

Green tea infusion prevents diabetic nephropathy aggravation in recent-onset type 1 diabetes regardless of glycemic control

Luiz Carlos Maia Ladeira, Eliziária Cardoso dos Santos, Talita Amorim Santos, Janaina da Silva, Graziela Domingues de Almeida Lima, Mariana Machado-Neves, Renê Chagas da Silva, Mariella Bontempo Freitas, Izabel Regina dos Santos Costa Maldonado

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Luiz Carlos Maia Ladeira, Eliziária Cardoso dos Santos, Talita Amorim Santos, Janaina da Silva, Graziela Domingues de Almeida Lima, et al.. Green tea infusion prevents diabetic nephropathy aggravation in recent-onset type 1 diabetes regardless of glycemic control. Journal of Ethnopharmacology, 2021, 274, pp.114032. 10.1016/j.jep.2021.114032. hal-03229076

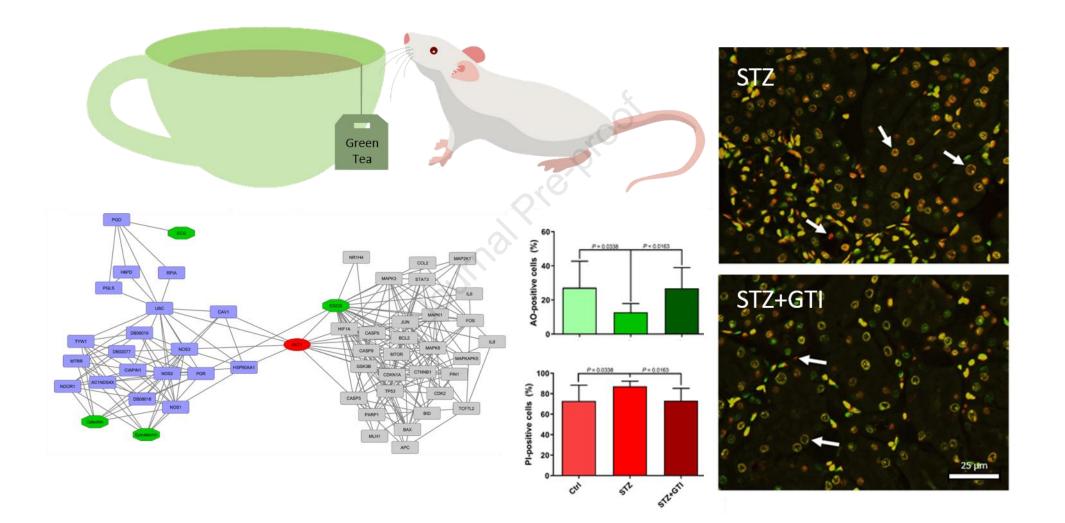
HAL Id: hal-03229076 https://hal.science/hal-03229076

Submitted on 31 May 2021 $\,$

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1	Green tea infusion prevents diabetic nephropathy's aggravation in recent-onset
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3	Running title: Tea and diabetic nephropathy
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34 Abstract

Ethnopharmacological relevance: Green tea, traditionally used as antidiabetic medicine, affects positively the diabetic nephropathy and it was assumed that these beneficial effects were due to the tea's hypoglycemiant capacity, reducing the glycemic overload and, consequently, the advanced glycation end products rate and oxidative damage. However, these results are still controversial because tea is not always able to exert a hypoglycemic action, as shown by previous studies.

40 Aim: Investigate if green tea infusion can generate positive outcomes for the kidney independently41 of glycemic control, using a model of severe type 1 diabetes.

42 Material and methods: We treated streptozotocin type 1 diabetic young rats with 100 mg/Kg of 43 green tea, daily, for 42 days, and evaluated the serum and tissue markers for stress and function, 44 also, we analyzed the ion dynamics in the organ and the morphological alterations promoted by 45 diabetes and green tea treatment. Besides, we analyzed, by an in silico approach, the interactions of 46 the green tea main catechins with the proteins expressed in the kidney.

47 Results: Our findings reveals that the components of green tea can interact with proteins 48 participating in cell signaling pathways that regulate energy metabolism, including glucose and 49 glycogen synthesis, glucose reabsorption, hypoxia management, and cell death by apoptosis. Such 50 interaction leads to reduced accumulation of glycogen in the organ, as well as protects DNA. These 51 results also reflect in a preserved glomerulus morphology, with improvement in pathological 52 features, and suggesting a prevention of kidney function impairment.

53 Conclusion: Our results show that such benefits are achieved regardless of the blood glucose status,
54 and are not dependent on the reduction of hyperglycemia.

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56 Keywords:

57 Diabetic nephropathy; type 1 diabetes; recent-onset diabetes; diabetic kidney disease; green tea.

58 **1. Introduction**

59 Diabetic nephropathy (DN) affects 25% - 35% of type 1 and 2 diabetic patients (Herman-60 Edelstein and Doi, 2016), and account for about 45% of the patients with end-stage renal disease 61 (Su et al., 2020). It progresses from the increase in the glomerular filtration rate to the total failure of the kidneys, passing through alterations that indicate damage to the renal glomeruli and tubules, 62 63 albuminuria, mesangial expansion, fibrosis, and vascular damage (Gilbert, 2017; Herman-Edelstein 64 and Doi, 2016). In addition, glycogenic accumulation in the proximal tubules is a common feature in DN, and one of the earliest signals of metabolic impairment in the organ (Gilbert, 2017; 65 66 Haraguchi et al., 2020). Such damage can progress in renal cells to pre-neoplastic lesions which, if 67 left untreated, may progress to renal cancer (Ribback et al., 2015).

Green tea (Camellia sinensis (L.) Kuntze (Theaceae)), popularly used as a traditional 68 medicine, in the form of infusion, for many porpoises including hyperglycaemia (Barkaoui et al., 69 70 2017; Chopade et al., 2008; Fallah Huseini et al., 2006; Rachid et al., 2012), is known to exert positive effects in diabetes management (Meng et al., 2019; Mohabbulla Mohib et al., 2016). 71 72 Recent studies have shed light on the mechanisms that tea catechins affect positively the DN, with 73 special focus on the podocyte (Hayashi et al., 2020), through the activation of the 67kDa laminin 74 receptor (67LR) by the epigallocatechin gallate (EGCG), the main polyphenol in green tea. Such interaction results in the preservation of podocyte morphology and the glomerular filtration 75 function, suggesting an improvement in DN. However, tubular alterations, with glycogen 76 77 accumulation, and aberrant activation of the advanced glycated end-products and its receptor 78 (AGE/RAGE system), affecting the cellular renovation and survival, are seem to be the primary cause of proximal tubular function disruptment (Haraguchi et al., 2020). This, in turn, can affect 79 80 glomerular function by the proximal tubule/glomerulus feedback system, leading to glomerular damage and contributing to the progression of DN. 81

82 It was assumed that the beneficial effects of the green tea on proximal tubules were due to the tea's hypoglycemiant capacity (Renno et al., 2008; Yokozawa et al., 2012), reducing the 83 84 glycemic overload and consequently AGE rate and oxidative damage. However, tea effects in 85 diabetic human subjects are still controversial. The first double-blind controlled trial treating diabetic patients (being 100% type 2 diabetic) with green tea polyphenols describes a reduction in 86 podocyte apoptosis and an improvement of kidney function by reducing microalbuminuria (Borges 87 88 et al., 2016). Another double-blind controlled trial conducted with diabetic adult patients (being 89 70.3% type 1 diabetic) fail to achieve glycemic control or improve renal function after green tea consumption (Vaz et al., 2018). On the other hand, tea catechins can inhibit gluconeogenesis by 90 91 activating the 5'AMP-activated protein kinase (AMPK) (Collins et al., 2007), possibly reducing 92 glycogenic nephrosis. Also, EGCG can activate the protein kinase B (AKT) pathway enhancing cell survival and preserving nephron morphology (Hayashi et al., 2020). These effects may contribute to 93 94 the prevention of DN development in recent-onset diabetes (Haraguchi et al., 2020).

In a previous study, we demonstrated that the infusion of green tea was not able to prevent hyperglycemia in animals with experimental type 1 diabetes induced by streptozotocin (STZ) in young male Wistar rats (Ladeira et al., 2020a). Therefore, in the same model, we tested the hypothesis that the beneficial effects of tea in DN go beyond glycemic control. In this way, we investigated the effects of green tea infusion treatment on diabetic kidney disease in recent-onset type 1 diabetic young rats. Also, we used bioinformatics tools to explore tea catechin interaction in signaling pathways in the kidney.

103 **2. Materials and methods**

104 2.1. Animals and ethics

Eighteen male Wistar rats (30 days old; 82.52 ± 10.83 g) were housed, two per cage, in polypropylene cages with autoclaved sawdust as cage bed, under controlled conditions of temperature (22 ± 2 °C) and light-dark cycles (12/12h), and received food (Presence Alimentos, Paulínea, SP, Brazil) and water *ad libitum*. The use of animals in the research was approved by the Ethics Committee of Animal Use of the Federal University of Viçosa (CEUA/UFV – protocol number 53/2018).

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112 2.2. Green tea infusion preparation and analysis

Green tea (*Camellia sinensis*) leaves were obtained from Leão[®] - Food and Beverages (Coca-Cola Company[®], lot LO159), and prepared as infusion, to mimic the way it is normally consumed by humans. The infusion was prepared mixing the leaves with warm distilled water (1:40 w/v, 80 °C) (Perva-Uzunalić et al., 2006). The mixture remained infused for 20 minutes on a magnetic stirrer. Then, it was filtered through a 0.45 µm porous filter, frozen at -80 °C and lyophilized. The lyophilized samples were resuspended in distilled water at the moment of use.

The chromatographic profile, or fingerprint, was determined as described by Kim-Park et al. 119 120 (Kim-Park et al., 2016), with some modifications. High-performance liquid chromatography (HPLC) (Prominence LC-20A, Shimadzu, Kyoto, Japan), equipped with Diode Arrangement 121 Detector (DAD), LC-20AD pump, SPD-M20A detector, CTO-20A oven and LabSolutions 122 123 software, was used to determine the EGCG content using a maximal absorption peaks at 272nm. It was used a Vydac C18 (4.6 x 250 mm) column, at 30 °C, with a 5µL injection volume. The mobile 124 phase was composed of water and 2.0% acetic acid (1:1). The infusion lyophilized powder was 125 126 suspended in methanol before analysis. The mobile phase flow rate was 1.0 mL/min and the run

time was 15 min. The retention time of the main component, EGCG, was 4.5 min and the total amount of it was calculated using a standard curve ($r^2 = 0.9967$) developed under the same conditions using an EGCG chemical standard ($\geq 98.0\%$, Sigma Aldrich Inc. - CAS Number 989-51-5. St. Louis, MO, USA). The EGCG content was shown to be 19.38% of the total GTI content. The fingerprint is presented in the Figure 1.

Also, we determined the total phenolic content and antioxidant capacity as previously described (Ladeira et al., 2020a). GTI presented a total amount of phenolic components of $3.88 \pm$ 2.49 mg gallic acid equivalent (GAE)/g GTI. The extract presented an antioxidant capacity of $3.26 \pm 0.06 \mu$ Mol Trolox equivalent (TE)/g GTI in the 2,2'-Azinobis-[3-ethylbenzthiazoline-6-sulfonic acid] (ABTS) assay and $46.38 \pm 4.10 \mu$ Mol FeSO4/g GTI in the ferric reducing antioxidant power (FRAP) assay.

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- 139

140 2.3. Experimental design, euthanasia, and tissue collection

141 Twelve rats were randomly selected to integrate the diabetics groups. After 12h fasting, diabetes 142 was induced by a single intraperitoneal (i.p.) injection of streptozotocin (STZ) (Sigma Chemical Co., St, Louis, MO, USA) at a dosage of 60 mg/kg of body weight (BW) diluted in 0.01 M sodium 143 144 citrate buffer, pH 4.5. The healthy control group (n=6) received the buffer alone (i.p.) to simulate 145 the injection stress. Fasting blood glucose levels were measured after 2 days using a glucometer 146 (Accu-Chek® Performa, Roche LTDA. Jaguaré, SP, Brazil) in blood samples collected at the tail vein. All STZ-injected animals presented the fasting glycemia levels higher than 250 mg/dL and 147 148 were included in the study. The diabetic rats were divided into two groups (n=6, each). Therefore, 149 the experiment consisted of three groups: the healthy control group (Ctrl, n=6), which received water as a placebo; the diabetic control group (STZ, n=6), which also received water; and the 150 151 diabetic group treated with the green tea infusion (STZ+GTI, n=6), that received the GTI (100

mg/kg body weight). All treatments were administered by gavage, daily, for 42 days. The dosage was equivalent to 7 cups (200mL) of tea, prepared according to the manufacturer instructions, mimicking a feasible human consumption dosage, considering survey data from the Asian population (Mineharu et al., 2011).

We monitored body weight and water consumption using a precision scale (BEL M503,
e=0.001g, Piracicaba, SP, Brazil), and 12h fasting blood glucose using test strips and a glucometer
(Accu-Chek® Performa, Roche LTDA. Jaguaré, SP, Brazil) in blood samples from the tail vein.

After the experimental period, the animals were euthanized by deep anesthesia (sodium thiopental, 60 mg/kg i.p.) followed by cardiac puncture and exsanguination. The kidneys were removed and weighed. One kidney (right) of each animal was frozen in liquid nitrogen and stored at -80 °C for enzymatic analysis, the other one (left) was immersed in Karnovsky fixative solution for 24h for histopathological analyses. The renal somatic index (RSI) was calculated using the ratio between the kidney weight (KW) and BW, where $RSI = KW/BW \times 100$ (Sertorio et al., 2019).

165

166 2.4. Renal function markers

Blood samples collected by cardiac puncture at the euthanasia were centrifuged at 4600 rpm for 168 15 min at 4 °C and the serum was separated. Then we performed the analysis for quantification of 169 urea and creatinine in the serum using biochemical kits (Bioclin Laboratories, Belo Horizonte, MG, 170 Brazil) at the BS-200 equipment (Bioclin Laboratories, Belo Horizonte, MG, Brazil) following the 171 manufacturer's instructions.

173 2.5. Antioxidant enzyme and nitric oxide analysis

174 The antioxidant enzyme analysis was performed with the supernatant obtained from 100 mg of frozen kidney tissue homogenized in ice-cold phosphate buffer (pH 7.0) and centrifuged at 12000 175 176 rpm for 10 minutes at 4 °C. The activity of the superoxide dismutase enzyme (SOD) was assessed by the pyrogallol method based on the ability of this enzyme to catalyze the reaction of the 177 superoxide (O^{-2}) and hydrogen peroxide (H_2O_2) (Dieterich et al., 2000). The glutathione S-178 179 transferase (GST) activity was measured according to the method of Habig et al. (1974), and calculated from the rate of NADPH oxidation. The activity of catalase (CAT) was determined by 180 181 measuring the kinetics of hydrogen peroxide (H_2O_2) decomposition as described by Aebi (1984). The nitric oxide $(NO_2^{-1} \text{ and } NO_3^{-1})$ levels were quantified by the Griess method (Ricart-Jané et al., 182 2002). The values of enzyme activities were normalized by the total protein content, determined 183 184 with the Folin–Ciocalteu method according to Lowry et al. (1994).

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186 2.6. Determination of Ca^{2+} , Na^+/K^+ , Mg^{2+} , and total ATPase activities

187 The ATPase activity was determined following the procedure described by Al-Numair et al (2015). Briefly, 100mg of kidney fragments were homogenized in Tris-HCl buffer (0.1M, pH 7.4) 188 and centrifuged at 12000 rpm for 10 min at 5°C. The supernatant was used for the determination of 189 190 the ATPase activity using NaCl, KCl, MgCl, and CaCl solutions at 0.1M. ATP solution (0.1M) was 191 used as a substrate to generate free phosphate by the ATPases. The reaction was stopped with a cold 192 solution of 10% TCA. Then, we centrifuged at 6000 rpm for 10 min and the supernatant was used to 193 determine the inorganic phosphorus content by the Fiske and Subbarow method (Fiske and 194 Subbarow, 1925). The ATPase activities were expressed as µMol of inorganic phosphorus/min mg of protein. 195

197 2.7. Chemical elements analysis

198 The proportion of chemical elements in the renal cortex was assessed per area in fragments of 199 frozen kidney, as described before (Ladeira et al., 2020b). We measured the proportion of sodium 200 (Na), magnesium (Mg), chlorine (Cl), potassium (K), and calcium (Ca). Fragments were dried at 60 201 °C for 96h, coated with carbon (Quorum Q150 T, East Grinstead, West Sussex, England, UK), and 202 analyzed in a scanning electron microscope (JEOL, JSM-6010LA) with a Silicon Drift type X-ray detector system. The analysis was performed in an area of 50 µm², using an accelerating voltage of 203 204 20 kV and a working distance of 10 mm. The results were expressed as a mean value of the 205 proportions between the elements present in the samples.

206 2.8. Histopathological and stereological analysis and assessment of DNA damage

207 The fragments fixed in Karnovsky solution were then dehydrated in a crescent ethanol series 208 and embedded in Historesin® (Leica, Nussloch, Germany). A rotary microtome (RM 2255, Leica Biosystems, Nussloch, Germany) was used to cut the material into histological sections of 3 µm 209 210 thickness, then, the section was mounted in glass slides and reacted with periodic acid and Schiff 211 reagent (PAS), and counterstained with hematoxylin for histopathological and stereological 212 evaluation. The analysis was carried as described before by Sertorio et al (2019). Also, slices 213 stained with Toluidine Blue - Sodium borate 1% were used to analyze qualitatively the glomeruli 214 morphopathological features. We analyzed 40 glomeruli, randomly photographed, per experimental 215 animal.

DNA damage was evaluated in sections of the kidney cortex stained with acridine orange (AO; green) and propidium iodide (PI; red) (Bernas et al., 2005; Suzuki et al., 1997). This fluorescent stain allows to evaluate the DNA damage, as damaged DNA presents red color, marked with PI, and integral DNA is marked in green by the AO (Dias et al., 2019). Digital images were captured using a photomicroscope (Olympus AX 70 TRF, Tokyo, Japan) and analyzed with Image-Pro Plus® 4.5 (Media Cybernetics, Silver Spring, MD) software according to Lima *et al* (2018).

223 2.9. Statistical analysis

224	All the results were submitted to the Shapiro-Wilk test to check normality. The data expressed
225	as percentages were transformed by angular transformation before the analysis. Results were
226	expressed as mean \pm standard deviation (mean \pm SD) and analyzed using unpaired <i>t</i> -test when the
227	variances are equal (by F test) and unpaired t -test with Welch's correction for data with unequal
228	variances (Ctrl vs STZ; STZ vs STZ+GTI). The non-parametric data were compared with the
229	Mann-Whitney test. The correlation analysis was carried out following Pearson's correlation
230	method, as the analyzed data were normally distributed. Statistical significance was established at P
231	$\leq 0.05.$

232

233 2.10. In silico pathway exploration

After the in vivo experiment, we explored, through an in silico approach, the interactions of green tea catechins with proteins, in search of possible signaling pathways involved in the generation of the observed effects. For this, we built and analyzed a network of interactions based on information from the STRING and STITCH databases (Szklarczyk et al., 2017, 2016).

238 A chemo-biology interactome network was built to elucidate the interactions between the tea 239 compounds (catechins) and proteins expressed in the kidneys related to the positive effects founded 240 in the in vivo experiment with diabetic rats. A prospective evaluation of compound-protein interactions (CPI) was done with the STITCH v.5.0 database (http://stitch.embl.de/) (Szklarczyk et 241 242 al., 2016). The CPI settings were done according to (de Godoi et al., 2020). Briefly, the network 243 downloaded from the database was limited to no more than 50 interactions, medium confidence 244 score (0.400), network depth equal to 1, and the following methods of predictions were activated: 245 experiments, databases, co-expression, and predictions. The search was set to retrieve results for

seven green tea catechins (Catechin, Catechin gallate, Epicatechin, Epicatechin Gallate, Epigallocatechin Gallate, Gallocatechin, and Gallocatechin Gallate), using the *Homo sapiens* species. All the catechins were imputed individually in the search, however, only four (Catechin, Epicatechin, Epicatechin Gallate, and Epigallocatechin Gallate) retrieve results of interactions, generating four small CPI subnetworks (data not showed), that were used in the posterior analysis.

251 The four catechin-proteins network analysis was performed using Cytoscape v.3.8.0 252 (Shannon, 2003). The four subnetworks were merged using the merge tool with the union function of the software. Then, we "STRINGfy" the resultant network, through the STRING v.1.5.1 253 (Szklarczyk et al., 2017) to enable the protein interaction functions analysis. After that, we 254 255 performed the Molecular Complex Detection analysis to detect clusters (i.e. densely connected regions) that may suggest functional protein complexes, with the MCODE v.1.6.1 app (Bader and 256 257 Hogue, 2003). To that, the app was set up as described before (de Godoi et al., 2020). An MCODE score was calculated for each cluster. Additionally, the Reactome Pathways (Jassal et al., 2020) 258 259 related to diabetic nephropathy pathogenesis were selected.

To identify proteins that could be considered as a key regulator of essential biological processes to the network da network, we performed a centrality analysis, using the CentiScaPe v.2.2 app (Scardoni et al., 2009) for Cytoscape. This app identifies the node (i.e. protein) that has a central position in the network by measuring the "betweenness" and "degree" of the node. Nodes with high betweenness and degree levels are named "bottlenecks" and are more probable to connect different clusters in the network (Yu et al., 2007).

The functional information about all the network proteins, as the tissue-specific expression score and the cellular location score, was accessed by the ClueGO v.2.5.7 and CluePedia v.1.5.7 apps (Bindea et al., 2013, 2009). The Specific Organ Expression Score (SOES) was accessed in this analysis and a filter to protein expression was used to apply the SOES to the PPI (Protein-Protein Interactome). Protein functions were accessed in the Human Gene database - GeneCards

(<u>http://www.genecards.org/</u>) (Rebhan et al., 1998) and compared with the functions related to their
effects in diabetic nephropathy, described in the scientific literature.

273

274 **3. Results**

275 3.1. Experimental results

Diabetic animals showed classical signs of polydipsia (Table 1) and polyuria observed during the experiment (noted in the cage bed). The initial body weight was maintained throughout the experimental period in the animals of the two diabetic groups, indicating a stagnation in the body weight gain, and a commitment of the body development by hyperglycemia, when compared to the healthy control group. Both diabetic groups remain severely hyperglycemic, and green tea infusion did not reduce blood glucose levels in the treated group.

The kidney weight was reduced in the diabetic groups when compared with the Ctrl group (P < 0.0001) and it was reflected in the kidney somatic index (P < 0.0001). In addition, this result may be related to the body development impairment due to hyperglycemia, as showed by bodyweight reduced values. These data are presented in Table 1.

The serological analysis revealed that diabetes increased the serum levels of urea and the GTI did not act modifying this parameter (Figure 2, A). In the same way, creatinine levels were also higher in the diabetic groups than the healthy control without effect by GTI treatment (Figure 2, B).

The GTI was capable of inducing a higher activity of GST enzyme (Figure 3, C), and nitric oxide levels were increased in both diabetics groups, without any effect of GTI treatment (Figure 3, D). The activity of SOD and CAT in the kidney were not impacted by diabetes or GTI treatment in the kidney.

Figure 4 shows the measurements of microelements and ions that participate in the filtration and reabsorption dynamics in the kidney. Despite diabetes have not affected any of the elements

analyzed (Figure 4, A – F), green tea infusion altered Mg and Cl amounts compared to the STZ group (Figure 4, B and D). Although all altered values (Mg and Cl) remain between the Ctrl normal reported values, the relationship between all these elements were impaired by diabetes (Figure 4, G), and GTI was not able to restore the homeostatic environment of ion dynamics. Additionally, we detected a reduced activity of the Na⁺/K⁺ ATPase pump in the diabetic group (Figure 4, H). The Ca²⁺ and Mg²⁺ ATPases, as the total ATPase activity were not affected.

301 Histopathological analysis revealed a reduced glomerular volume in the diabetic groups (Figure 5, C), despite no differences in the glomeruli number per area (mm²) (Figure 5, B). Sections 302 303 of the healthy control group did not show any pathological feature, and the measurements are compatible with the described ones for the species. However, the diabetic groups presented an 304 abnormal accumulation of glycogen in the tubules, known as glycogen nephrosis. The volume of 305 glycogen accumulation in the diabetic group was increased compared with the Ctrl group (Figure 5, 306 D), however the GTI treatment was able to prevent the glycogen granules accumulation in the 307 308 diabetic animals (Figure 5, D).

Diabetes led to a reduced proportion of AO-positive cells in the renal cortex (Figure 6, A), indicating a reduced proportion of cells without DNA damage. A direct consequence of that is the increased proportion of IP-positive cells, shown in Figure 6, B. On the other hand, GTI was able to counteract these effects, improving the proportion of AO-positive cells (Figure 6, A), and reducing the proportion of the IP-positive cells (Figure 6, B).

Glomerular morphological analysis reveals diabetic glomerulus surrounded by flattened epithelial cells, with pathological alterations that were less frequent in the group treated with GTI. Diffuse mesangial expansion was more frequent, present in almost every glomeruli in the STZ group. Bowman's capsule lesions were more frequent in the untreated diabetic than in the STZ+GTI group. Nodular mesangial expansion was not observed in any group. Moderate dilation in the lumen of the proximal tubule was more frequent in the STZ group. Also in the STZ group, the basal region

of the proximal tubular cells presented the accumulation of aggregated stained granules, more densely than in the healthy group, possible mitochondria aggregation (Itagaki et al., 1995).
Furthermore, karyocytomegaly was frequently observed in the STZ group and less frequency in the STZ+GTI group, as so as cytoplasmatic microvesicles, possibly lipid droplets, in the proximal tubule cells (Figure 7).

325 3.2. Virtual analysis

The STRING network is presented in Figure 8, A, and highlights the two main functional clusters (Cluster 1 and Cluster 2). The Reactome Pathway analysis for each cluster is summarized in Table 2. The centrality analysis showed that protein kinase B 1 (AKT1) is the protein classified as the "bottleneck" in the network and has the capacity to integrate the functional pathways that participate in the catechins effects in the kidney (Figure 8, B). The implications of AKT1 in green tea induced signaling in diabetic nephropathy are discussed below. All proteins in the PPI network are expressed in the normal kidney in different degrees.

333

334 4. Discussion

335 Our results showed that green tea infusion treatment was able to prevent glycogen 336 accumulation in the renal tubules, reduce the DNA damage caused by the hyperglycemic state in renal cortex cells, and act preventing the aggravation of glomerular morphological alterations, 337 independently of any hyperglycemia reduction. These outcomes confirm that green tea positive 338 339 effects in diabetic nephrosis are broader than glycemic regulation related effects. Although our study has not shown a strong improvement in organ function. DNA preservation is determinant in 340 341 cell survival and proper function, and glomerular morphological integrity is elemental to the 342 filtration process. Such results, together with the *in silico* considerations, may indicate key points in

the signaling pathways to improve diabetic nephropathy treatment, as coadjuvant, and prevention,
with an herbal medicine, widely distributed and highly accepted around the world.

In adult animals, the weight of the kidney is increased by the damage caused by 345 346 hyperglycemia. Such injuries lead to hypertrophy and compensatory hyperglasia in the tubules, in 347 order to preserve the glomerular filtration function, thus increasing the kidney's weight (Herman-348 Edelstein and Doi, 2016). However, our animals were induced to diabetes at a younger age, so that 349 they had not passed the full development process of the body and organs, including the kidneys, that 350 would still go through a period of growth, with subsequent weight gain (Arataki, 1926). The 351 damage caused by hyperglycemia at this stage of life seems to have been severe enough to delay the progression of the organ's normal growth, stagnating the weight gain together with the entire body 352 353 development of the animal, as described in other experimental conditions with young animals (da Silva et al., 2016; Haraguchi et al., 2020; Silva et al., 2009). Besides, such damage may have 354 extended to prevent green tea's positive effects on kidney function markers found in other studies 355 356 with adult animals (Hayashi et al., 2020; Renno et al., 2008). Our data suggest that diabetes, when 357 rises early, impairs the development of the kidney, as well as the glomerulus, reflected in the low volume of the glomerulus and appearance of pathological features (e.g. mesangial expansion, 358 359 karyocytomegaly, and glomerular basal membrane alterations) in the diabetic animals compared to 360 healthy control. Although we have not observed statistical difference, the size of glomerulus was 361 observed to have a higher mean and a lower variance (SD) in the group treated with green tea 362 compared with the diabetic one, approaching the characteristics that describe the control group. Such data are in line with the protective effects on glomerular morphology exercised by EGCG, the 363 main catechin found in green tea (Yoon et al., 2014). 364

365 It is known that catechins in green tea have a hypoglycemic and preventive effect on high 366 glucose levels (Fu et al., 2017), and it was assumed that the beneficial effects of green tea in 367 diabetic nephropathy, especially concerning the tubular glycogen nephrosis, were due to this 368 hypoglycemiant capacity (Renno et al., 2008). However, green tea treatment, or its isolated catechin

administration, can generate positive outcomes without the achievement of proper glycemic control
(Hayashi et al., 2020), confirming that tea's effect on diabetes goes beyond improving glucoserelated harms.

372 The glycogen accumulation in renal tubules, as presented in our study, is a hallmark of 373 experimental diabetic nephropathy induced by STZ or Alloxan in experimental models (Kang et al., 374 2005). In normal conditions, glucose is reabsorbed almost completely in the proximal tubule by 375 sodium-dependent glucose transporter 2 (SGLT2) and, in lower levels, by sodium-dependent glucose transporter 1 (SGLT1), and appears in the urine when the absorptive capacity is 376 377 extrapolated (Bailey, 2011; Vallon and Thomson, 2017). Additionally, proximal tubule cells have a 378 greater capacity to perform gluconeogenesis from lactate, glutamine, and glycerol, and this is an 379 upregulated process in diabetes (Eid et al., 2006). The glycogen accumulated in the tubule may 380 result from the sum of factors including abnormally increased absorption, and increased gluconeogenesis (Herman-Edelstein and Doi, 2016; Mather and Pollock, 2011). 381

Green tea catechins are shown to act as SGLT1 inhibitors in vitro (Kobayashi et al., 2000), 382 383 suggesting that tea treatment forces the glucose reabsorption process in the kidney to be done by 384 SGLT2 alone. At the time, there is no evidence suggesting an inhibitory effect of catechins on 385 SGLT2. However, EGCG was shown to inhibit glucose production via gluconeogenesis in cells by 386 activating the AMPK (Collins et al., 2007). Also, EGCG suppresses gluconeogenic gene expression 387 (e.g. glucose-6-phosphatase and phosphoenolpyruvate carboxykinase) via the phosphoinositide 3-388 kinase (PI3K) pathway (Waltner-Law et al., 2002). Such a mechanism in kidney cells could lead to 389 a reduced glucose overload and the improvement of glycogen accumulation in proximal tubules and 390 may explain the positive outcomes of GTI treatment in our study.

Furthermore, diabetes can increase the expression of SGLT2 and sodium-hydrogen antiporter 3 (NHE3), in response to the higher demand for adenosine triphosphate (ATP) to maintain the glucose reabsorption flow (Herman-Edelstein and Doi, 2016). The great capacity of

394 tubular cells to perform gluconeogenesis, a process that consumes a lot of ATP, further increases 395 the demand for the molecule (Gilbert, 2017). Such increased demand for energy therefore enhances 396 the oxygen (O₂) demand creating a hypoxic environment in the tubular cells (Herman-Edelstein and 397 Doi, 2016). However, the blood supply of O_2 in this case is severely affected by the endothelial 398 damage caused by glucose, leading to loss and obstruction of capillaries, worsen the oxygen supply (Herman-Edelstein and Doi, 2016). In this way, a deeper hypoxic environment is generated, 399 400 favorable to the activation of apoptosis via the Caspase pathway, and the fibrosis development in the organ by stimulating the Transforming growth factor-beta (TGF-B) pathway. In turn, the 401 progression of fibrosis further worsens hypoxia, aggravating cell death in the organ (Gilbert, 2017). 402 403 This mechanism is also accompanied by increased expression of stem cell factor (SCF) and proto \Box oncogene c \Box kit (c-kit) (Yin et al., 2018). In contrast, ellagic acid, a derivative polyphenol 404 found in green tea (Yang and Tomás-Barberán, 2019), is shown to inhibit tyrosinase activity 405 406 (Yoshimura et al., 2005) inhibiting the SCT-Kit pathway and alleviating the damages caused by 407 hypoxia.

In this same line, green tea extract can inhibit the fibroblast growth factor receptor (FGFR) signaling by reducing the expression of fibroblast growth factor (FGF) (Sartippour et al., 2002), and EGCG impedes the signaling pathway of the platelet-derived growth factor (PDGF), other profibrotic factors (Park et al., 2006).

412 Hypoxia can aggravate diabetic kidney disease by upregulating the expression of Toll-Like 413 Receptor 4 (TLR4) ligands in diabetes, as fibronectin (Zhang et al., 2018) and high-mobility group 414 box 1 (HMGB1) (Feng et al., 2020). The activation of the TLR4 signal mediated by the TIR-415 domain-containing adaptor-inducing Interferon- β (TRIF) culminate in the activation of the nuclear 416 factor κ B (NF- κ B) that lead to inflammation and fibrosis in the kidney (Feng et al., 2020). However, EGCG was shown to inhibit the TLR pathway activation in vitro (Youn et al., 2006) and 417 418 to reduce the NFkB expression (Yamabe et al., 2006) suggesting that tea may act through this 419 mechanism to promote anti-inflammatory and antifibrotic protection in the kidney.

420 Our results showed that green tea was able to reduce the binding of propidium iodide to DNA and enhance GST activity, suggesting an improvement in DNA integrity or that there was 421 422 some reduction in the damage caused by hyperglycemia or oxidizing agents. A previous study 423 showed that EGCG can inhibit apoptosis induced by oxidative stress (Itoh et al., 2005) preserving 424 renal cells in an *in vitro* model. Also, green tea polyphenols can contribute to reduce apoptosis 425 levels in diabetic nephropathy by blocking the glycogen synthase kinase-3 β (GSK3 β) interaction 426 with the tumor protein 53 (TP53), reducing Caspase 3 activity in podocytes leading to higher cell 427 survival rates (Borges et al., 2016; Peixoto et al., 2015). A review study by Mohabbulla Mohib et al. (2016) summarizes other possible mechanisms that green tea protects the nuclear envelope and the 428 429 genome, including the stabilization of the DNA strand and also the reduction of NF-kB expression culminating in the already discussed positive outcomes. 430

The homeostatic maintenance of the ions inside the cell may influence the antioxidant enzyme activities (Soetan et al., 2010). Our results show that green tea was not able to reverse the dysregulation in the relationship between the ions in the kidneys, which actively participate in the functioning of antioxidant enzymes. Also, oxidative stress may be responsible to inhibit Na^+/K^+ ATPase activity by oxidation of thiol groups in the pumps (Al-Numair et al., 2015), and despite the increased GST activity shown in our study, Na^+/K^+ ATPase function was not recovered.

The PI3K/AKT/mammalian target of rapamycin (mTOR) pathway is linked to metabolic 437 438 regulation in diabetic nephropathy and also in the development of human kidney cancer. This signal 439 cascade is upregulated in diabetes and is closely related to glycogen tubular accumulation (Ribback 440 et al., 2015). EGCG is shown to inhibit both PI3K and mTOR, by competitively binding in the 441 ATP-binding sites in these proteins (Van Aller et al., 2011). Additionally, mTOR inhibition can 442 restore the autophagy mechanism, reduced by mTOR overexpression in diabetes, and contribute to cellular renovation in the kidney. Also, the PI3K/AKT/mTOR pathway is related to de novo 443 444 lipogenesis in the kidney (Ribback et al., 2015), which can lead to lipid accumulation, as in line

with the microvesicles showed in Figure 6 D. Green tea treated animals didn't present thiscytoplasmic microvesicles.

Our in silico results show that protein kinase B (AKT) is the central protein in the catechin 447 448 mediated effects in the kidney. EGCG can activate the diacylglycerol kinase (DGK) pathway, promoting the inactivation of protein kinase C beta (PKC- β) and improving the condition of 449 450 diabetic nephropathy (Hayashi et al., 2020). Such a process is initiated the interaction of EGCG 451 with the 67-kDa laminin receptor (67LR), which is known as an EGCG receptor (Tachibana et al., 2004), and is also capable of activating the AKT in the kidney (Kumazoe et al., 2020). Hayashi et al 452 (2015) showed that EGCG activates DGK-a via 67LR binding. In a recent study (Hayashi et al., 453 454 2020), the authors proposed that this mechanism occurs by activating 67LR receptors in the cell membrane, which, when activated, promotes the translocation of the DGK to the membrane, 455 through the formation of 67LR-DGK- α and α 3- β 1 integrin's complex, promoting greater focal 456 adhesion of podocyte foot process in the glomerular basement membrane, ensuring cell adhesion, in 457 458 addition to inhibiting α and β PKC (Hayashi, 2020), preserving glomerular morphology. This 459 mechanism may be responsible for the positive effects concerning glomerular preservation by green tea ingestion. Other catechins present in green tea composition may exert effect by AKT pathway 460 activation by a different receptor, as they do not bind with the 67LR (Tachibana et al., 2004), 461 462 however the primary membrane receptor for them are still unknown.

463

464 **5. Conclusion**

The components of green tea can interact with proteins participating in cell signaling pathways that regulate energy metabolism, including glucose and glycogen synthesis, glucose reabsorption, hypoxia management, and cell death by apoptosis. Such interaction leads to reduced accumulation of glycogen in the kidney's cells of the proximal tubules in diabetes, as well as to reduce DNA damage. These results also reflect in a preserved glomerulus morphology, with

- 470 improvement in pathological features, and suggesting a prevention of kidney function impairment.
- 471 Our results show that such benefits are achieved regardless of the blood glucose status, and are not
- 472 dependent on the reduction of hyperglycemia to be achieved.

474 Abbreviations

475 476 477 67LR - 67kDa laminin receptor; ABTS - 2,2'-Azinobis-[3-ethylbenzthiazoline-6-sulfonic acid]; NOS1 - Nitric Oxide Synthase 1; AGE/RAGE - advanced glycated end-products and its receptor; AKT - protein kinase B; AMPK - 5'-AMP-activated protein kinase; AO - acridine Orange; APC - APC Regulator Of WNT Signaling Pathway; ATP - adenosine triphosphate; BAX - BCL2 Associated 478 X; BCL2 - BCL2 Apoptosis Regulator; BID - BH3 Interacting Domain Death Agonist; BW - body weight; Ca - calcium; CaCl -479 480 calcium chloride; CASP3 - Caspase 3; CASP8 - Caspase 8; CASP9 - Caspase 9; CAT - catalase; CAV1 - Caveolin 1; CCL2 - C-C Motif Chemokine Ligand 2; CDK2 - Cyclin Dependent Kinase 2; CDKN1A - Cyclin Dependent Kinase Inhibitor 1; CIAPIN1 -481 482 483 484 485 486 485 486 487 488 489 Cytokine Induced Apoptosis Inhibitor 1; c-kit - proto-oncogene c-kit; Cl - chlorine; CPI - compound-protein interactions; CTNNB1 - Catenin Beta 1; Ctrl - control group; DB02077 - L-N(omega)-nitroarginine-(4R)-amino-L-proline amide (NOS3); DB08019, DB08018 and NOS3- Nitric Oxide Synthase 3; DKG - diacylglycerol kinase; DN - Diabetic nephropathy; EGCG - epigallocatechin gallate; FGF - fibroblast growth fator; FGFR - fibroblast growth factor receptor; FOS - Fos Proto-Oncogene; FRAP - ferric reducing antioxidant power; GSK $_{3\beta}$ - glycogen synthase kinase-3 β ; GST – glutathione S-transferase; GTI – Green tea infusion; H₂O₂ hydrogen peroxide; H6PD - Hexose-6-Phosphate Dehydrogenase/Glucose 1-Dehydrogenase; HIF1A - Hypoxia Inducible Factor 1 Subunit Alpha; HMG1 – high-mobility group box 1; HSP90AA1 - Heat Shock Protein 90 Alpha Family Class A Member 1; i.p. – intraperitoneal; IL6 - Interleukin 6; IL8 - Interleukin 8; JUN - Jun Proto-Oncogene; K - potassium; KCl - potassium chloride; KW kidney weight; MAP2K1 - Mitogen-Activated Protein Kinase Kinase 1; MAPK1 - Mitogen-Activated Protein Kinase 1; MAPK3 -490 Mitogen-Activated Protein Kinase 3; MAPK8 - Mitogen-Activated Protein Kinase 8; MAPKAPK5 - MAPK Activated Protein 491 492 493 Kinase 5; Mg - magnesium; MgCl - magnesium chloride; MLH1 - MutL Homolog 1; mTOR - mammalian target of rapamycin; MTRR - 5-Methyltetrahydrofolate-Homocysteine Methyltransferase Reductase; Na - sodium; NaCl - sodium chloride; NADPH reduced nicotinamide adenine dinucleotide phosphate; NDOR1 - NADPH-dependent diflavin reductase; NF κ B - nuclear factor κ B; 494 495 496 NO2⁻/NO3⁻ - nitric oxide; NOS2 - Nitric Oxide Synthase 2; NR1H4 - Nuclear Receptor Subfamily 1 Group H Member 4; O2 oxygen; O₂ - superoxide; PARP1 - Poly(ADP-Ribose) Polymerase 1; PDGF - platelet-derived growth fator; PGD -Phosphogluconate Dehydrogenase; PGLS - 6-Phosphogluconolactonase; PI – propidium iodide; PI3K – phosphoinositide 3-kinase; PIN1 - Peptidylprolyl Cis/Trans Isomerase, NIMA-Interacting 1; PKC- β – protein kinase C beta; POR - Cytochrome P450 497 498 Oxidoreductase; PPI - Protein-Protein Interactome; RPIA - Ribose 5-Phosphate Isomerase A; RSI - renal somatic index; SCF - stem 499 cell fator; SD - standard deviation; SGLT1 - sodium-dependent glucose transporter 1; SGLT2 - sodium-dependent glucose 500 501 transporter 2; SOD - superoxide dismutase; SOES - Specific Organ Expression Score; STAT3 - Signal transducer and activator of transcription 3; STZ - streptozotocin; TCA - Trichloroacetic acid; TCF7L2 - Transcription Factor 7 Like 2; TE - Trolox equivalente; 502 TGF- β - transforming growth factor-beta; TLR4 - toll-like receptor 4; TP53 - tumor protein 53; TRIF - TIR domain-containing 503 adaptor-inducing Interferon- β; TYW1 - TRNA-YW Synthesizing Protein 1 Homolog; UBC - Ubiquitin C.

504

505 Disclosures

506 The authors have no conflicts of interest to disclose.

507

508 Authors' contributions

509 LCML planned and carried the experiment, performed the analysis and interpreted the results,

510 wrote the original draft, reviewed and final edited the manuscript. ECS participate in the

511 conceptualization of the experiment, interpretation of results and writing of the manuscript. TAS, 512 JS, GDAL, performed the analysis, interpreted results, reviewed and approved the final manuscript. 513 MMN participate in the conceptualization of the experiment, provided resources, reviewed and 514 approved the final manuscript. RCS and MBF provided resources, participate in the interpretation 515 of results, reviewed and approved the final manuscript. IRSCM participate in the conceptualization 516 of the experiment, interpretation of results, supervision and administration of the project, reviewed 517 and approved the final manuscript.

518

519 Availability of data and material

520 The datasets used and/or analyzed during the current study are available from the 521 corresponding author on reasonable request.

522

523 Acknowledgments

524 The authors are grateful to Bioclin Laboratories for kindly providing the biochemical kits used in this work; "Laboratório de Microscopia Eletrônica" of the Physics Department of the 525 Federal University of Vicosa; Eliana Alviarez Gutierrez, for the green tea infusion chemical 526 527 analysis; Letícia Monteiro Farias, of the "Laboratório de Biodiversidade" of the Biochemistry and Molecular Biology of the Federal University of Viçosa, for the chemical analysis in HPLC of the 528 529 green tea infusion; Professor Dr. Marcio Roberto Silva, for the statistical insights; Enedina 530 Sacramento, for the English proofreading service; and Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), for the L. C. M. Ladeira Ph.D. scholarship provided (Procs. Nr. 531 532 88882.436984/2019-01).

534 Ethics statement

- 535 The use of animals in this study was approved by the Ethics Committee of Animal Use of the
- 536 Federal University of Viçosa (CEUA/UFV protocol number 53/2018).

537

538 Funding

- 539 This paper was supported by a grant from the Brazilian agency Capes (Coordenação de
- 540 Aperfeiçoamento de Pessoal de Nível Superior, Procs. Nr. 88882.436984/2019-01) and resources
- 541 from the CNPq (Conselho Nacional de Desenvolvimento Científico e Tecnológico, Chamada
- 542 UNIVERSAL 2018; Procs. Nr. 431330/2018-2).

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786 787 788 789 790 **Figure captions** Figure 1. Chromatogram of the green tea infusion (*Camellia sinensis*). In detail: peak of the major 791 792 compound (Epigallocatechin gallate). 793 Figure 2. Renal function markers of male Wistar diabetic rats treated or not with green tea infusion 794 and a healthy control group. A – Urea (mg/dL). B – Creatinine (mg/dL). Mean \pm SD. The statistical 795 796 differences are indicated with lines with the *P*-value above or below them. Data were compared by Student *t*-test (Ctrl vs STZ; STZ vs STZ+GTI) considering statistical differences when $P \le 0.05$. (n 797 798 = 6 animals/group). 799 Figure 3. Antioxidant enzymes and nitric oxide levels of male Wistar diabetic rats treated or not 800 801 with green tea infusion and a healthy control group. A - Superoxide dismutase. B - Catalase. C - Catalase802 Glutathione S-Transferase. \mathbf{D} – Nitric oxide. Mean \pm SD. The statistical differences are indicated 803 with lines with the *P*-value above or below them. Data were compared by Student *t*-test (Ctrl vs 804 STZ; STZ vs STZ+GTI) considering statistical differences when $P \le 0.05$. (n = 6 animals/group). 805 806 Figure 4. Microelement proportions and its correlations, and ATPase activity in the kidney of male 807 Wistar diabetic rats treated or not with green tea infusion and a healthy control group. A – Sodium (%). **B** – Magnesium (%). **C** – Phosphorus (%). **D** – Chlorine (%). **E** – Potassium (%). **F** – Calcium 808

809 (%). **G** – Elemental correlations. **H** - Na⁺/K⁺, Ca²⁺, Mg²⁺ and total ATPase activity. Mean \pm SD.

The statistical differences are indicated with lines with the *P*-value above or below them. Data were compared by Student *t*-test (Ctrl vs STZ; STZ vs STZ+GTI) considering statistical differences when $P \le 0.05$. The correlations were calculated by Pearson's method and the r² is shown in the upper number of each graph cell, the bottom number in each graph cell corresponds to the *P*-value of each correlation. (n = 6 animals/group).

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816 Figure 5. Representative PAS stained photomicrographs, histopathological and stereological 817 parameters of the kidney's cortex of male Wistar diabetic rats treated or not with green tea infusion 818 and a healthy control group. A – Kidney's cortex photomicrography. The glomeruli are delimited 819 by the dotted line. The glycogen nephrosis areas are indicated by the arrowheads. The scale bar is indicated in the figure. **B** – Glomeruli / mm^2 . **C** – Total glomerular volume (mm^3). **D** – Glycogen 820 821 nephrosis volume (mm³). The box represents the interguartile interval with the median indicated 822 (horizontal line), and the whiskers represent the superior and inferior quartiles. The statistical differences are indicated with lines with the *P*-value above or below them. Data were compared by 823 824 Student *t*-test (Ctrl vs STZ; STZ vs STZ+GTI) considering statistical differences when $P \le 0.05$. (n = 6 animals/group). 825

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Figure 6. Representative acridine orange (AO) and propidium iodide (IP) stained photomicrographs of the kidney's cortex of male Wistar diabetic rats treated or not with green tea infusion and a healthy control group. A – Kidney's cortex photomicrography. Green nuclei – AO-positive; Yellow to reddish nuclei – IP-positive; Arrows indicate PI-positive nuclei. Scales bars are indicated in the figure. B – AO-positive cells (%). C – IP-positive cells (%). Mean \pm SD. The statistical differences are indicated with lines with the *P*-value above them. Data were compared by Student *t*-test (Ctrl vs STZ; STZ vs STZ+GTI) considering statistical differences when $P \le 0.05$. (n = 6 animals/group).

835 Figure 7. Representative photomicrographs of the glomerulus, stained with Toluidine Blue -Sodium borate 1%, of male Wistar diabetic rats treated or not with green tea infusion and a healthy 836 control group. A - A normal glomeruli of an animal from the healthy control group. B - Diabetic837 glomeruli. Arrowhead indicates a thickening in the glomeruli basal membrane. C – Diabetic 838 839 glomeruli. Arrow indicates a region of diffuse mesangial expansion. **D** – Diabetic glomeruli. Thick 840 arrow indicates a remarkable vacuolization in the macula densa region. Thin arrows indicate 841 cytoplasmic microvesicles in the proximal tubule cells. **E** – Diabetic glomeruli. Squares indicate 842 karyocytomegaly in the proximal tubule. Dotted circles indicate basal regions in the tubular cells 843 with accumulation of stained granules, possible mitochondria aggregation. The glomeruli present a 844 dilated Bowman's space.

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Figure 8. *In silico* exploration of catechins effects in the kidney. **A** – Compound-Protein Interactome network, highlighting tea catechins (green nodes), bottleneck protein (red node), cluster 1 (grey nodes), and cluster 2 (light blue nodes). **B** – Centrality analysis for the CPI network, the blue lines represent the threshold of the parameter.

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869	Table 1.	

870 Blood Glucose, biometric parameters and water consumption of male Wistar diabetic rats treated or

871 not with green tea infusion and a healthy control group.

	Ctrl	STZ	STZ+GTI
Blood Glucose (mg/dL)	85.38 ± 7.53	$475.00 \pm 33.14*$	$542.80 \pm 42.20^{\#}$
Initial body weight (g)	84.26 ± 14.97	81.27 ± 9.46	81.75 ± 7.57
Final body weight (g)	288.10 ± 44.16	$93.08 \pm 23.42*$	99.75 ± 13.04
Body weight gain (g)	203.80 ± 30.81	$11.82 \pm 21.87*$	18.00 ± 16.18
Kidney weight (g)	0.98 ± 0.07	$0.78\pm0.18^{\#}$	$0.86~\pm~0.08$
Renal somatic index (%)	0.34 ± 0.05	$0.84 \pm 0.13^{*}$	0.87 ± 0.10
Initial water consumption (mL/day)	44.45 ± 10.02	44.48 ± 9.87	41.78 ± 11.16
Final water consumption (mL/day)	39.25 ± 6.13	$118.8 \pm 17.45*$	$139.8 \pm 10.26 \#$

872 Mean ± SD. Data were compared by Student *t*-test (Ctrl vs STZ; STZ vs STZ+GTI) considering

873 statistical differences when $P \le 0.05$. Asterisk (*) indicates difference with P < 0.0001, and the

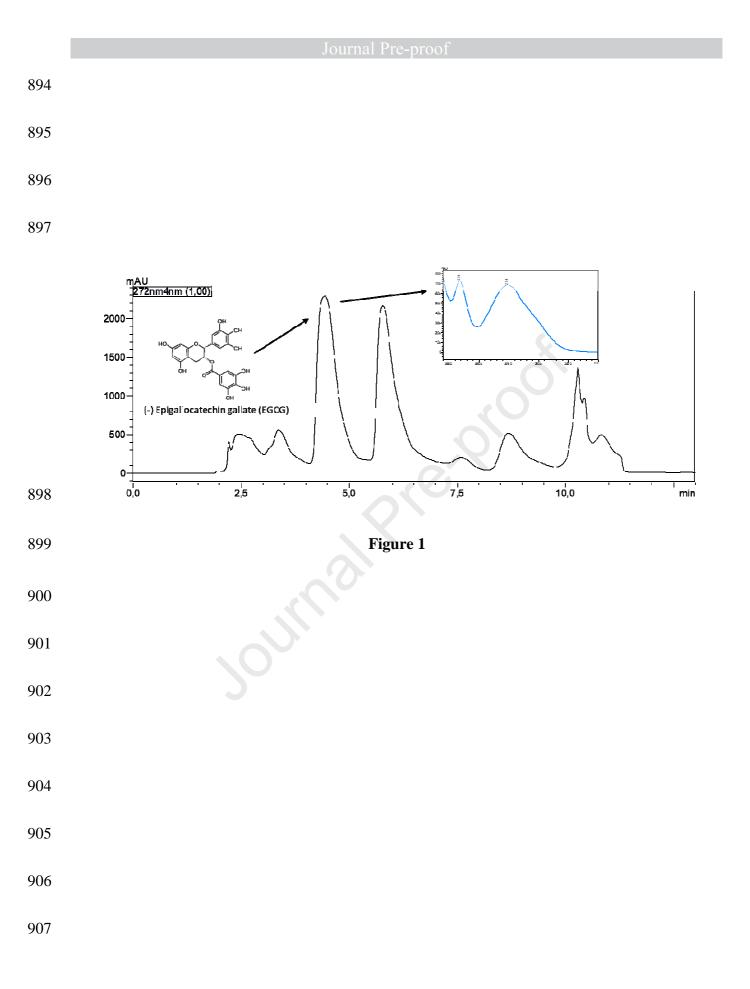
- hash (#) indicates different means with P < 0.05. (n = 6 animals/group).
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883	Table 2.
884	Reactome pathways identified for each cluster with specific interest to the diabetic nephropathy

pathological state, identified by the comparison of the CPI network with the Reactome Pathway

886 database with the corresponding adjusted *P*-values.

Cluster	Proteins	Reactome Pathway	Adjusted <i>P</i> - value
Cluster 1	NR1H4, CCL2, IL8, IL6,	Apoptosis	1.76 x 10 ⁻⁷
	MAPKAPK5, STAT3, PIN1,	Signaling by SCF-KIT	1.06 x 10 ⁻⁶
	PARP1, CASP8, MTOR, MAPK3,	Signaling by FGFR in disease	4.35 x 10 ⁻⁶
	MAPK8, MLH1, CASP3, CASP9, GSK3B, HIF1A, BID, MAPK1,	Signaling by PDGF	6.00 x 10 ⁻⁶
	MAP2K1, BAX, BCL2, FOS, JUN,	TRIF-mediated TLR3/TLR4 signaling	6.00 x 10 ⁻⁶
	APC, AKT1, CDKN1A, CDK2, TP53, CTNNB1, TCF7L2		1.15 x 10 ⁻⁵
Cluster 2	DB02077, RPIA, POR, H6PD,	eNOS activation	1.05 x 10 ⁻⁶
	PGLS, PGD, AKT1, TYW1,	Pentose phosphate pathway	1.30 x 10 ⁻⁵
	MTRR, NOS2, DB08019, DB08018, AC1NDS4X, NOS1,	AKT phosphorylates targets in the cytosol	3.70 x 10 ⁻⁵
	CAV1, NDOR1, CIAPIN1,	Metabolism of carbohydrates	1.53 x 10 ⁻⁴
	HSP90AA1, UBC, NOS3	Cellular response to hypoxia	$1.50 \ge 10^{-3}$
		PI3K/AKT/mTOR activation	6.29 x 10 ⁻³



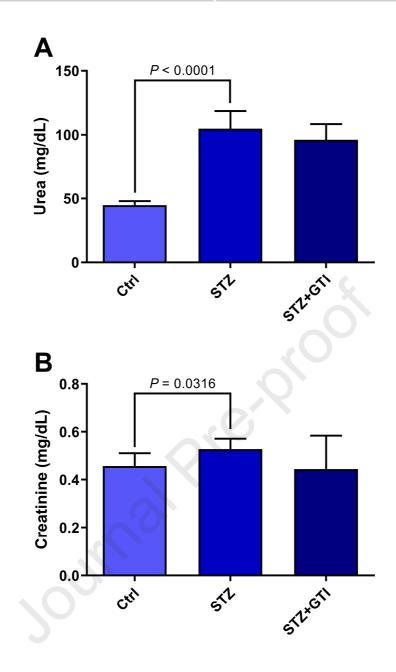


Figure 2

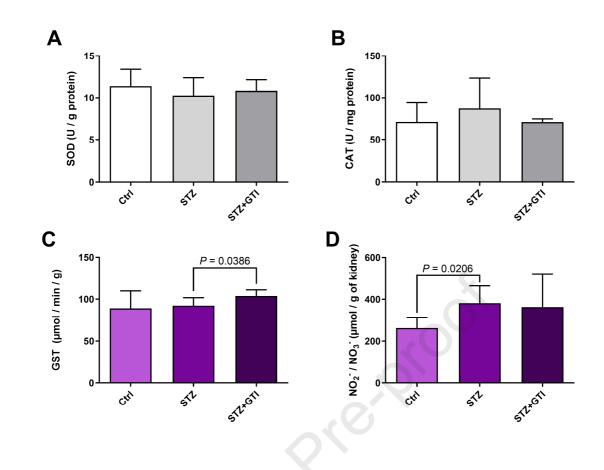
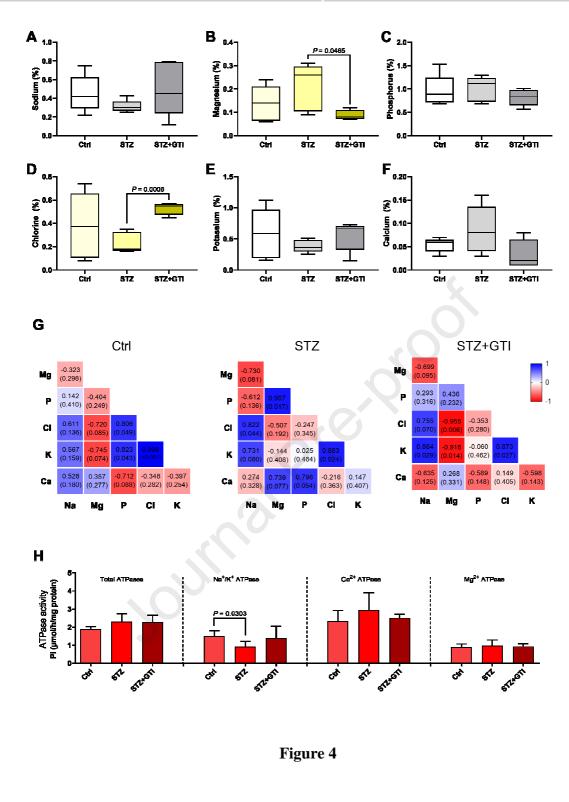
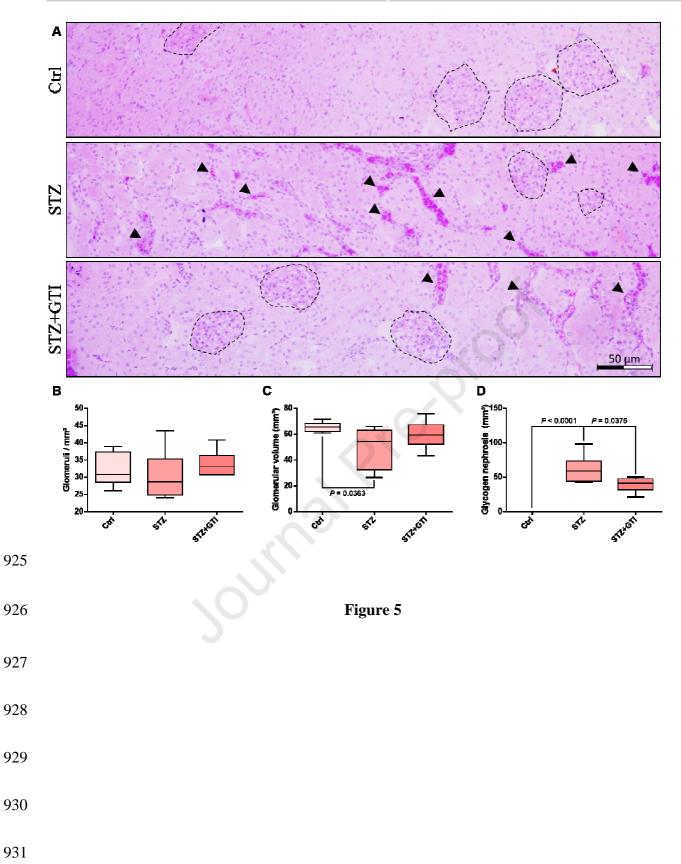
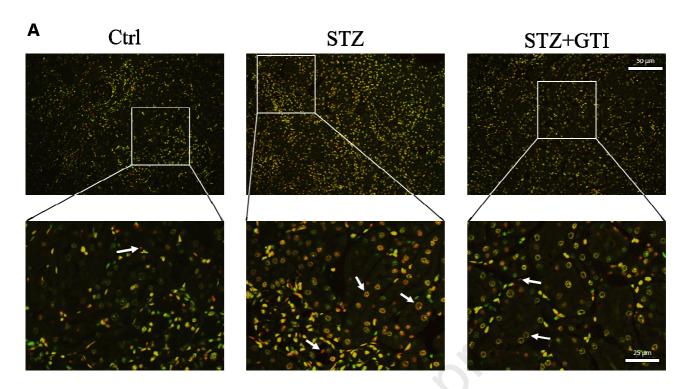


Figure 3







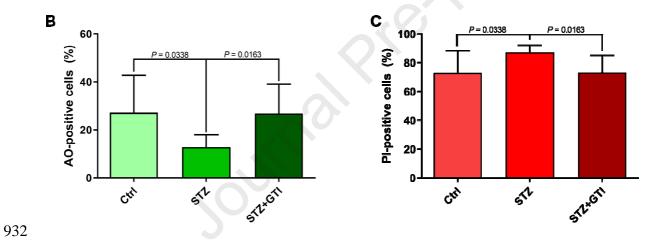


Figure 6

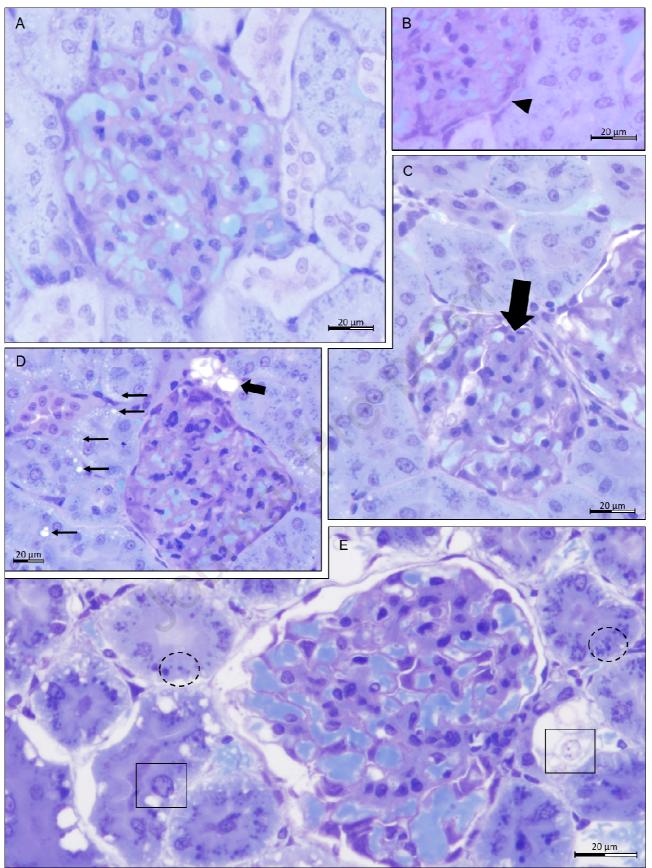


Figure 7

