

# Energy depletion by cell proliferation sensitizes the kidney epithelial cells to injury

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# 1 RESEARCH ARTICLE

- 2 RUNNING HEAD: Viability of proliferating cells
- 3 Energy depletion by cell proliferation sensitizes the kidney epithelial cells to injury.
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# 34 **ABSTRACT**

Acute kidney injury activates both proliferative and anti-proliferative pathways, the consequences of 35 which are not fully elucidated. If an initial proliferation of the renal epithelium is necessary for the 36 successful repair, the persistence of proliferation markers is associated with the occurrence of chronic 37 kidney disease. We hypothesized that proliferation in stress conditions impacts cell viability and renal 38 outcomes. We found that proliferation is associated with cell death after various stresses in kidney 39 cells. In vitro, the ATP/ADP ratio oscillates reproducibly throughout the cell cycle, and cell 40 41 proliferation is associated with a decreased intracellular ATP/ADP ratio. In vivo, transcriptomic data from transplanted kidneys revealed that proliferation was strongly associated with a decrease in the 42 expression of the mitochondria-encoded genes of the oxidative phosphorylation pathway, but not of 43 the nuclear-encoded ones. These observations suggest that mitochondrial function is a limiting factor 44 45 for energy production in proliferative kidney cells after injury. The association of increased 46 proliferation and decreased mitochondrial function was indeed associated with poor renal outcomes. In summary, proliferation is an energy demanding process impairing the cellular ability to cope with 47 an injury, highlighting proliferative repair and metabolic recovery as indispensable and 48 interdependent features for successful kidney repair. 49

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# 51 NEW & NOTEWORTHY

ATP depletion is a hallmark of acute kidney injury. Proliferation is instrumental to kidney repair. We show that ATP levels vary during the cell-cycle and that proliferation sensitizes renal epithelial cells to superimposed injuries *in vitro*. More proliferation and less energy production by the mitochondria are associated with adverse outcomes in injured kidney allografts. This suggests that controlling the timing of kidney repair might be beneficial to mitigate the extend of acute kidney injury.

- 57
- 58 **Keywords:** acute kidney injury ; cell proliferation ; energy metabolism

# 60 INTRODUCTION

Cell proliferation is essential for any life form. As the multiplication of organized structures, 61 proliferation uses energy to decrease entropy. In his book "whant is Life?", Erwin Schrodinger coined 62 the term "negentropy" to define Life.(44). Thus, proliferation requires energy. It is the cornerstone not 63 only of development in multicellular organisms but also of several processes of organ repair. In the 64 presence of various stresses, however, anti-proliferative pathways are triggered, suggesting that 65 uncontrolled proliferation can be deleterious, even in non-cancerous diseases (12, 34). This is the case, 66 for example, in the context of acute kidney injury (AKI). If it is known that cell proliferation is 67 indispensable for the organ repair (37), it was also shown that alleviating cell cycle blockade by P21 or 68 P53 aggravates the course of toxic or ischemic AKI (9, 27, 32, 33, 37, 49). These observations 69 demonstrate the essential role of cell proliferation control in pathological situations. 70

A high cellular energy level is generally accepted as a marker of viability (6) and is considered 71 a prerequisite for cell proliferation (10, 60). Conversely, a persistent decrease in the level of 72 73 intracellular ATP is associated with cell injury and ultimately death, both in tumor and non-tumor cells (26, 57). It is generally assumed that the ATP level is regulated prior to changes in proliferation (15, 74 31, 45, 47). Indeed, a low ATP level stimulates AMPK, which induces cell cycle arrest through P27, 75 P53 and P21 activation in various organs (16). By contrast, in cancer, a low ATP level is considered to 76 allow cell proliferation by stimulating aerobic glycolysis and the Warburg effect (30). Although the 77 effect of ATP variations on proliferation has been studied, the reverse mechanism, i.e. the effect of cell 78 cycle progression on the cellular energy status, is yet unexplored. Since energy depletion leads to cell 79 death (19, 57), the effect of proliferation on the energy level of the cell might critically impact cell 80 viability. In particular, we hypothesized that cell proliferation in the context of energy depletion, such 81 as an ischemic AKI, could be detrimental. We investigated the relationship between proliferation and 82 viability in human renal epithelial cells. By quantifying the ATP/ADP ratio in live cells using a single 83 cell approach, we studied the effect of proliferation on the cellular viability and characterized the 84 pattern of variation of the intracellular energy level throughout the cell cycle. Lastly, we investigated 85 how the balance between cell proliferation and energy production influences the outcomes of kidney 86 allografts. We thus identified the downregulation of mitochondrial-encoded genes of the oxidative 87 phosphorylation pathway in proliferating epithelial cells as a limiting factor for successful recovery 88 after an episode of acute kidney injury. 89

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- 91

# 92 MATERIALS AND METHODS

- 93 Reagents are referenced in Supplemental Table S4.
- 94 Cell cultures

95 HK2 (ATCC<sup>®</sup> CRL-2190<sup>™</sup>) cells are immortalized male adult human renal proximal tubular cells 96 cultured at 37°C in DMEM with 10% fetal bovine serum. The live microscopy experiments were 97 conducted in Leibovitz's L-15 medium with no phenol red (Fisher, #21083027). Pharmaceutical 98 inhibitors were purchased from Selleckchem: tenovin-1 (#S8000), pifithrin-alpha (#S2929), Rigosertib 99 (#S1362) and KU-55933 (#S1092). Cell count was performed on live microscopy data using the Fiji 100 Trackmate plugin (53).

101

# 102 Western Blot

Proteins were extracted from HK2 cells with RIPA buffer containing protease and phosphatase inhibitor cocktails. Total protein concentration was measured using the BCA assay (Pierce). Samples were fractionated by SDS-PAGE under reducing conditions and then transferred to a nitrocellulose membrane. Membranes were incubated in TBST (TBS 1X with 0.1% Tween) with the appropriate primary antibodies: anti-ATP5a (Abcam ab14748), anti-MTCO1 (Abcam ab203912) and anti-HIF1a (Novus NB100-449). HSC70 (Abcam, ab51052, 1:500) was used as loading control. ImageJ software (National Institutes of Health) was used for quantification.

110 Viability experiments

111 Cells were grown in DMEM with 10% fetal bovine serum in the presence or absence of puromycin (2µg/mL). Energy depletion was achieved in cells grown in Leibovitz's L-15 medium without glucose 112 113 supplementation and hypoxia obtained by applying a 100% N2 atmosphere (ref 26700 from Air products) in an airtight chamber (ref 27310 and 27311 from Stemcell) during 24h. The control cells 114 were grown in L-15 medium with 4.5 g/dL glucose supplementation under ambient atmosphere. The 115 expression of mitochondrial proteins ATP5A and MTCO1 and the induction of Hypoxia inducible factor 116 1 in hypoxic conditions were verified by western blot (Fig S1). Flow cytometry analysis for assessment 117 of dead cells was performed with the fixable viability dye Viobility 405/452 Fixable Dye (Miltenyi 118 Biotec<sup>®</sup>). 119

# 120 Mitochondrial potential assay

121 Cells were grown for 24 hours in L-15 medium with 1µmol/L JC-1 (ref 65-0851-38 from Thermo 122 Fisher) under control conditions or energy depleting conditions (as described above). Mitochondria 123 were identified by the presence of JC-1 aggregates fluorescing in red, and we assessed the 124 mitochondrial potential by quantifying the red/green fluorescence ratio in mitochondria (reflecting 125 aggregates/monomers), using Fiji(42).

## 126 ATP/ADP ratio measurements

127 ATP and ADP measurements were performed with the ApoSENSOR ADP/ATP ratio assay (Enzo Life 128 Sciences), in accordance with the manufacturer's instructions.

PercevalHR was used to study the ATP/ADP ratio in live individual cells in real-time experiments, spanning multiple cell cycles. Using lentiviral transformation, we generated proximal tubular cells with stable expression of PercevalHR as well as pHRed, in order to adjust the PercevalHR signal on pH variations(51). ATP/ADP ratio and pH were assessed by dual signal acquisition for PercevalHR (ex 436/495; em 540) and pHRed (ex 436/550; em 640), followed by ratiometric normalization using the Ratio Plus plugin in Fiji(42). PercevalHR (ATP/ADP ratio) was further corrected for pH by normalization on pHRed (51), using the Ratio Plus plugin.

136 Bioinformatic analysis

ATP/ADP ratio. The Fiji Trackmate plugin was used to monitor single-cell ATP/ADP ratio over time, and to determine the time of cytokinesis for each cell(53). Briefly, every cell was assigned to a single trajectory at a specific timepoint, with a corresponding ATP/ADP value. The times of cytokinesis were noted for each cell trajectory. ATP/ADP values were represented on the y-axis as mean+/-standard error, and time was represented on the x-axis in hours from either the start of the experiment or from the time of cytokinesis. The full script is available as Supplemental data.

143 Computation of proliferation index, overall OXPHOS index, nuclear and mitochondrial OXPHOS index in

bulk RNAseq data. We then used available RNA-seq data from kidney allograft biopsies in order to test 144 the relationship between proliferation and energy metabolism in vivo in 163 kidney allograft biopsies 145 from 42 patients (7). The clinical and research activities being reported are consistent with the 146 Principles of the Declaration of Istanbul as outlined in the 'Declaration of Istanbul on Organ Trafficking 147 and Transplant Tourism'. We applied a previously published and validated method to compute a 148 proliferation index as the median value of a list of proliferation associated genes (56). Similarly, we 149 computed the overall OXPHOS index as the median value of the genes listed in the human OXPHOS 150 pathway of the (Kyoto Encyclopedia of Genes and Genomes database(22). We performed the same 151 computation on the subset of mitochondria-encoded genes to obtain the mitochondrial OXPHOS 152 index. We used median value by analogy to the previously determined proliferation index, and 153 because it has the theoretical advantage over mean values of mitigating the effect of extreme values 154 in only a small subset of genes within the predefined list. However mean values correlated closely 155  $(r \ge 0.8)$  with median values suggesting non-skewed expression data for the studied genes. 156

157 Computation of proliferation index, overall OXPHOS index, nuclear and mitochondrial OXPHOS index in

single-cell RNAseq data. We used the human rejecting kidney data set (61) and the Seurat package from R (14, 40) to identify the different cell types (Fig. 5). We computed the proliferation index, mitochondrial encoded OXPHOS and nuclear encoded OXPHOS in the epithelial cells as described for bulk RNA-seq in the previous paragraph. Because the single-cell depth of sequencing is much lower than for bulk RNA-seq, we used the sum of copies within the lists of genes instead of the median value.

Pathway analysis of proliferation associated genes. We computed Kendall's tau rank correlation 164 coefficient to evaluate the correlation of every gene expression value with the proliferation index. The 165 166 correlations' p-values and coefficient were then processed with the LrPath web-based software 167 allowing a logistic regression pathway analysis to identify the gene sets enriched in genes with 168 proliferation-correlated expression levels. Three prespecified genesets for energy-producing pathways were analyzed: "OXidative PHOSphorylation", "Tricarboxylic Acid Cycle", and "glycolysis". P-169 170 values and Odds Ratios were computed as indicators of the significance and the magnitude of the enrichment of these gene sets in genes with proliferation-correlated expression values. 171

# 172 Statistical analysis

Statistical analyses were conducted using JMP 11 (SAS). Log-transformation was performed to 173 174 obtain normal distribution, when necessary. Proportions, 95% confidence interval and p-values were computed using the exact binomial test. Correlations were evaluated using Kendall's tau rank 175 correlation coefficient. P-values were considered significant when <0.05. Comparison between groups 176 were considered significant when the p-value was <0.05 using a Kruskall-Wallis non-parametrical test, 177 and secondary comparisons between pairs were considered significant when the p-value was <0.05 by 178 Wilcoxon signed-rank test. Differences in ATP/ADP changes between treatment groups over time 179 180 were assessed by analysis of variance using a standard least square model.

# 182 **RESULTS**

#### 183 Proliferating cells are more sensitive to an injury than non-proliferating ones

184 We subjected human renal epithelial cells (HK2 cell line) to a metabolic stress and compared their consequences in conditions of stimulated or inhibited proliferation. HK2 cells express markers of 185 mitochondrial ATP production but are also known to be glycolytic. Thus we caused energy depletion 186 by oxygen and glucose deprivation. Oxygen deprivation was confirmed by HIF1a induction. Although 187 the expression of OXPHOS proteins remained stable in this model, it caused a decrease in 188 mitochondrial potential (Figure 1a-b and S1A), mimicking the mitochondrial dysfunction observed in 189 190 the injured renal tubules in vivo (20, 50). Proliferation was either enhanced by pifithrin-2 (a P53 antagonist promoting G1/S and G2/M transition) or inhibited by tenovin-1 (a P53 agonist inhibiting 191 the G1/S transition) (Fig. 1c-d and S1B). . Pifithrin-22 alone or tenovin-1 alone were not toxic, as they 192 did not cause cell death in the absence of puromycin. We observed that the stimulation of cell 193 proliferation promoted the death of energy-depleted cells, whereas inhibition of cell proliferation was 194 195 protective (Fig. 1c). Similar results were obtained when cells were exposed to puromycin, a wellcharacterized toxicant acting through inhibition of protein synthesis (Fig1 d). 196

Taken together, these data show that proliferation enhances susceptibility to noxious stimuli and/or impairs the ability of cells to survive an injury. Given that proliferation requires energy and that a decreased cellular energy level results in cell death, we hypothesized that the depletion of cellular energy in proliferating cells could be responsible for this enhanced susceptibility to toxic influences.

202

#### 203 The ATP/ADP ratio decreases when cells proliferate

Adenosine triphosphate (ATP) is the main energy source for intracellular processes, through its cleavage into adenosine diphosphate (ADP) and hydrogen phosphate (4, 55). The intracellular 206 ATP/ADP or ATP/AMP ratio is a more reliable marker of the cellular energy status than the absolute ATP concentration (8, 30). PercevalHR is a genetically encoded markers of the ATP/ADP ratio, 207 providing a reliable indicator of the intracellular energy status (2, 51). To monitor the single cell-208 ATP/ADP ratio over time in proliferating epithelial cells, we generated human renal tubular cells (HK2 209 cell line) stably expressing PercevalHR (Fig. S2A). We first validated the quantification of the 210 ATP/ADP ratio (ATP/ADP[Perceval]) by an independent technique based on the measurement of 211 luciferin/luciferase bioluminescence (ATP/ADP[Luciferin]). The total ATP/ADP[Perceval] signal 212 correlated well with the ATP/ADP[Luciferin] (r=0.96, p=0.0001) with an intraclass correlation of 0.87. 213 We observed the expected decrease of ATP/ADP[Perceval] after chemical energy depletion with 214 215 blockage of glycolysis and oxidative metabolism using 2-deoxyglucose (2 DG) and sodium azide (NaN<sub>3</sub>) (Fig. S2B-C). 216

217 We then quantitated the single cell ATP/ADP[Perceval]. The mean ATP/ADP values over time were reproducible between wells under basal conditions or during energy depletion (Fig. S2C, middle 218 panel). However, this ratio was highly variable among proliferating cells in the same well and at the 219 same time (Fig. S2C, right panel). This observation suggests that the ATP/ADP ratio is a dynamic 220 221 parameter, undergoing variations that are at least partly independent of the extracellular environment. We hypothesized that the ATP/ADP ratio could be correlated with the cell cycle stage. To test this 222 hypothesis, PercevalHR-expressing epithelial cells were plated at various densities to achieve different 223 levels of contact inhibition of proliferation (Fig. 2A, left panel). The intracellular ATP/ADP ratio 224 increased when the cells were more confluent. To rule out a direct effect of the confluency, we cultured 225 the cells at the same densities in the presence of rigosertib, a potent polo-like-kinase 1 (PLK1) inhibitor 226 inducing G2/M arrest. Non-proliferating cells showed a significant increase in the ATP/ADP ratio, 227 regardless of their degree of confluence. Conversely, performing a scratch assay on confluent cells 228

induced the proliferation and migration of the cells, which then displayed a low ATP/ADP ratio (Fig.
230 2A, right panel). Rigosertib increased the cellular ATP/ADP ratio while inhibiting wound closure.

To exclude a possible cell cycle-independent effect of rigosertib, a panel of pharmaceutical compounds was used to study the changes in the ATP/ADP ratio over time when the cell cycle is perturbed (Fig. 2B-C). Tenovin-1 and Rigosertib were used to inhibit the cell cycle during the G1/S or G2/M transition, respectively. Conversely, pifithrin- $\alpha$  and KU-55933 (an ATM inhibitor promoting G2/M transition) were used to stimulate cell proliferation. Single-cell monitoring demonstrated that the ATP/ADP ratio increased progressively over time when cell proliferation was inhibited whereas it decreased when cell proliferation was stimulated (Fig. 2C).

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#### 239 Cell cycle and proliferation-dependent variations in the intracellular ATP/ADP ratio

We then followed the variation of single-cell ATP/ADP ratio throughout the cell cycle. We thus 240 observed that the ratio was maximal around cytokinesis (Fig. 3A, left panel). This analysis was 241 performed using single cell tracking in non-synchronized cells, ruling out an effect of time or an effect 242 of the extracellular environment and suggesting a direct association with the cell cycle stage. Variations 243 of the ATP/ADP ratio before and after cytokinesis follow a systematic pattern (Fig. 3A, right panel): 244 after a gradual increase, the ratio peaks at mitosis before dropping dramatically. This pattern was 245 highly reproducible, including in cells exposed to pharmaceutical inhibition or stimulation of the cell 246 cycle (Fig. 3B). The cell cycle inhibitor tenovin-1 increased the mean ATP/ADP ratio over time 247 compared to the cell cycle facilitator pifithrin- $\alpha$  (Fig. 3B). Thus, the intracellular energy level, 248 evaluated by the ATP/ADP ratio, is directly influenced by the cell cycle. 249

In order to study the variations of the ATP/ADP ratio during successive cell cycles within the same cell, the trajectories of this ratio were evaluated in cells undergoing division twice in the same live-imaging experiment. The cells had the same pattern of ATP/ADP variations for each of the two successive mitoses. After a first mitosis, cells treated with tenovin-1 reached the second mitosis with a significantly higher ATP/ADP ratio than the first mitosis, compared to cells treated with pifithrin- $\alpha$ , in which such an increment did not occur (Fig. 3B). We conclude that cell cycle inhibition increases the ATP/ADP ratio in cells independently of the cell cycle stage, in a time-dependent manner: the slower the cell cycles, the more positive the cellular energy balance.

#### 258 Association of a mitochondrial defect with proliferation in injured kidney allografts

The proliferation of tubular cells is indispensable for the repair of the kidney after an acute 259 injury. However, the inhibition of anti-proliferative factors such as P21 and P53 (35, 38, 49, 52) leads 260 to the aggravation of the kidney lesions and loss of function. Therefore, to test the relevance of our 261 findings in proliferating cells in vivo, we performed an unbiased gene enrichment analysis to identify 262 pathways associated with cell proliferation in injured kidneys by analyzing the RNA-sequencing data 263 from kidney allografts before and after transplantation by Cippa and colleagues (7). Indeed, all 264 allografts undergo an episode of acute ischemic injury between the organ procurement and the 265 transplantation into the recipient. 266

The level of proliferation was estimated using a previously published and validated proliferation 267 index, which corresponds to the median value of a list of proliferation associated genes (56). We found 268 that the KEGG items that are the most significantly associated with cell proliferation are 'Metabolic 269 270 pathways' (FDR: 2.87e-39) and 'Oxidative phosphorylation (OXPHOS)' (FDR: 2.94e-20). Proliferation 271 and the expression level of OXPHOS genes of the pathway were negatively correlated in kidney allografts immediately after transplantation (Fig. 4A and Tables S1 and S2). A further analysis showed 272 that this decrease in OXPHOS genes expression with proliferation was in fact due to a profound 273 274 downregulation of the expression of mitochondria-encoded genes. In contrast, the transcription of the nucleus-encoded OXPHOS genes was moderately upregulated with proliferation (Fig. 4B-C,Fig. S3 275

Table S3), suggesting that mitochondrial failure is characteristic of proliferating epithelial cells in the acutely injured kidney.

In order to verify this hypothesis at the single-cell level, we used single-cell RNA-seq data from rejecting human kidneys (61) to analyze the relationship between proliferation and OXPHOS related genes specifically in renal epithelial cells, identified by unsupervised analysis and verified by the expression of tubular-specific markers (Fig. 5A and S4). Our analysis confirmed that proliferation was negatively correlated with mitochondria-encoded OXPHOS genes, but not with nuclear-encoded OXPHOS genes (Fig. 5B).

#### Association of proliferation, mitochondrial status and outcomes.

The study reported by Cippà and colleagues was performed on biopsies performed on the same 285 kidney allografts before, just after, 3 and 12 months after transplantation (7). The first two series of 286 samples constituted the 'early' group, while the last two constituted the 'late' group. Furthermore, three 287 types of evolution were distinguished within the late biopsies: recovery, transition towards chronic 288 kidney disease and established chronic kidney disease (CKD) (7). As shown in Fig. S5A, the computed 289 proliferation index was higher in the kidney biopsies performed 3 or 12 months after transplantation 290 than in biopsies performed immediately before or after transplantation. Moreover, a higher proliferation 291 index was associated with the progression towards CKD (Fig. S5B). OXPHOS transcripts were found 292 to be downregulated in the nucleus only during the acute phase of injury (reperfusion), whereas they 293 were downregulated in the mitochondria during the transition towards chronic kidney disease (Fig. 294 S5D, E, G,H). 295

We then studied the relationship between proliferation, the regulation of OXPHOS genes and the long-term clinical outcomes, i.e. the glomerular filtration rate (GFR) and incidence of fibrosis (Fig. S5C, F, I and Fig. S6). We found that the timing dramatically modified the relationship between proliferation, the OXPHOS level and the incidence of fibrosis in the kidney. Although there was no correlation between the proliferation index and fibrosis in the early biopsies, a low mitochondrial
OXPHOS index in the early biopsies (immediately before and after transplantation) was associated
with a lesser incidence of fibrosis in the kidney between 3 and 12 months after transplantation (Fig.
S5I). In contrast, a decrease in the mitochondrial OXPHOS index and an increase in the proliferation
index in the late biopsies (3 and 12 months after transplantation) were associated with an increased
fibrosis and a decreased GFR at 12 months (Fig. S5I and Fig. S6).

Taken together, these transcriptomic analyses suggest that the decrease of mitochondria-encoded genes represents a limiting factor for energy production by OXPHOS required for the adaptive proliferative repair of the kidney allografts after injury.

## 310 **DISCUSSION**

Here we show that proliferating cells are more sensitive to injury than non-proliferating ones, 311 and that the inhibition of proliferation is protective. Proliferation causes a decrease in intracellular 312 energy with superimposed energy oscillations depending on the cell-cycle stage. In vivo, we found that 313 314 mitochondria-encoded genes were profoundly downregulated in the proliferating kidney after injury, indicating mitochondrial shutdown. This is in contrast with the upregulation of nucleus-encoded genes 315 of the OXPHOS gene set (Fig. 4c). This dissociated transcriptomic pattern between mitochondrial and 316 317 nuclear-encoded genes suggests that the cellular energy production is limited by mitochondrial damage. Finally, we found that the persistence of proliferation associated with the downregulation of 318 mitochondrial OXPHOS genes is a pattern associated with an unfavorable evolution towards chronic 319 kidney disease. 320

## 321 Proliferation and energy metabolism are interdependent

The fact that a low intracellular ATP induces molecular pathways downstream of AMPK to control 322 proliferation suggests the presence of a regulatory feedback to mitigate the decrease in intracellular 323 ATP levels caused by increased energy consumption. Such an effect of proliferation on ATP could 324 explain why alleviating cell cycle blockade by P21 or P53 aggravates the course of acute kidney injury 325 caused by an ischemic episode (37), and why highly proliferative tumors frequently undergo 326 spontaneous necrosis (57). The kidney energy turnover is very high. It is thus very sensitive to injury 327 (and especially ischemia), which causes an immediate decrease in energy production, overall energy 328 depletion and epithelial cell death (58). After an injury, cell proliferation is necessary to replace lost 329 330 cells (18). However, an increase in cell proliferation caused by the inactivation of the anti-proliferative factors P53 and P21 was shown to worsen the lesions caused by an episode of ischemia-reperfusion in 331 the kidney (27, 32, 49). The p53 pathway is important to arrest the cell cycle in case of DNA damage, 332 delaying proliferation until DNA is repaired (24). Short-term blockage of p53 performed after the acute 333 phase of ischemia reperfusion may have beneficial effects on subsequent fibrosis due to a decrease in 334

the senescence-associated secretory phenotype (63) whereas earlier or continued blockade actually
 enhances fibrosis (9)

DNA repair is a highly energy-demanding process fueled by mitochondrial ATP generation (39). Thus, 337 proliferation arrest might be an energy-saving mechanism, especially in an injured state. In agreement 338 339 with this hypothesis, we found an association between increased proliferation, ATP depletion and increased cell death in renal epithelial cells in which Nupr1 (Nuclear Protein 1) was inactivated (11). 340 Nupr1 is a downstream effector of ATF4, a master regulator of endoplasmic reticulum stress, the 341 activation of which leads to excessive protein synthesis, causing energy depletion and cell death (13). 342 343 Taken together, these studies suggest that an increase in cell proliferation in conditions of stress might 344 cause critical energy depletion due to enhanced energy needs for both cell maintenance and biosynthetic processes, thus resulting in cell death if a critical energy threshold is not maintained (29). 345 Ultimately if the cells do not die, they may enhance the population of DNA-damaged, cell cycle 346 347 arrested senescent cells and lead to fibrosis.

#### 348 Intercellular and intracellular variations in energy metabolism

Our observations change the understanding of energy variations in proliferating cells (Fig. 7). Previous 349 experiments were limited by the fact that timed bulk cell analysis did not allow the study of the 350 ATP/ADP trajectories of single cells within the same extracellular environment. We show by single-351 cell analysis that a progressive increase in the ATP/ADP ratio in proliferating cells can be observed 352 when confluence and contact inhibition increase, whereas proliferation itself (at the single-cell level) is 353 associated with a decreased ATP/ADP ratio. In addition, we show that within proliferating cells, the 354 ATP/ADP ratio oscillates with the cell cycle. These oscillations in ATP/ADP ratio are reminiscent of 355 cyclic variations of the TCA cycle flux described by Ahn and colleagues (1). This is also in keeping 356 with our in vivo transcriptomic data showing that nuclear OXPHOS transcripts are overexpressed in 357 proliferating cells. The intracellular energy level not only varies during the cell cycle but also depends 358

on the proliferation rate. The live monitoring in single cells demonstrates a transient physiological
 decrease in ATP/ADP in proliferating cells.

# 361 Effect of proliferation on cell viability upon injury

In certain conditions, inhibiting proliferation might be a protective mechanism to prevent lethal energy depletion in epithelial cells or prevent propagation of cells with damaged DNA. This mechanism might be responsible for the protective effect of the extensively studied phenomenon of ischemic preconditioning (3, 5, 28), where a mild and transient ischemia triggers cytoprotective pathways concomitant with transient cell cycle arrest (35, 41). Among these pathways, p53, p21 and AMPK were shown to protect the kidneys from the early lesions induced by ischemia-reperfusion injury while suppressing cell proliferation (21, 34).

However, cell proliferation is absolutely necessary for vital processes. Following a renal 369 epithelial injury, epithelial proliferation is known to be instrumental to organ repair (18). Proliferation 370 demands a high energetic input, and oxidative phosphorylation is the most efficient pathway for energy 371 production. In keeping with that, we found that proliferation is associated with increased expression of 372 nucleus-encoded OXPHOS genes in injured kidneys. Kidneys transitioning to fibrotic chronic kidney 373 disease display a dissociated transcriptomic pattern: high proliferation index with maintained 374 expression of nucleus-encoded OXPHOS genes but decreased expression of mitochondria-encoded 375 OXPHOS genes. This mitochondrial imbalance is known to be deleterious (48). In vitro, hypoxia and 376 glucose deprivation did decrease mitochondrial potential, and caused cell death in proliferating cells, 377 without causing mitonuclear imbalance, suggesting proliferating cells are sensitive to mitochondrial 378 dysfunction in general (Figure S1). This is in keeping with recent studies showing that maintaining 379 oxidative phosphorylation during and after acute kidney injury (AKI) is protective (23, 36, 54). Other 380 studies also suggested that energy-parsimonious approaches might mitigate renal damage at the early 381 382 stage of acute kidney injury. For example, the stabilization of the hypoxia inducible factor (HIF) shifts

the energy metabolism to anaerobic glycolysis, inhibits cell proliferation (12, 17, 25) and protects against ischemic acute kidney injury (43, 46, 59).

# 385 Proliferation as a therapeutic target in kidney diseases

We identified kidney epithelial proliferation as a state of energy crisis with increased sensitivity to cell 386 death. However, epithelial cell proliferation is necessary for kidney repair. Thus, an interesting strategy 387 to mitigate necrosis would be to delay proliferative repair in kidneys with ongoing injury, and allow 388 proliferation after cessation of the injury. However, identifying the optimal time frame for the 389 inhibition of proliferation after kidney injury in individual patients will necessitate the implementation 390 of dynamic biomarkers of acute kidney injury. In this perspective, the cell cycle arrest markers IGFB7 391 and TIMP2 are clinically available urinary markers that might help to refine the different stages of 392 injury and repair after acute kidney injury (62). Urinary guinolinate/tryptophan ratio is another 393 emerging non-invasive marker allowing to pinpoint the mitochondrial defect during acute kidney injury 394 (36). 395

Targeting the cell cycle to orchestrate kidney repair is an attractive option, but raises the concern of extrarenal side effects, as proliferation is both necessary for the self-renewal of certain tissues like gut or blood cells, and also instrumental in the development of cancers. Thus, targeting proliferation in a time and tissue specific manner would be an advantageous strategy to improve renal outcomes while minimizing the risk of side effects.

401

# 402 PERSPECTIVES AND SIGNIFICANCE

Proliferation is an energy demanding process impairing the cellular ability to cope with a toxic or ischemic injury. We postulate that interventions to mitigate proliferation and restore energy production can enhance cell survival and organ recovery (Fig. 7).

# 407 SUPPLEMENTAL MATERIAL:

# 408 https://doi.org/10.6084/m9.figshare.24504028

409

410 Fig. S1. A. Expression of HIF1alpha, ATP5A and MTCO1. B. Proliferation in cells incubated with

- 411 vehicle, Pifithrin alpha or tenovin-1, represented as relative cell count per field.
- 412 **Fig. S2.** Monitoring of intracellular ATP/ADP ratio.
- Fig. S3. Transcriptomic signature associated with proliferation at different time points of kidney
  transplantation.
- 415 Fig. S4. Proliferation index and renal epithelial cell differentiation markers in single cells from a
- 416 rejecting human kidney.
- 417 **Fig. S5.** Association of proliferation index and OXPHOS with chronic kidney disease progression.
- 418 **Fig. S6.** Association of the proliferation index and the OXPHOS indexes with long term outcomes.
- 419 Table S1. Association of proliferation-associated genes with energy metabolism pathways from the
- 420 KEGG encyclopedia.
- 421 **Table S2.** Metabolic pathways and genes associated with proliferation in injured kidneys (reperfusion).
- 422 **Table S4.** Key resources.
- 423 **Data File S1.** Fiji Jython script for single cell ratiometric analysis
- 424 **Movie S1.** Live PercevalHR video: scratch assay.
- 425 **Movie S2.** Live PercevalHR video: effect of various cell-cycle acting molecules.
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429 Authors declare that they have no competing interests.

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#### FIGURE LEGENDS 643

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Figure 1. Consequences of cell proliferation on susceptibility to cell death. (a) Representative images 645 646 of JC-1 staining in control conditions (CTL) or under energy depletion (ED). The red fluorescence indicates aggregates forming in high potential mitochondria. The green fluorescence indicates JC-1 647 monomers in low potential mitochondria. The composite image shows the increase in JC-1 monomers 648 under energy depletion. (b) Quantification of mitochondrial potential by JC-1 in control condition, and 649 energy depletion, showing the ratio of red/green fluorescence intensity in arbitrary units. (c) Effect of 650 cell cycle inhibition by tenovin-1 or cell cycle facilitation by pifithrin- $\alpha$  on cellular death caused by 651 puromycin (pre-incubation for 4 hours before puromycin exposure). (d) Effect of cell cycle inhibition 652 by tenovin-1 or cell cycle facilitation by pifithrin- $\alpha$  on cellular necrosis caused by energy depletion 653 (preincubaiton for 4 hours before oxygen and glucose deprivation). \*: p-value <0.05 ; NS: statistically 654 non-significant. 655

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657 Figure 2. Cell cycle interventions and their effects on ATP/ADP ratio. (A). Left panel: Wells were

plated with increasing numbers of PercevalHR expressing cells to obtain various levels of confluence 658

in control condition or with 1µM rigosertib to inhibit the cell cycle. Right panel: Representative 659 pictures obtained 0 and 15 hours after a scratch performed under control condition or with exposure to 660

1µM rigosertib to inhibit wound closure. (B) Pharmaceutical interventions on the cell cycle using

661 various compounds on PercevalHR expressing cells over an 18-hr time course (total= 7345 events): 662 663 KU55933 (10 µM), pifithrin-alpha (50 µM), rigosertib (10 µM), tenovin-1 (10 µM). C Quantification of changes in single cell intracellular ATP/ADP ratio over an 18-hr exposure to various cell cycle 664

665 666 modifiers.

Figure 3. ATP/ADP variations throughout the cell cycle. (A, left panel): Live imaging on a single 667 PercevalHR expressing cell undergoing mitosis. (A, right panel): Quantification of the intracellular 668 ATP/ADP ratio in single cells during the perimitotic period with in silico synchronization on time of 669 mitosis (n= 117 mitoses). (B) ATP/ADP changes in PercevalHR expressing cells incubated with the 670 cell cycle facilitator pifithrin-alpha or with the cell cycle inhibitor tenovin-1 between 2 successive 671 mitoses (n= 42 mitoses). ATP/ADP ratio values are represented as means and whiskers indicate the 672 673 standard error. P-values represent the significance of the comparison between the first and second mitosis within each treatment group, using a Wilcoxon signed-rank test. 674 675

Figure 4. Transcriptomic signature associated with proliferation. (A). KEGG pathways enrichment 676 associated with proliferation in kidney allografts immediately after reperfusion. The 20 most significant 677 pathways are labeled. (B). Vulcano plot showing the correlation between OXPHOS gene expression 678 679 and the computed

proliferation index in kidney allografts (right panel). x-axis: Kendall's k correlation coefficient; y-axis: 680 significance represented by the -log(p-value) of the correlation (Kendall); blue: mitochondria-encoded 681 genes; red: nuclear-encoded genes. (C). Differential correlations of nuclei and mitochondria-encoded 682 OXPHOS with the proliferation index in kidney allografts. 683

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Figure 5. Oxidative phosphorylation in proliferating epithelial cells. (A) Single-cell RNA-seq analysis 685 of human rejecting kidney showing clusters corresponding to different cell types within the kidney. The 686 subset of epithelial cells is circled in red. (B) In the subset of renal epithelial cells (PT, LOH and CD), 687 an increased proliferation correlated with a decreased expression of mitochondria-encoded OXPHOS 688 genes (mean values of oxphos gene expression with standard-error whiskers, by proliferation index 689

values rounded to the nearest  $10^{-5}$ ). 690

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**Figure 6.** Association of proliferation index and OXPHOS mitochondrial genes expression with chronic kidney disease progression. (A) Expression of nucleus-encoded OXPHOS genes was not correlated with proliferation index or evolution towards chronic kidney disease. (B) Expression of mitochondria-encoded OXPHOS genes was strongly correlated with proliferation index and evolution towards chronic kidney disease.

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**Figure 7.** Impact of energy metabolism changes leading to cellular injury and proliferation in injured kidneys. Top: the lines show the physiological changes in oxidative phosphorylation (pink) and proliferation (blue) leading to full recovery. Bottom: the lines show pathological processes with excessive proliferation leading to cell death by energy depletion (hatched purple area) and persistent oxidative phosphorylation defect leading to chronic kidney disease and fibrosis (hatched green area).















# Viability of proliferating kidney cells

