh weight)
211 were cut and submerged in glutaraldehyde triphosphate in Eppendorf tubes for fixation. After three
212 days the samples were dehydrated in gradients of alcohol (from 25 to 100%) and fixed with epoxy
213 resin following Kurth et al. (2009).²⁴ To analyse potential variations in local structures within the
214 tissues, bulk X-ray Absorption Spectroscopy (XAS) analyses at BM08 “LISA” beamline at ESRF
215 have been performed. The protocols described in Marmioli et al. (2020)²⁵ were applied. Briefly,
216 samples were mixed with pure cellulose powder (Sigma Aldrich, St. Louis, MO, USA) and pressed
217 into 1.3 cm diameter pellets using an amount of material sufficient to keep the total absorption (μ)
218 ≤ 1.5 above the edge.

219

220 *Low Energy μ -XRF (LE μ -XRF)*

221 μ -XRF analyses in the soft X-ray regime were performed at the TwinMic beamline at
222 ELETTRA, Sincrotrone Trieste, Italy.²⁶ For the present experiment, the TwinMic microscope was
223 operated in scanning transmission mode (SXM), the beam was focused on the sample through a zone
224 plate (600 μ m in diameter with a 50 nm outermost zone width), and a micrometric or sub-micrometric
225 probe size was delivered. While the sample was raster-scanned perpendicularly to the incoming
226 monochromatic beam, a fast readout CCD camera collected the transmitted X-rays and an 8-silicon
227 drift detector-based XRF system acquired the emitted fluorescence photons.²⁷ The obtained
228 absorption and phase contrast images outline the morphological features of the sample at sub-

229 micrometer length scales, whereas the simultaneous detection of the low energy μ -XRF correlates the
230 elemental distribution to the morphology. The elemental distribution was then obtained by
231 deconvolving and fitting the XRF spectra with PyMCA software.²⁸ A photon energy of 1.26 keV was
232 used to excite and obtain optimal emission conditions for the elements of major interest (Cu, Na, Ni
233 and Fe) with a spot size of 1.45 μm and a dwell time of 8 s per pixel for XRF mapping and a CCD
234 dwell time of 50 ms per SXM imaging. Each map lasted approximately 5-7 h, depending on the
235 dimensions of the scanned area.

236

237 *XRF and X-ray absorption near edge structure (XANES) mapping*

238 Zucchini root and flower thin section samples were also investigated by means of XRF
239 mapping and XAS at the XRF beamline, ELETTRA Sincrotrone Trieste (Italy)²⁹ which covers a
240 different energy range compared to TwinMic and allows detection of heavier elements and K lines of
241 transition metals. The experiment was conducted using a Si(111) monochromator and standard
242 45°/45° geometry for fluorescence mode measurements, using an XFlash 5030 SDD (Bruker, Berlin,
243 Germany). Higher order harmonics contamination was suppressed by a pair of parallel plane mirrors
244 intercepting the beam in grazing incidence. Thin sections of samples embedded in resin were sealed
245 between two Mylar foils and fixed on the Al sample holder using a Delrin interlocking ring. This
246 design was necessary to secure the samples and to have a system compatible with the working
247 conditions of the Ultra High Vacuum Chamber (UHVC, 10^{-7} mbar) available at the XRF beamline.
248 XRF maps were collected with an incident beam energy of 10 keV and a beam size at the exit slits of
249 200x100 μm^2 (HxV) to inspect the elemental distribution. Based on the XRF maps acquired on the
250 samples (data not shown), the areas with higher content of Fe, Cu and Zn were selected to collect
251 XANES spectra at the relative K-edges. The Si(111) monochromator was calibrated before the
252 measurements using reference metal foils. All spectra were collected using 5 seconds per step and a
253 variable energy step as a function of the energy: Large step (5 eV) in the first 200 eV of the spectrum,

254 smaller step (0.2 eV) in the near-edge region and a k-constant step of 0.07 \AA^{-1} further above the
255 absorption edge. Multiple spectra were collected and merged in order to increase the signal to noise
256 ratio. The oxidation state was determined using least-squares Linear Combination Fitting (LCF) based
257 on reference spectra collected on compounds of known oxidation state. Background removal,
258 normalization of XANES spectra and LCF analyses were performed using the ATHENA software
259 package.³⁰

260

261 *Extended X-ray absorption fine structure (EXAFS)*

262 Extended X-ray absorption fine structure (EXAFS) measurements at the Cu K-edge (8978.9
263 eV) were performed at the LISA CRG beamline (BM08)³¹ at the European Synchrotron Radiation
264 Facility (ESRF, Grenoble, France) using plant samples and three model compounds: CuO (bulk),
265 CuO NPs and $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$. The main optical features of the beamline were a fixed exit
266 monochromator with a pair of Si(111) crystals (energy resolution $\Delta E/E \approx 1.33 \cdot 10^{-4}$); Si mirrors were
267 used for harmonics rejection (E cutoff $\approx 15 \text{ KeV}$). Energy was calibrated with a Cu reference foil
268 (8978.9 eV). Spectra of plant samples were acquired at 80 K, in order to minimize beam-induced
269 damage, with a constant k step of 0.05 \AA^{-1} up to a maximum k value of 12.5 \AA^{-1} ; model compounds
270 were measured at room temperature with a k step of 0.03 \AA^{-1} up to $k=18 \text{ \AA}^{-1}$. Plant samples were
271 measured in fluorescence mode with a 12-element HP-Ge detector,³² while model compounds were
272 measured in transmission mode. Multiple spectra were collected and merged in order to increase the
273 signal to noise ratio. ATHENA software³⁰ was used to calibrate the energy and to average multiple
274 spectra. Standard procedures were followed to extract the structural extended EXAFS signals
275 ($k \cdot \chi(k)$), including pre-edge background removal, spline modelling of bare atomic background, edge
276 step normalization, and energy calibration.³³ Model atomic clusters centered on the absorber atom
277 were obtained by ATOMS;³⁴ theoretical amplitude and phase functions were generated using the

278 FEFF8 code.³⁵ EXAFS spectra were fitted through the ARTEMIS software in the Fourier-Transform
279 (FT) space.³⁰

280

281 **Results and Discussion**

282 *Pollen morphology and viability*

283 Pollen grain morphology was analysed by ESEM of transverse sections of developing mature
284 anthers; no overt differences were observed across treatments (Figure S2a). Pollen viability was also
285 evaluated to determine the male gametophyte developmental stage and the preservation of plant
286 reproductive fitness. Similar to morphology, there were no differences across CuO NP, CuO bulk and
287 CuSO₄ treatments as compared to the untreated control, with a pollen viability approximately 100%
288 in all cases (Figure S2b).

289 Previous studies have demonstrated that copper can be toxic to seed and pollen germination,
290 pollen viability and pollen tube growth; Sharafi (2014)³⁶ showed that high concentrations (250 mg
291 Kg⁻¹) of copper cause an almost complete inhibition of pollen germination and pollen tube
292 lengthening in almond (*Prunus dulcis* (Mill.) D.A. Webb cultivars). Similar results were observed in
293 *Pisum sativum*, where copper (35-700 mg Kg⁻¹) was highly toxic to pollen germination.³⁷ It is unclear
294 if zucchini exhibits a unique tolerance to copper; importantly, few studies have investigated the
295 potential effects of copper nanomaterials on pollen formation and maturation. Kumbhakar *et al.*
296 (2016)³⁸ showed that both copper and cadmium-based NPs reduced pollen fertility in black cumin
297 (*Nigella sativa* L.), both during pollen formation and in developmental maturation process. Similarly,
298 in *Coriandrum sativum* L. CdS NPs and CuO NPs induced physiological alterations and cytological
299 aberrations in meiotic cells, and decreased viability of pollen.³⁹ The alteration types and frequencies
300 in meiotic cells of *C. sativum* following NPs treatments (0.25-1 mg L⁻¹) were less severe than those
301 reported in *Nigella sativa*.³⁸ Notably, in the present study the Cu concentration used was specifically
302 selected to be below the limit considered for Cu contamination in soil.¹⁹⁻²⁰

303

304 *Plant biomass and metal content*

305 After flowering, plants were harvested, and the fresh mass of roots and shoots was measured
306 (Table S1-S2). Treatment with CuO, CuO NPs and CuSO₄ had no impact on zucchini biomass (fresh
307 weight) compared to untreated control. These results align with much of the present literature,
308 showing that exposure to CuO NPs did not negatively impact the biological parameters in agricultural
309 crops. Tamez et al. (2019)⁴⁰ reported no significant changes in zucchini root and leaf biomass upon
310 exposure to comparable concentrations of CuO NPs. Pagano et al. (2016)²¹ demonstrated that CuO
311 NPs had no effect on *C. pepo* biomass at a higher concentration (500 mg Kg⁻¹) and with an
312 experimental design that provided greater direct interaction between NPs and tissues (vermiculite
313 growth media). Alternatively, studies conducted with the model plant *Arabidopsis thaliana* grown in
314 hydroponic conditions showed a strong reduction in root length after exposure to CuO NPs (10-20
315 mg L⁻¹).⁴¹ These contrasting results demonstrate the importance of CuO NPs dose to biological
316 response, and also highlight the influence of growth medium, plant species, and the exposure time to
317 observed effects.

318 The Cu content in soil and in the different tissues of zucchini plants was determined by Atomic
319 Absorption Spectroscopy (AAS), as shown in Table S3. The Cu content in soil was determined (14.18
320 mg Kg⁻¹) in order to justify the concentrations utilized for the experiment, highlighting a different
321 metal release percentage within the soil, starting from the same relative concentration of Cu
322 potentially available of 80 mg Kg⁻¹ (salt > NP > bulk). Although there was a trend for increased Cu
323 content of tissues with all Cu treatments, only plant roots from the CuSO₄ exposure were significantly
324 increased. To validate the AAS results on flowers, analysis of the Cu content was performed also by
325 Inductively Coupled Plasma Mass Spectrometry (ICP-MS). Here, results show that the Cu content
326 from the CuO NPs and bulk material treatment was 43 and 30% (significant at p<0.05) greater than
327 the untreated control, respectively (Table S4). This finding demonstrates that CuO NPs addition to
328 the soil does result in Cu accumulation in the reproductive tissues, although there is no difference

329 based on particle size. However, these results were impacted by instrument limits of detection (ICP-
330 MS: $0.04 \mu\text{g L}^{-1}$ vs AAS: 0.05mg L^{-1}) and quantitation (ICP-MS: $0.1 \mu\text{g mL}^{-1}$ vs AAS: 0.1mg L^{-1}).
331 A previous study from our group focused on zucchini exposed to nanoscale Cu evaluated a broad set
332 of physiological assays, including chlorophyll content, mitochondrial functionality, and metal content
333 in different plant tissues (roots, stems, leaves), and also demonstrated significant Cu translocation
334 from roots to both stems and leaves.²¹

335

336 *RNA-seq data analysis: critical aspects related to the CuO NP molecular response*

337 Given the evidence of an active translocation of Cu into reproductive tissues, the plant
338 transcriptomic response of different tissues and organs to exposure was evaluated using the high-
339 quality assembly of the *C. pepo* genome (NCBI BioProject PRJNA386743, sequences length 263
340 Mbps; 34240 ORFs) published on Cucurbitgenomics database.²³ Statistical analysis of RNA-seq
341 datasets showed high homogeneity between treatments in the different tissues, with comparable
342 averages and dispersions (Figures S3-S6). After normalization to the untreated control, comparison
343 across CuO NPs, CuO bulk and CuSO₄ exposure in roots showed 4420, 6540, and 4747 differentially
344 expressed genes in the three treatments, respectively. In leaves, the CuO NPs treatment showed a
345 lower number of differentially expressed genes compared to the other treatments: 3122 genes were
346 up- or down-regulated with CuO exposure, whereas the values for CuO bulk and CuSO₄ were 9924
347 and 9103, respectively. The number of differentially expressed genes in CuO NPs exposed pollen
348 was also markedly lower in comparison to the treatments in the other tissues: 1829, 2112 and 2163
349 respectively for CuO NPs, CuO bulk and CuSO₄ treatments. This large quantitative difference in gene
350 expression was certainly related with a larger number of different biological processes performed in
351 roots and leaves, as compared to pollen, but could be also due to the lower amount of the Cu (in
352 different forms) translocated to pollen.

353 Venn diagrams of up- and down-regulated genes in roots (Figure 1) and the relative GO
354 enrichment (Supplementary Information, SI2) data show that the transcripts in common among all
355 the tested conditions were only 4.3% and 16.3% of total genes up- and down-regulated, respectively.
356 In the roots, the specific molecular responses to the three different treatments were largely
357 independent of each other, as shown by the low percentage of gene functions common among all the
358 three conditions tested and by the two-by-two common classes. Metabolic processes and ribosome
359 translation were the most highly represented groups in biological processes related to CuO NPs and
360 CuO bulk (Figure 2; details in Supplementary Information, SI2), together with mitochondrial activity.
361 In the CuSO₄ treatment, unlike the NPs and bulk exposure, a nuclear component was represented,
362 and this can be related to greater Cu ion toxicity.⁴² The percentage of genes commonly up- or down-
363 regulated in leaves was similar to that observed in roots: 4.7% and 16.4% total shared genes,
364 respectively (Figure 1). The percentage of genes in common between CuO bulk and CuSO₄ increased
365 dramatically, both for up- and down-regulated transcripts, to 40.1% and 46.6%, respectively. This
366 observation may correlate with the Cu ion release from the CuO bulk material within the plant tissues,
367 which seems to be higher than for CuO NPs, in spite of the similar dissolution rate in ddH₂O. Genes
368 involved in metabolic and energetic processes are among the more enriched genes; in addition, GO
369 terms related to chloroplast genes are well represented, as are genes for abiotic stimuli response
370 (Figure 2; details in Supplementary Information, SI3). Previous studies with *A. thaliana* highlighted
371 the role of chloroplast as a potential target of ENMs exposure.⁴³ Wang *et al.* (2016)⁴⁴ showed that
372 CuO NPs block electron transport between the two photosystems which can cause an excessive ROS
373 accumulation and oxidative stress, damaging biological molecules and disrupting of cellular
374 metabolism. Furthermore, CuO NPs strongly up-regulate ZAT12, a transcription factor implicated in
375 abiotic stress response, with a key role in ROS signalling pathway and co-expressed with ORF31, a
376 chloroplastic electron carrier involved in photosynthesis that has been identified as a potential
377 biomarker of ENM exposure.²¹ In pollen, the percentage of genes up- or down-regulated common to
378 all treatments increased as compared to the leaves and roots: 25.5% and 33%, respectively (Figure

379 1). The percentage of genes up- and down-regulated specifically related to CuO NPs response is
380 significant (21.1% and 12.5%), when compared to the other two treatments. This data strengthens the
381 idea that CuO NPs were not only translocated (intact or modified) into the floral parts of the plant,
382 but once there, they trigger a “nanoscale-specific” response which is different from the response
383 observed in roots and leaves. These results likely reflect a multifaceted response, including partial
384 dissolution of CuO NPs and CuO bulk giving rise to a “non-specific Cu response”, along with a non-
385 dissolved component exerting a nanoscale-specific response. It is also reasonable to suppose that
386 amount of Cu²⁺ derived from the three treatments increased as a consequence of the interaction with
387 plant organs and tissues.

388 Pollen has a significantly lower number of expressed genes as compared to the vegetative
389 tissues, but data highlight some pollen-specific functions and other components which have been
390 described as unique to sporophyte tissues.⁴⁵ The difference between the leaves was related to the low
391 level of expression of genes involved in energy metabolism, especially photosynthesis, since pollen
392 is not photosynthetically active. Another difference between treated and untreated plants was in
393 pollen with higher expression level of genes with functions in ion transport, cell-wall and starch
394 metabolism, and cytoskeleton dynamics (Figure 2; details in Supplementary Information, SI4).
395 Previous studies showed that polarized internal gradients and/or external fluxes of protons, potassium,
396 and chloride had a role in pollen tube function,⁴⁶ but that ion channel and transporter involvement in
397 ion fluxes across the plasma membrane in pollen tubes is still largely unknown. Starch biosynthesis
398 during the final phases of pollen maturation is fundamental because starch is a reserve source of
399 energy for pollen survival and it may also act as a metabolic checkpoint for pollen maturity. This
400 pathway is prematurely aborted whenever starch levels remain below a critical amount, strongly
401 linking pollen viability to starch deficiency.⁴⁷ A key aspect of pollen tube tip growth is the constant
402 construction of new cell wall and plasma membrane at the tube apex. Vesicles delivering this material
403 are mediated by the actin cytoskeleton.⁴⁸

404 The whole transcriptome analysis of *C. pepo* treated with CuO NPs showed interesting
405 insights from a functional point of view. Chloroplast and mitochondrial function were critical in
406 regulating the response to CuO NPs and the energy metabolism in all plant tissues, which becomes
407 primarily mitochondrial functionality in pollen formation and development (Figure 2; details in
408 Supplementary Information, SI5). A network analysis produced for chloroplast genes in leaves, and
409 for mitochondrial genes in roots, leaves and pollen, respectively, shows the physical interactions
410 between the reported gene targets (Figures S7-S10). Genes highlighted in heatmaps and Venn
411 diagrams (Figure 3) showed a certain specificity to CuO NPs response, in particular in roots and
412 leaves. In the case of pollen, the percentage of common regulated genes among CuO NPs, CuO bulk
413 and CuSO₄ treatment is increased (Figure 3), suggesting that during translocation from roots to shoots
414 there was an increase in ionic Cu presence. Additional information about potential sensitive targets
415 in pollen development, derived from the study of orthologue genes in the yeast *S. cerevisiae*, were
416 investigated, highlighting a certain level of commonality in the response with the RNA-seq analyses.
417 Results are reported and described in Supplementary information (Table S5, and Figure S11).

418

419 *CuO NPs biotransformation*

420 μ -XRF analyses performed at the TwinMic beamline,²⁶ an example of which is depicted in
421 Figure 4, showed that in the root sections, Cu in general was mainly detectable on cell walls and more
422 visible in the treatments with CuSO₄, followed by nanoparticle and bulk forms where Cu content was
423 very close to TwinMic detection limits; the higher presence of Cu in the treatments with CuSO₄ salt
424 is due to the salt dissociation in the soil and followed by ready Cu accumulation in the roots. Notably,
425 the roots were thoroughly washed before the resin embedding procedures to avoid external
426 contamination. Fe was highly present in all root samples, including the controls, likely because it was
427 abundant in the soil. The roots maps for Cu (Figure 4a) are consistent with those obtained by Servin
428 *et al.* (2017).¹⁸ In the flower samples (Figure 4b), it is possible to observe the pollen sacs and the

429 completely developed pollen grain; one exception is for the CuSO_4 treatment, where the pollen sacs
430 were noticeably smaller and possessed fewer pollen grains. Interestingly, Cu was present in the roots,
431 in particular in the cell wall, where other elements such as Ca, which is an important cofactor in
432 building of the cell wall, are known to be present.⁴⁹ In CuO bulk treatment Cu was almost not
433 detectable in roots. Although the resolution of the maps does not allow nanoparticle visualization, the
434 EXAFS analyses (Table S6, Figure 5) confirm that CuO NPs in the plants were biotransformed. This
435 suggests that cellular and molecular activities remodel and biotransform the nanoparticles. Cu was
436 present in the flowers treated with all the three types of Cu-based materials, but there were minimal
437 differences in the signal intensity and in the localization of the element. The treatment with CuO NPs
438 did not hinder formation of the flower or pollen and did not result in overt phytotoxicity, but there
439 were nanoscale-specific molecular effects at the transcriptomic levels as described by RNA-seq
440 analysis. The same was true for the bulk Cu treatment, although treatment with CuSO_4 did appear to
441 negatively affect gamete formation. The idea of a biotransformation of CuO NPs once within the
442 plant tissues has been reported in the literature; Servin et al. (2017) reported that after treatment,
443 transformed CuO NPs products were detected in roots as Cu_2O , Cu_2S and Cu-acetate.¹⁸ These
444 biotransformation processes significantly influence NPs bioavailability and effects in plants,
445 including broad main metabolic and physiological processes, as well as gametogenesis.^{18,50}

446 Figure 5 shows normalized XANES and EXAFS spectra of the plant samples, together with
447 those of the model compounds CuO, CuO NPs and $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ and the EXAFS multiparameter fits.
448 Both XANES (results shown in Figure S12) and EXAFS features show that the CuO NPs structure is
449 closely related to the CuO bulk structure. EXAFS multiparameter fits (Table S6) were performed on
450 both CuO samples based on the tenorite structure,⁵¹ yielding the same results in terms of interatomic
451 distances and path degeneracies, with both refined parameters closely agreeing with the theoretical
452 ones. EXAFS quantitative results on plant samples (Figure 5, Table S6) clearly indicate that the CuO
453 structure is not fully preserved within the plants tissues, in particular in the roots, and that after uptake,
454 the particles are biotransformed over time, leading to Cu^{2+} release starting in roots and increasing up

455 to the flower. Specifically, the prominent signal at $R > 4.5 \text{ \AA}$ in the Fourier Transform (FT) spectra
456 in both CuO bulk and NPs is not visible any longer in plant samples. Moreover, the peaks at $R < 4.5$
457 \AA are markedly weakened. In addition, no overt differences are observable among plant samples
458 treated with two different CuO types. First, shell distances in both roots and flowers are typical of
459 Cu^{2+} in square planar coordination with O and thus compatible with a remnant structure of CuO.
460 However, the Cu local environment in the higher shells shows small differences between roots and
461 flowers. Indeed, a second Cu-O shell path is systematically present in both flowers and roots at
462 significantly different distances: $\approx 2.7 \text{ \AA}$ in roots and 2.8 \AA in flowers. Moreover, a Cu-Cu path at
463 $\approx 3.55 \text{ \AA}$ is always present in roots while the same path could not be fitted in flowers, the only
464 exception being plants treated with CuSO_4 , where the path distance is much longer (3.79 \AA). In shoots
465 of the Cu hyperaccumulator plant *Crassula helmsii*, Kupper et al. (2009)⁵² reported Cu^{2+} O ligands
466 at 2.001 \AA , indicating Cu bonds with small organic acids. Mijovilovich et al. (2009)⁵³ studied the
467 leaves of *Nocca caerulescences* (ecotype Ganges), an hyperaccumulator plant of Cd and Zn but
468 sensitive to Cu, reported ligands for Cu^{2+} at 1.9 \AA sulfur atoms, indicating ligands with S rich
469 molecules, and at 4.5 \AA , a double ligand Cu-Cu that they attributed to Cu biomineralization. These
470 findings do not align with our results and this is likely due to plant species differences;
471 hyperaccumulator plants having a unique and specific metabolic profile that is different from that of
472 non-hyperaccumulator species such as *Cucurbita pepo*.

473

474 *Environmental implications*

475 Given the essential role of Cu to the plant life cycle and its biotic response to disease, there
476 has been significant interest in its use as a potential nanofertilizer. However, in certain plants and
477 under certain concentrations, phytotoxicity has been observed. In the present study, the effect of three
478 types of Cu (CuO NPs, CuO bulk, and CuSO_4) was compared in *C. pepo* using a broad range of
479 physiological and molecular endpoints, with a focus on the process of male gametogenesis and pollen

480 production, which are essential to reproduction and from fruit formation and ultimately, to plant yield.
481 In a dioic species such as zucchini, gamete fertilization depends primarily on pollen quality and
482 vitality of the parental plant, which then mediates fruit production. From the morphological and
483 physiological perspective, as inferred by ESEM and XRF analyses, there were few differences
484 between the three forms of Cu (CuO NPs, CuO bulk and CuSO₄) in the roots, but as the Cu was
485 translocated to the flower, the CuSO₄ treatment exerted a more marked negative effect on pollen
486 viability. This increasing toxic response likely was a function of the complete dissolution to Cu²⁺ ions
487 in this medium and the increased reactivity of Cu in this form. Conversely, the NP form exerted
488 almost no effects on pollen and exhibited a reduced stimulation of Cu uptake, possibly being a
489 function of Cu complexed to organic ligands within the plant tissues that mitigated chemical
490 dissolution. The CuO bulk material results for the molecular and physiological endpoints were more
491 similar to CuSO₄, in spite of the CuO bulk and CuO NPs dissolution behavior in ddH₂O being quite
492 similar. Interesting, some nanoscale materials release ions at a greater rate than bulk materials, due
493 to increased surface area and volume.¹⁴ However, coatings, complexation and corona formation could
494 modulate dissolution. The transcriptomic analysis of the different tissues and flowers showed that
495 metabolic processes and ribosome translation were highly represented among the most responsive
496 pathways. Chloroplast and especially mitochondrial functions were particularly affected in response
497 to CuO NPs, which agrees with previous data and aligns with the organelle's role in energy
498 metabolism in all plant tissues,⁴⁴ and specifically in pollen formation and development. In addition,
499 the EXAFS features demonstrate the occurrence of CuO NPs biotransformation, highlighting a
500 similar Cu local environment from roots to flowers. The similarity of the Cu environment after
501 different treatments seemed to depend more on the plant tissue than on the type of treatment,
502 suggesting that the biotransformed Cu environment is reached after substantial dissolution of Cu ions,
503 followed by stabilization of Cu in complexes whose nature is more dependent on the plant
504 characteristics than on the type of treatment. Indeed, the transcriptomic data showed that at the
505 molecular level, the response was partially nanoscale-specific, including in the pollen. Similar

506 phenomena have been reported for other nanomaterials such as CeO₂ NPs and CdS QDs.^{25,54} The
507 evidence for the formation of Cu ions when CuO NPs are accumulated by the plants and the fact that
508 still there is a certain level of nanoscale-specific response suggests that *in planta* biotransformation
509 processes are significant and critical to overall plant response. Overall, this suggests nanoscale CuO
510 NPs as nanofertilizers likely presents minimal concerns to general plant health. A thorough and
511 mechanistic understanding of these processes such as that provided by this study will be necessary to
512 ensure the safe and sustainable application of Cu-based and other nanoscale materials in nano-enabled
513 agricultural strategies.

514

515

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525

526 **Authors contribution**

527 MM, LP, NM and JCW coordinated the study and designed the experiments. RR, LP and RD
528 performed individual experiments and analysed the physiological and molecular data in with
529 collaboration of MM and RRu. AG, GA, performed the synchrotron analyses in Trieste with
530 collaboration of SP, GG and VB. AP, FA and GOL (remotely) performed the XAS measurements at

531 LISA BM08 beamline at ESRF; GOL performed EXAFS data analysis in collaboration with FA. All
532 authors contributed to manuscript revision and approved the final version.

533

534 **Conflict of interest**

535 The authors declare no conflict of interest.

536

537

538 **Supplementary Information (SI) description:**

539 *Supplementary information included (SI1):*

540 Method section and results for qPCR of genes involved in gametogenesis

541 Results of LCF analysis of XANES spectra

542 Figure S1: CuO nanoparticles visualization by TEM

543 Figure S2: ESEM micrographs pollen grains and pollen viability assay

544 Figure S3: Statistics of the genes datasets from roots samples

545 Figure S4: Statistics of the genes datasets from leaves samples

546 Figure S5: Statistics of the genes datasets from pollen samples

547 Figure S6: PCA of all data profiles

548 Figure S7: Gene network of chloroplast targets observed in leaves treated with CuO NPs

549 Figure S8: Gene network of mitochondrial targets observed in roots treated with CuO NPs

550 Figure S9: Gene network of mitochondrial targets observed in leaves treated with CuO NPs

551 Figure S10: Gene network of mitochondrial targets observed in pollen treated with CuO NPs

552 Figure S11: Heatmap transcriptomics genes involved in meiosis and gametogenesis

553 Figure S12: XANES fits and relative K-edge data

554 Table S1: Biomass of roots and shoots

555 Table S2: Flower biomass

556 Table S3: Copper concentration measured in soil, roots, shoots and flowers by AAS

557 Table S4: Copper concentration measured in flowers by ICP-MS

558 Table S5: Genes' information and primer sequences utilized in Real time PCR assay

559 Table S6: EXAFS multiparameter fit details for studied samples and
560 reference compounds

561

562 *Supplementary information reported in excel format:*

563 Supplementary Information 2 (SI2): GO analysis of up- and down-regulated genes exposed to CuO
564 NPs, CuO bulk and CuSO₄ in roots.

565 Supplementary Information 3 (SI3): GO analysis of up- and down-regulated genes exposed to CuO
566 NPs, CuO bulk and CuSO₄ in leaves.

567 Supplementary Information 4 (SI4): GO analysis of up- and down-regulated genes exposed to CuO
568 NPs, CuO bulk and CuSO₄ in pollen.

569 Supplementary Information 5 (SI5): *A. thaliana* ortholog genes analysis of relevant chloroplast and
570 mitochondrial targets isolated from *C. pepo* exposed to CuO NPs, CuO bulk and CuSO₄ in roots,
571 leaves and pollen.

572

573

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742 **Figure captions:**

743 Figure 1. Comparison of high-throughput transcriptional datasets related to the molecular response
744 of *C. pepo* in condition of treatment with CuO NPs, CuO bulk and CuSO₄, in the roots (a), leaves (b),
745 pollen (c), represented with Venn diagrams. Up-regulated and down-regulated genes are reported on
746 left and right side, respectively. Percentage of identity between CuO NPs, CuO bulk and CuSO₄ is
747 also reported. Data were normalized on the untreated controls, with a 2.3 threshold of raw data (in
748 log₂). Data highlighted an increase in the percentage of common genes involved in the response to
749 the three different Cu-based forms from roots to pollen, suggesting an increased bioavailability of
750 free Cu in the plant shoots.

751

752 Figure 2. GO biological processes expressed in percentage (%) of gene cluster enriched, related to
753 roots (a), leaves (b), and pollen (c) related to the treatment with 100 mg kg⁻¹ of CuO NPs. Up-
754 regulated and down-regulated genes are reported as blue and orange bars, respectively. Additional
755 details related to GO analyses in the different tissues are available in Supplementary Information,
756 SI2-SI4.

757

758 Figure 3. Heatmaps and Venn diagrams comparison of the genes involved in chloroplast functions in
759 response to CuO NPs, CuO bulk and CuSO₄, in leaves (a), and in mitochondrial functions identified
760 in roots (b), leaves (c) and pollen (d) tissues. Data related to the specific genes are reported in
761 Supplementary Information, SI5. Data confirmed the increase in percentage of common modulated
762 genes from roots to pollen in response to the three different Cu-based forms utilized for the treatments.

763

764 Figure 4. μ -XRF maps of (a) roots and (b) flowers from plants treated with CuO NPs. Names of the
765 mapped elements are on top of each figure. The maps are related to the black and white square on top
766 left (Abs) which is the 20x image of the cells in the root tissue and pollen sac tissues treated with
767 CuO NPs. Cu map is always the last in the second row for (a) and (b).

768

769 Figure 5. XANES spectra of the measured samples and model compounds (a). Cu K-edge k^2 -weighted
770 EXAFS region (b) and Fourier transforms (c) of plant tissues and model compounds. Solid lines are
771 data, red lines are fits. Energy was calibrated with a Cu reference foil (8978.9 eV). In order to
772 minimize beam-induced damage, spectra of samples were acquired at 80 K with a constant k step of
773 0.05 \AA^{-1} up to a maximum k value of 12.5 \AA^{-1} for plant tissues while model compounds were measured
774 at room temperature with a k step of 0.03 \AA^{-1} up to $k=18 \text{ \AA}^{-1}$. Plant samples were measured in the
775 fluorescence mode with a 12-element HP-Ge detector.

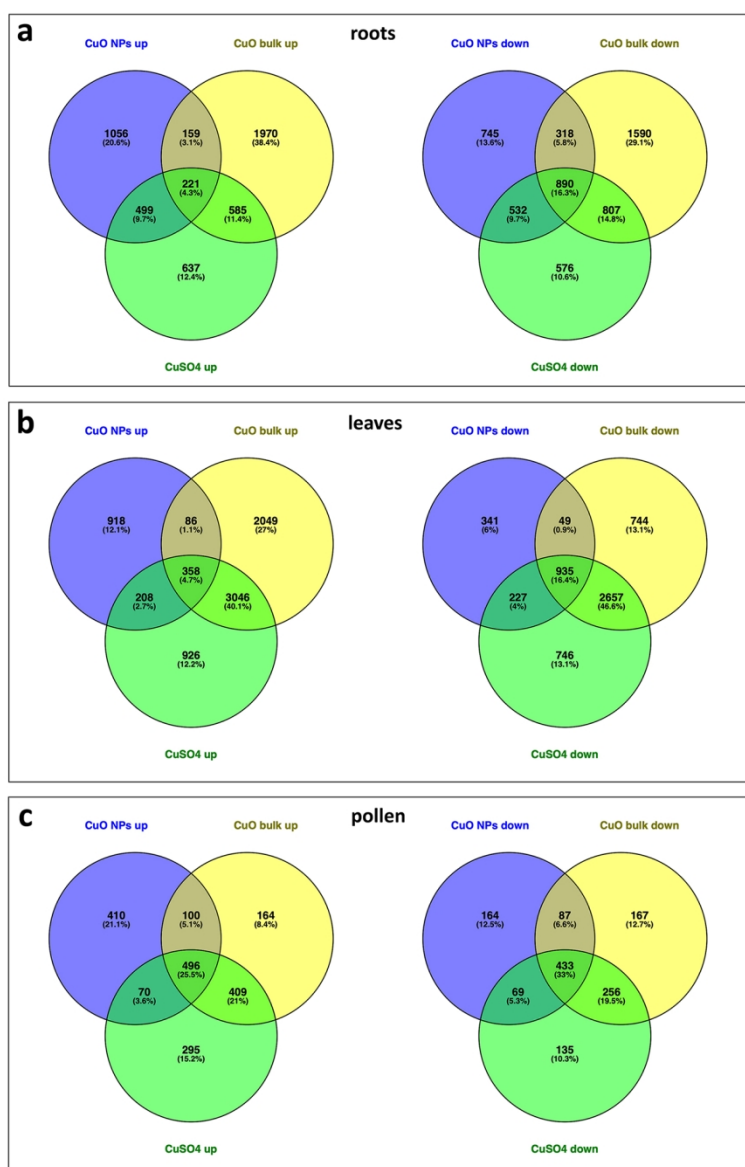


Figure 1. Comparison of high-throughput transcriptional datasets related to the molecular response of *C. pepo* in condition of treatment with CuO NPs, CuO bulk and CuSO₄, in the roots (a), leaves (b), pollen (c), represented with Venn's diagrams. Up-regulated and down-regulated genes are reported on left and right side, respectively. Percentage of identity between CuO NPs, CuO bulk and CuSO₄ is also reported. Data were normalized to the untreated controls, with a 2.3 threshold of raw data (in log₂). Data highlighted an increase in the percentage of common genes involved in the response to the three different Cu-based forms from roots to pollen, suggesting an increased bioavailability of free Cu in the plant shoots.

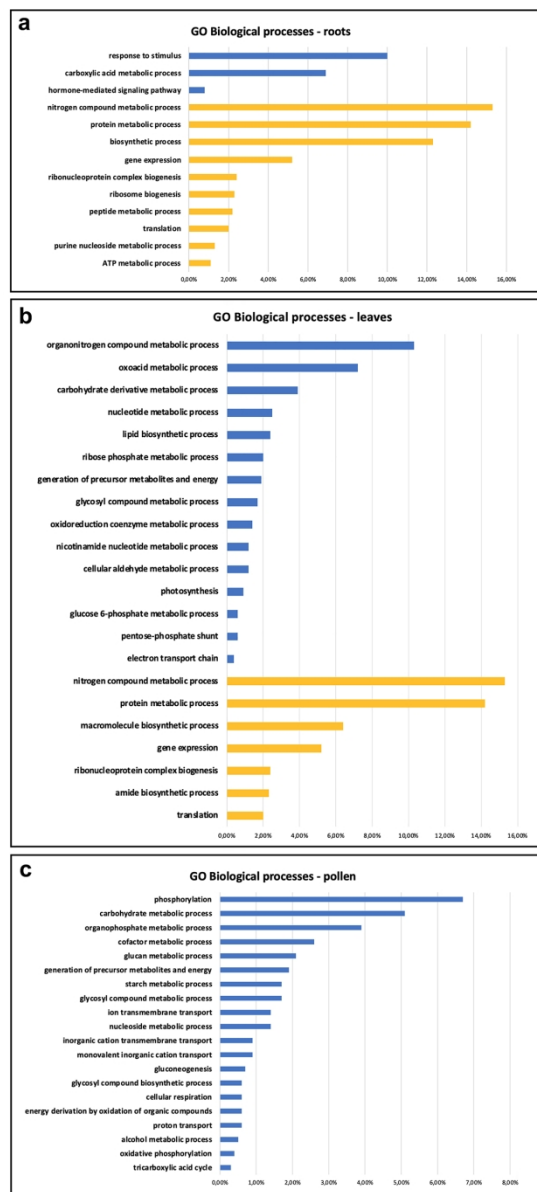


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101x223mm (300 x 300 DPI)

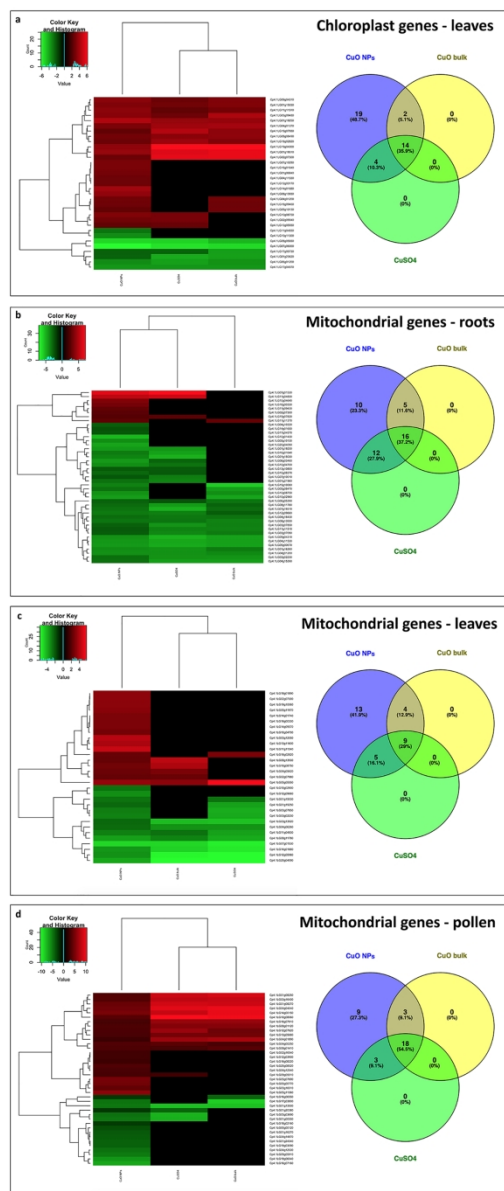


Figure 3. Heatmaps and Venn's diagrams comparison of the genes involved in chloroplast functions in response to CuO NPs, CuO bulk and CuSO₄ in leaves (a), and in mitochondrial functions identified in roots (b), leaves (c) and pollen (d) tissues. Data related to the specific genes are reported in Supplementary Information, SI5. Data confirmed the increase in percentage of common modulated genes from roots to pollen in response to the three different Cu-based forms utilized for the treatments.

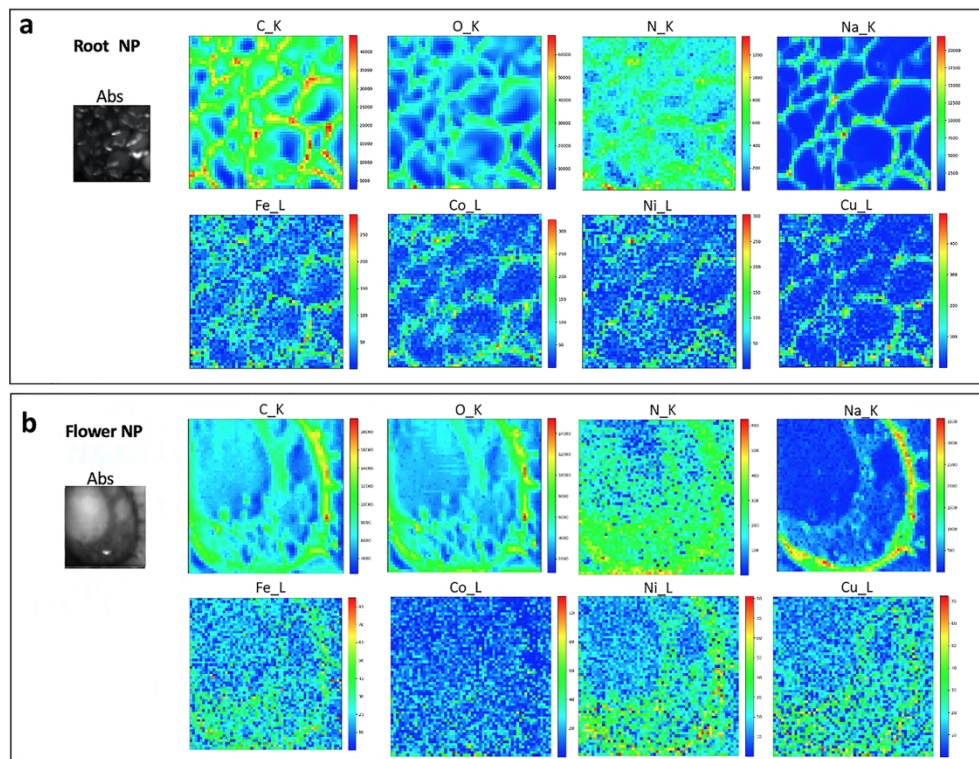


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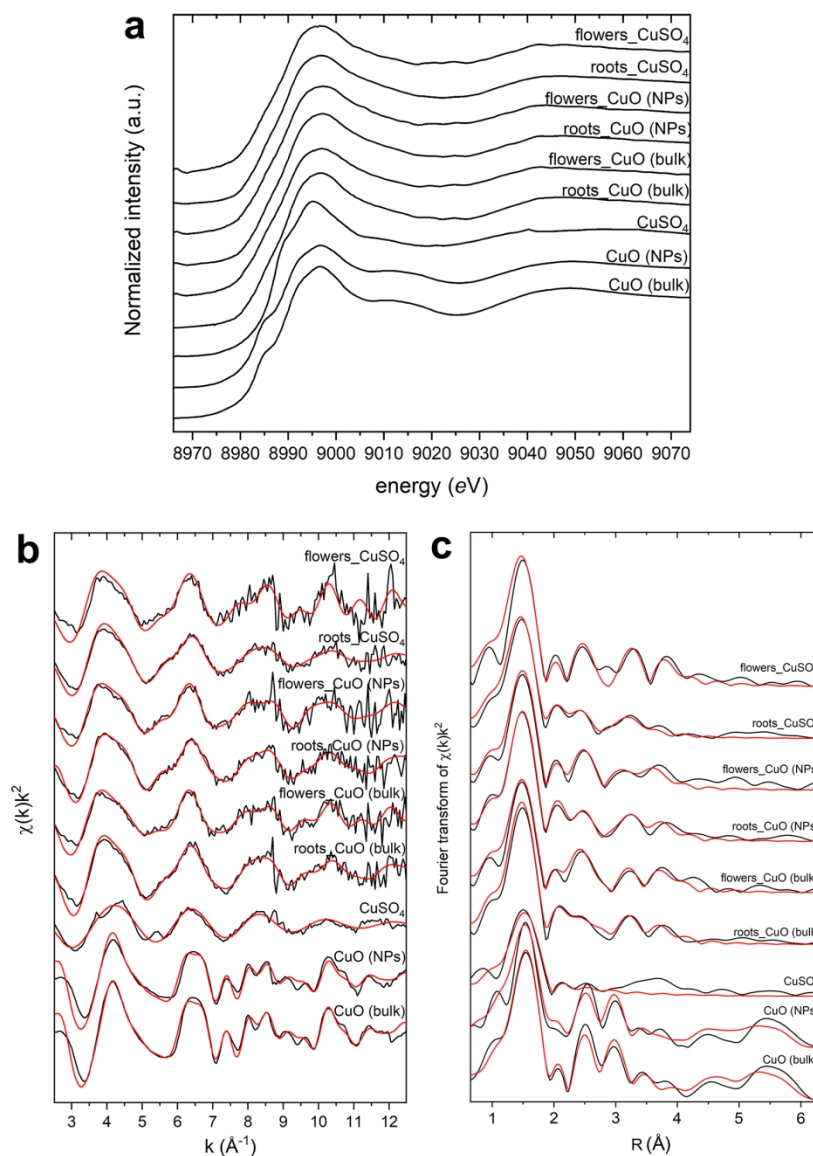


Figure 5. XANES spectra of the measured samples and model compounds (a). Cu K-edge k²-weighted EXAFS region (b) and Fourier transforms (c) of plant tissues and model compounds. Solid lines are data, red lines are fits. Energy was calibrated with a Cu reference foil (8978.9 eV). In order to minimize beam-induced damage, spectra of samples were acquired at 80 K with a constant k step of 0.05 Å⁻¹ up to a maximum k value of 12.5 Å⁻¹ for plant tissues while model compounds were measured at room temperature with a k step of 0.03 Å⁻¹ up to k=18 Å⁻¹. Plant samples were measured in the fluorescence mode with a 12-element HP-Ge detector.