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DISSERTATION

**Analysis of circadian regulation in a cellular model of
pancreatic cancer**

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1. Abstract:

Perturbations of circadian rhythms are instrumental in carcinogenesis and facilitate the development of cancer hallmarks. TGF β acts as a tumour suppressor in the early stages of tumourigenesis due to its growth inhibitory effect, and is able to prompt the tumour malignancy in the advanced stage. As a core component of the TGF β canonical signal pathway, SMAD4 (DPC4) is frequently mutated in pancreatic cancer, usually causing poor prognosis for PDA patients.

Despite current findings revealing the circadian rhythmicity of elements in the TGF β pathway, the bidirectional interplay between the TGF β pathway, the circadian clock, and its potential impact on cancer development remains largely uncharacterized.

In this doctoral dissertation work, we used Pancreatic adenocarcinoma (PDA) as an experimental model and carried out a systematic analysis to investigate the mechanistic interplay between circadian rhythms and the TGF β canonical signalling. Particularly, we explored its impact on tumour malignancy in PDA cells, and further verified the influence of genes involved in the crosstalk on patient survival. We identified oscillatory transcriptional expression of *TGF β 1*, *SMAD3*, *SMAD4* and *SMAD7*, notably in SMAD4 wild-type (WT) PDA cells. Furthermore, the circadian perturbation via knockdown of *BMAL1* and *NR1D1* impaired mRNA dynamics of these TGF β signalling components. In particular, we verified that possible mediators (*DEC1*, *DEC2* and *CRY1*) among the crosstalk elements were altered depending on SMAD4 expression level. We further identified a link of the TGF β signalling pathway toward the circadian clock in SMAD4-WT cells, which is altered in SMAD4-mutant (Del) cells. Remarkably, the activation of the TGF β canonical pathway results in an altered clock with a shorter period, cell cycle arrest, accelerated apoptosis, increased metastatic ability and enhanced chemosensitivity.

Taken together, our data indicate that SMAD4-WT and SMAD4-mutant pancreatic cancer cells upon the dysregulation of the circadian clock, result in a significant differential change in cell survival, invasiveness and drug response, highlighting the importance of the associations between the TGF β pathway, the cellular clock and drug timing which affect chemosensitivity and patient prognosis in a cancer context. TGF β modulates the circadian clock differentially via the canonical and non-canonical pathways in our model system. This work provides novel evidence concerning the crosstalk between the circadian clock and TGF β signalling in PDA with an indispensable role for SMAD4 and further highlights new connections between both systems with possible roles in drug response, cancer progression and patients' prognosis.

1. Zusammenfassung:

Gestörte zirkadianen Rhythmen sind maßgeblich an der Karzinogenese beteiligt und tragen zur Entwicklung von Krebsmerkmalen bei. TGF β wirkt aufgrund seiner wachstumshemmenden Wirkung im Krebsfrühstadium als Tumorsuppressor und kann im fortgeschrittenen Krebsstadium die Tumormalignität auslösen. Als Kernkomponente im kanonischen TGF β -Signalweg ist SMAD4 (DPC4) häufig bei

Bauchspeicheldrüsenkrebs mutiert, was normalerweise schlechte Folgen für die Patienten hat.

Trotz aktueller Erkenntnisse, welche die zirkadiane Rhythmicität von Elementen des TGF β -Signalwegs offenbaren, ist das bidirektionale Zusammenspiel zwischen dem TGF β -Signalweg, der zirkadianen Uhr und ihren möglichen Auswirkungen auf die Krebsentwicklung weitgehend uncharakterisiert. In dieser Dissertation verwendeten wir das Pankreas-Adenokarzinom (PDA) als experimentelles Modell und führten eine systematische Analyse durch, um das mechanistische Zusammenspiel zwischen zirkadianen Rhythmen und dem kanonischen TGF β -Signalweg zu untersuchen. Insbesondere untersuchten wir die Auswirkungen auf die Malignität von Tumoren in PDA-Zellen und verifizierten die Einflüsse von Genen, die am Crosstalk beteiligt sind, auf das Überleben der Patienten. Wir identifizierten oszillatorische transkriptionelle Expression von *TGF β 1*, *SMAD3*, *SMAD4* und *SMAD7*, insbesondere in *SMAD4* Wild-Typ (WT) PDA-Zellen. Darüber hinaus beeinträchtigte die zirkadiane Störung durch Herunterregulieren von *BMAL1* und *NR1D1* die mRNA-Dynamik dieser TGF β -Signalkomponenten. Insbesondere überprüften wir, ob die möglichen Mediatoren (*DEC1*, *DEC2* und *CRY1*) im Crosstalk in *SMAD4*-abhängiger Weise verändert wurden. Wir haben ferner eine Verbindung der TGF β -Signalübertragung zur zirkadianen Uhr in *SMAD4*-WT-Zellen identifiziert, die in *SMAD4*-Mutanten (Del) -Zellen verändert ist. Bemerkenswerterweise führt die Aktivierung des kanonischen TGF β -Weges zu einer kürzeren Periode, einem Stillstand des Zellzyklus, einer beschleunigten Apoptose, einer erhöhten Metastasierungsfähigkeit und einer erhöhten Chemosensitivität.

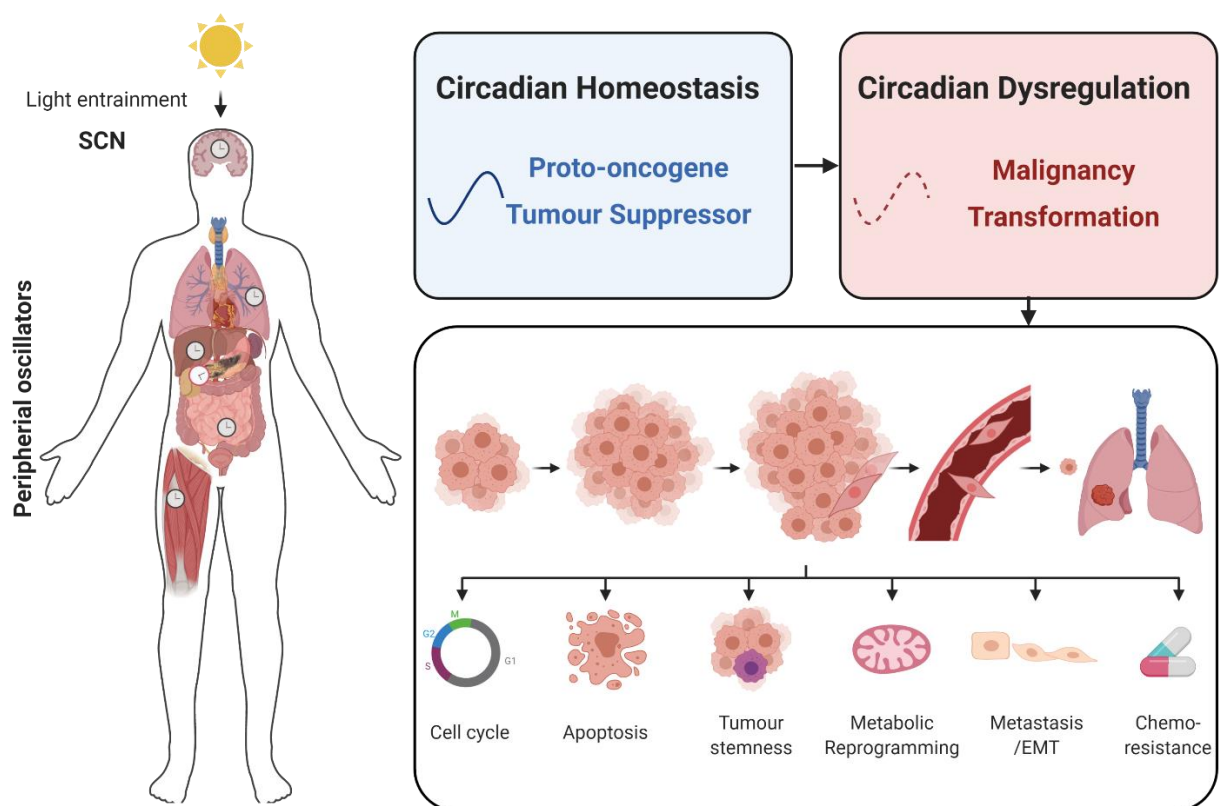
Insgesamt zeigen unsere Daten, dass *SMAD4*-WT und *SMAD4*-mutierte Pankreaskrebszellen bei einer Dysregulation der zirkadianen Uhr zu einer signifikanten unterschiedlichen Veränderung des Zellüberlebens, der Invasivität und der Arzneimittelantwort führen, was die Bedeutung der Verbindung zwischen der Uhr und dem TGF β -Signalweg hervorhebt. Die zelluläre Uhr und der Zeitpunkt der Arzneimittelgabe beeinflussen die Chemosensitivität und das Patientenüberleben in einem Krebskontext. In unserem Modellsystem moduliert TGF β die zirkadiane Uhr über die kanonischen und nichtkanonischen Pfade unterschiedlich. Diese Arbeit liefert neue Belege für das Zusammenspiel zwischen der zirkadianen Uhr und der TGF β -Signalübertragung in PDAs, die für *SMAD4* eine unverzichtbare Rolle spielen, und zeigt neue Verbindungen zwischen beiden Systemen auf, die möglicherweise eine Rolle bei der Reaktion auf Arzneimittel, dem Fortschreiten des Krebses und der Prognose der Patienten spielen.

2. Introduction:

2.1 Circadian system

A wide variety of behavioural activities and physiological processes of most organisms follows a daily cycle, which is regulated by an endogenous biological timing-system, known as circadian rhythms. In humans, circadian rhythms have a period of approximately 24 hours, similar to the geophysical time of the Earth, following the entrainment of optical or non-optical stimuli. The mammalian circadian system consists of a main pacemaker located in the suprachiasmatic nucleus (SCN) in the hypothalamus and numerous peripheral oscillators exist in a variety of organs, tissues and virtually every single cell. The main pacemaker can be entrained by external “Zeitgebers”, including light, food and temperature and in turn, drives the peripheral oscillators through neuronal and hormonal signals ¹ (Figure 1). Once the retinal cells receive light stimuli, the photic input will be transmitted to the main pacemaker (in SCN) via the retinohypothalamic tract ². Upon signal transmission, the main pacemaker generates and maintains rhythms, and subsequently synchronizes the peripheral clocks to one and another through output hormonal pathways (e.g., glucocorticoid pathways ³).

Figure 1. The circadian system in humans and its dysregulation influence cancer transformation and tumour malignancy (Created by Biorender.com).



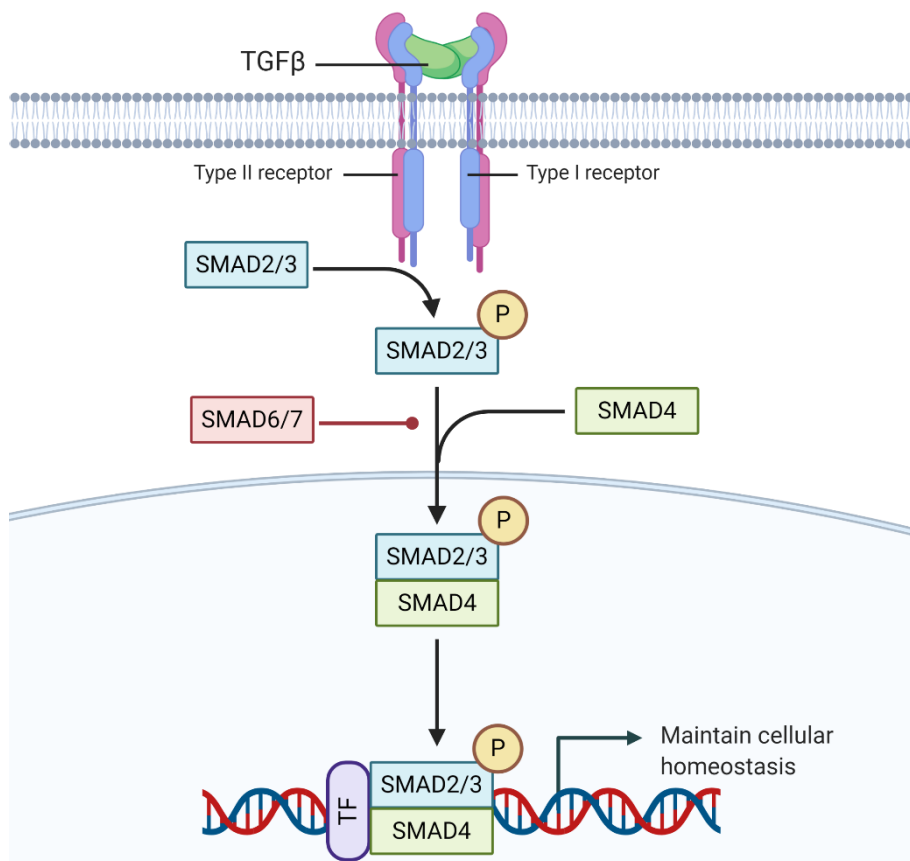
2.2 Cellular clocks and clock-controlled genes

Cellular oscillators are driven by transcriptional/translational feedback loops (TTFL) that constitute tight gene/protein regulatory networks ¹. In mammalian cells, 14 core-clock genes form the endogenous core clock network (CCN), which is involved in the circadian regulation of cellular processes, including the cell cycle, apoptosis, DNA repair, metabolism, immunity and epithelial-to-mesenchymal transition (EMT) ^{4,5}. Clock-controlled genes (CCGs) that display daily rhythms in their expression are involved in various cellular processes from cell cycle regulation (e.g. *INK4A*) ⁶, immune function (e.g. *TNF*) ⁷ to metabolism programming (e.g. *SIRT1*) ⁸. Impairment of these components has widespread implications and can prompt severe pathological phenotypes including cancer ⁹ (Figure 1).

2.3 Basics of the TGF β system

The transforming growth factor β (TGF β) signalling pathway maintains cellular homeostasis and plays a major regulatory role in fetal development, immune response, wound repair, bone formation and cell immortalization in various cell types and tissues ¹⁰. Perturbations of the TGF β pathway are implicated in oncogenic transformation ¹⁰. As for the TGF β subfamily, three distant isoforms have been identified (including TGF β 1, TGF β 2 and TGF β 3), each encoded by a different gene sharing around 70% homology within their sequence ¹¹. TGF β 1 is the most well-studied isoform, hence it has also been used for the present dissertation.

Figure 2. Schematic representation of Canonical TGF β pathway in human cells (created by Biorender.com).



The basic system of the canonical TGF β pathway consists of TGF β cytokines, receptors, Smads (receptor-Smads and inhibitory-Smads) and the common-Smad (Smad4, *Figure 2*). The precursor molecule of TGF β is stored in the extracellular matrix that functions as a reservoir for TGF β ligands ¹⁰. The canonical TGF β signalling is transduced from the cytomembrane to the cytoplasm by binding to receptors known as TGF β type I and type II receptors ¹⁰ (*Figure 2*). Once bound to the ligand TGF β , the receptors are activated and propagate the signal by phosphorylating receptor-Smads (R-Smads) ¹⁰. The activated R-Smads (Smad2 and Smad3) translocate to the nucleus and form a complex with Smad4. Hence the Smads complex operates on downstream gene expression by regulating transcriptional activity, whereas Smad7, known as inhibitory-Smad, prevents this complex formation ¹⁰.

2.4 Roles of TGF β in pancreatic adenocarcinomas

Pancreatic ductal adenocarcinoma (PDA) is a fatal disease, and over half of patients harbour SMAD4 mutations (mostly deletions, Del). In the early stage of PDA, TGF β acts as a tumour suppressor by regulating cryostasis, the cell cycle, apoptosis and its inflammation-inhibitory effects ¹⁰. Related to these vital regulatory functions of TGF β are the severe consequences that often result from malfunctions of this signalling pathway, known as tumorigenesis ¹⁰. Inactivation of TGF β canonical pathway has implications in hyperproliferation, tumour formation, inflammation, immunosuppression and tumour metastasis, leading to a poor prognosis and a low survival rate ¹². As tumours grow and progress, genetic alterations often arise in the TGF β canonical components (e.g., SMAD4 mutations), meanwhile tumour cells release a large amount of TGF β in the tumour microenvironment ¹¹. As a consequence, the overwhelming released TGF β not only activates the TGF β non-canonical pathways such as RAS-ERK further promoting tumorigenesis, but also affects the tumour microenvironment by impairing cell adhesion, suppressing immunity, promoting angiogenesis, and degrading the extracellular matrix ¹¹. Ultimately, these genetic modifications override the growth inhibitory effects of TGF β , further contributing to cancer development and the metastatic progress.

2.5 The reciprocal interplay between the circadian clock and the TGF β canonical pathway

Previous studies reported a rhythmic expression of *Tgfb1* and *Smad3* at the transcriptome and proteome levels in mouse brown adipocyte ¹³, mouse kidney ¹⁴ and mouse heart ¹⁵. Furthermore, the circadian expression of *Tgfb1* was found to be perturbed upon *Clock*-knockout in mice ¹⁶. In addition, former work from our group demonstrated that SMAD4 is a member of the network of circadian regulated genes (NCRG) ¹⁷. These findings suggest that the TGF β pathway is regulated by the circadian clock. In turn, the Smads complex has been found to bind to the promoter region of the clock gene *Dec1* in mouse fibroblasts ¹⁸, human keratinocytes ¹⁹ and pancreatic cancer cells ²⁰, thereby regulating circadian patterns. Additionally, activation of TGF β signalling has been found to induce phase-shifts of the tissue clock in mouse kidney

and adrenal gland¹⁸, indicating that peripheral oscillators are regulated by the TGF β canonical pathway. This evidence hints at a mutual interaction bridging the TGF β pathway and the circadian clock.

Despite a few studies pointing to the crosstalk between TGF β and circadian pathways in normal tissues and cells as above-mentioned¹³⁻¹⁶, it remains unclear whether this crosstalk also exists in human cancer cells and whether it has an impact on tumour malignancy. The molecular mechanisms underlying this crosstalk in PDA cells remain largely uncharacterized.

2.6 Aims of the thesis:

The main aim of this work is to investigate whether the reciprocal interaction between the clock network and the TGF β pathway exists in PDA cells and its underlying molecular mechanism, and to dissect the role of this crosstalk on cell-fate determination, cancer progress and susceptibility of gemcitabine in PDA cells.

Hence, we used an *in vitro* model system consisting of SMAD4-WT and SMAD4-Del PDA cells derived from the primary tumour and metastatic lesions, respectively.

- a) To profile the clock phenotypes in SMAD4-WT and SMAD4-Del PDA cells, and characterize the role of circadian rhythms (via knockdown of core clock genes) in cell-fate decisions, metastatic progress, drug response in both PDA cells.
- b) To investigate thoroughly the reciprocal crosstalk between the TGF β (canonical or non-canonical) pathway and circadian rhythms in SMAD4-WT and SMAD4-Del PDA cells and the possible genes involved in this crosstalk, and further study the effect of expression levels of these genes on patient survival.
- c) To optimize the therapeutic efficiency using a timing administration approach applied for SMAD4-WT and SMAD4-Del PDA cells, and investigate the influence of the TGF β -Clock coupling in cell-fate decisions (e.g., proliferation, apoptosis and cell cycle dynamics), metastatic properties and patient survival.

Our data show that mRNA expression of *SMAD3*, *SMAD4*, *SMAD7* and *TGF β 1* exhibits circadian rhythms in SMAD4-proficient cells and that these cycling transcripts were perturbed by circadian malfunctions, hinting at a circadian regulation of these TGF β components. Remarkably, we found that the activation of the TGF β pathway with the overexpression of SMAD4 affects the clock phenotype in these PDA cells, resulting in a shorter period. Additionally, the expression level of clock genes (e.g. *DEC1*, *DEC2* and *CRY1*) is SMAD4-dependent, pointing to these genes as putative mediators of the hypothesized interplay in our model system.

Furthermore, we investigated key biological processes (including proliferation, apoptosis, the cell cycle, migration and invasion) and drug response in clock-disrupted (*shBMAL1*, *shPER2* and *shNR1D1* knockdown) and SMAD4 up- or down-regulated PDA cells. Our data indicate that clock disruption and the different treatment timings affect drug response in SMAD4-WT cells, which is distinct from SMAD4-

deficient cells, highlighting the important role of SMAD4 as a key regulator of clock components. Our results illustrate the pivotal role of the bidirectional crosstalk between the molecular clock and the TGF β pathway in the cell cycle, apoptosis, cancer metastasis and treatment response in PDA cells, which further affects PDA patient's survival.

Taken together, by means of a comprehensive *in vitro* study on PDA cells combined with clinical analyses using the public database (TCGA), the present study provides novel evidence for a SMAD4- and clock-dependent drug response in PDA cells. Particularly, this study highlights the role of the reciprocal link between the clock and the TGF β canonical pathway in cell-fate determination and cancer metastasis in PDA cells, which further affects patient prognosis.

3. Methodology:

3.1 Cell culture

Panc1(ATCC: CRL-1469) and AsPC1 (ATCC: CRL-1682) cells were used as our *in vitro* model system. Cells were maintained in RPMI 1640 (Gibco) supplemented with 1% penicillin-streptomycin (PS, Gibco) and 10% fetal bovine serum (FBS, Gibco). All cells were incubated at 37°C in a humidified atmosphere with 5% CO₂.

3.2 Lentivirus and γ -retrovirus production and viral transduction

Lentiviral vectors containing a *BMAL1*- and a *PER2*-promoter-driven-Luciferase were generated as previously described²¹. For the knockdowns, a TRC lentiviral shRNA glycerol set (Dharmacon) for a corresponding gene consists of 5 - 6 individual shRNAs vectors. The best knockdown efficiency was determined by RT-qPCR.

For lentiviral production, HEK293T (ATCC: CRL-3216) cells were cultured and co-transfected with psPAX, pMD2G and expression plasmid. The transfection efficiency was enhanced by CalPhos mammalian transfection kit (Clontech Fremont). For retrovirus generation, HEK293T cells were maintained and co-transfected with pBabe-puro empty vector or pBabe-Smad4-Flag along with PMD2.G and pUMVC plasmids using FUGENE (Promega). Virus particles were harvested by centrifugation and the supernatant was stored in -80°C and used for the subsequent viral transduction.

Cells were transduced with the virus filtrate along with protamine sulphate (Sigma) and polybrene (Sigma). The supernatant was subsequently removed after 6 - 8 hours. To obtain the cells stably expressing a specific gene, transduced cells were selected with corresponding antibiotics according to the manufacturer's instruction concerning plasmids.

3.3 Cell synchronisation and real-time bioluminescence recording

Cells were synchronised by medium change; the time point of medium change is defined as 0 h. Live-cell bioluminescence was measured by a LumiCycle (Actimetrics). Cells were maintained in phenol-red free media containing D-luciferin (PJK). For TGF β 1 stimulation, cells were maintained with 10ng/ml TGF β 1 for five consecutive days. TGF β 1 concentration was determined as previously described²². The Chronostar software was used for the data analysis.

3.4 RNA isolation, cDNA synthesis and RT-qPCR

Cell pellets were collected and lysed with RLT plus buffer (Qiagen). The plus RNeasy Mini kit (Qiagen) was used to extract total RNA from cell lysate. To digest genomic DNA, homogenized cell lysates were passed through a gDNA eliminator spin column. Total RNA was eluted in 20 μ l TE buffer.

1000 ng RNA was subsequently reverse-transcribed to cDNA with random hexamers (Eurofins) and Reverse Transcriptase (Life technologies). The qPCR reaction and the subsequent melting curve were

carried out using a CFX Connect Real-Time PCR Detection System (Biorad). GAPDH was used as a reference gene. Relative gene expression was calculated using the $2^{-\Delta\Delta Ct}$ method²³. Mean and SEM were calculated including biological and technical replicates.

3.5 Proliferation and apoptosis assays

Cells were seeded and allowed to adhere in a 96-well plate. The medium was subsequently replaced. Plates were placed in the IncuCyte® S3 Live Cell System Analysis (Sartorius). For proliferation, images were immediately recorded with a 10x objective using phase channel. For apoptosis, the cell media were replaced with fresh media containing the caspase 3/7 apoptosis reagent (Sartorius, ratio: 1:2000). Cell images were scanned with a 20x objective using phase and green channels. For proliferation and apoptosis assays, the analysis was performed using the IncuCyte S3 Software (Sartorius). The replicates were included in the data. For TGFβ1 stimulation, cells were maintained with 10ng/ml TGFβ1 or its solvent (0.1% BSA).

3.6 Migration and invasion assays

For migration assays, cells were seeded in a 96-well Essen Image Lock TM microplate (Essen BioScience) and incubated till attached to the plates. Reproducible wounds were created by the Wound Maker (Essen BioScience), and the plate was placed in the IncuCyte® S3 Live Cell System Analysis. The images were analysed using the scratch wound method of the IncuCyte S3 Software. Then, the wound width of each time point was exported. The migration speeds were calculated using the following equation:

$$\text{Migration speed} = \frac{\text{Final wound width} - \text{Initial wound width}}{\text{Time}}$$

Time is taken by either the timepoint for wound closed or cutting off at 48h.

For invasion assays, cells were mixed with 20μl Basement Membrane Matrix (Trevigen) and seeded in the inner chamber of a 96-well Incucyte Chemotaxis invasion clear-view plates (Sartorius). Basement Membrane Matrix was allowed to polymerise at 37°C for 45 minutes. Cell invasion was measured using the IncuCyte® S3 Live Cell System Analysis using the phase channel.

3.7 Cytotoxicity assays

Cells were seeded in a 96-well plate overnight. Subsequently, the supernatant was replaced with fresh medium containing IncuCyte® Cytotox Reagents (Red, Sartorius) supplemented appropriate concentrations of gemcitabine (IC50: Panc1, 9.5μM; AsPC1, 23.9μM)²⁴.

To determine the accurate cell viability, cells were labelled with an IncuCyte® NucLight Rapid Red Reagent (Sartorius) for 30 mins before measurements. After treatment, viable cells were counted by IncuCyte® S3 Live Cell System Analysis (Sartorius) using phase and red channels.

3.8 Western blot

Cell pellets were collected and resuspended in lysis buffer. 20mg proteins were subjected to SDS

polyacrylamide gel electrophoresis and transferred to a Nitrocellulose Membranes (GE Healthcare Amersham™). Membranes were probed with primary antibodies, then incubated with corresponding secondary antibody. Signals were acquired by Image Quant LAS 4000 series (GE Health care).

3.9 Cell cycle analysis

Cells under the logarithmic phase were collected, washed with 1x PBS (Gibco) and fixed with ice-cold 80% ethanol. Subsequently, samples were washed with PBS and incubated in PBS solution containing 0.5% Tween20, 1% BSA, 2 N HCl/Triton x-100 and 10 mg/mL of Rnase (AppliChem) for 30 minutes at room temperature. For PI staining, the fixed cell pellets were resuspended and stained in 50μM PI (Sigma) for 30 minutes at 37°C. The stained cells were read by FACS Cabilur (Becton Dickinson). The data was analysed by fitting a univariate cell cycle model using the Watson pragmatic algorithm as implemented in FlowJo v10.2 (FlowJo LLC).

3.10 Statistical analysis

The significant differences between groups (* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$) was validated using one- or two-way ANOVA followed by Tukey's comparisons and two-tailed (multiple) t-tests using the GraphPad Prism v.6 (GraphPad Prism).

3.11 Cosinor analysis

To detect the circadian rhythmicity of a specific gene, the cosinor analysis was used to verify robustly oscillating transcripts with a p -value < 0.05 . The p -value was calculated by QUICK CALCS (GraphPad, <https://www.graphpad.com/quickcalcs/pValue1/>). The oscillations were estimated by the following equation:

$$Y(t) = B + A \cdot \left(\cos \frac{2\pi \cdot t}{P} + \varphi \right) + S \cdot t$$

t = time, B = baseline, A = amplitude, S = slope, φ = acrophase, P = period

3.12 Survival analysis of PDA patients

Clinical data for PDA patients including overall patient survival were obtained from the TCGA research network (National Cancer Institute). OncoPrint functionality was used for mutation frequencies of 10 candidate genes. For the candidate genes, we plotted survival curves using a Cox model that includes coxph (Surv (times, died) ~ gene + grade1 + grade2 + grade3 + age) using OncoLnc (<http://www.oncolnc.org>). Based on the mean expression value of each gene, the patient cohort was equally divided into patients with high-expression ($n = 87$) and low-expression ($n = 87$) for a specific gene. Survival data of PDA patients in high- and low-expression groups for each candidate gene were analysed.

4. Results:

4.1 The bidirectional interplay between the circadian clock and the TGF β canonical pathway

Refer to Figure. 1 - 2, Table. 1 - 3, and Figure. S1 - S4 in the publication.

To investigate the impact of a disrupted clock in cell-fate decisions, we established an *in vitro* model of SMAD4-WT (Panc1) and SMAD4-mutant PDA cells (AsPC1), derived from primary tumours and metastasis ascites, respectively. Both cell lines show similar cell cycle dynamics (doubling time \approx 52h)^{25,26}, and harbour mutated forms of *KRAS*, *Ink4a* and *TP53*²⁷⁻²⁹, making them appropriate for this study. Both cell lines further exhibit circadian rhythms, with a smaller amplitude and shorter period (26.1 ± 0.3 h) found for Panc1 in comparison with AsPC1 cells (27.4 ± 0.6 h) as observed based on bioluminescence measurements of *BMAL1* promoter activity. A 48h time-course RT-qPCR analysis confirmed the clock phenotypes observed in the bioluminescence data, and both cell lines showed anti-phasic behaviour for *BMAL1* and *PER2*. Accordingly, these data indicate that the endogenous circadian clock operates robustly but differentially in both PDA cell lines.

Subsequently, we performed knockdowns (KDs) for the core-clock genes *BMAL1*, *PER2*, and *NR1D1* in both cell lines, and evaluated the output concerning gene expression. In addition, we examined SMAD4 expression at gene and protein level and ascertained that AsPC1 is a SMAD4-deficient cell line, as previously reported³⁰. Intriguingly, KDs of *BMAL1* and *NR1D1* not only affect *SMAD4* expression level but also disturb the rhythmicity of *SMAD4* in the Panc1 cell line.

Given that our results point to a linking between SMAD4 and core-clock components, we decide to further investigate this interplay in greater detail. Therefore, we quantified mRNA dynamics of *SMAD3*, *SMAD4*, *SMAD7* and *TGF β 1* in our *in vitro* model using a 39h time-course RT-qPCR analysis. Our data showed a rhythmic expression of *TGF β 1* in both SMAD4-proficient and SMAD4-deficient cells. Interestingly, transcripts of *SMAD3* and *TGF β 1* oscillated with similar phases and periods as *BMAL1* in Panc1 (WT) cells. In contrast, in AsPC1 (SMAD4-mutant) cells, *TGF β 1* oscillated with a longer period (\sim 27h) than *BMAL1* ($22.3\text{h} \pm 0.9\text{h}$), indicating that the linking between the rhythmic *TGF β 1* and *BMAL1* is altered in absence of SMAD4. From a comparison of these elements' expression for both cell lines, we observed reductions of *SMAD3* and *SMAD7* and an increased expression level of *TGF β 1* in AsPC1 relative to Panc1. This further points to mutational inactivation of the TGF β canonical pathway via SMAD4 (AsPC1), which may lead to the activation of the non-canonical TGF β pathway such as RAS-ERK, and an altered interaction with the circadian clock.

We further explored links from the core-clock bridging to the canonical TGF β pathway. A previous study reported that the core clock components *Bmal1* and *Nr1d1* are linked with the TGF β pathway in mouse adipose cells, *Bmal1* activates the expression of *Smad3* or *Nr1d1* by binding to the promoter region at a specific time point (CT8 in mice)¹³. Therefore, we verified the effects of *BMAL1* and *NR1D1* KDs on the

rhythmic expression of *TGFβ1*, *SMAD3*, *SMAD4* and *SMAD7* using a 24h time-course RT-qPCR analysis. Our data showed that clock dysregulation (*BMAL1*-KD) repressed the transcripts of *SMAD3* and *SMAD7* at 21h after synchronization of Panc1 cells, implying that disruption of the circadian system by *BMAL1*-KD inactivates the TGFβ canonical pathway at a specific time point. In addition, our results show that circadian perturbation by silencing of *BMAL1* and *NR1D1* abolish the rhythmic expression of *TGFβ1*, *SMAD3*, *SMAD4* and *SMAD7*, indicating these genes are likely to be clock-regulated.

To obtain further insights into the impact of the TGFβ pathway on the clock phenotype, we measured the promoter activity of *BMAL1* and *PER2* in *SMAD4*-KD and overexpression (-OE) cells stimulated with additional TGFβ1. Remarkably, the over-activation of the TGFβ pathway (*SMAD4*-OE + TGFβ1) resulted in significantly shortened periods of circadian oscillations ($p < 0.05$), in particular for *PER2*, indicating regulatory roles of SMAD4 and the extrinsic TGFβ in the circadian rhythms. Additionally, we examined the impact of SMAD4 on the expression of the core-clock genes *BMAL1*, *PER2*, *NR1D1* and *CRY1*, and of the clock-regulated genes *DEC1* and *DEC2*, which have been reported as mediators of the hypothesized TGFβ-clock networks^{14,18,31}. Remarkably, the restoration of *SMAD4* expression (*SMAD4*-OE) led to a decrease of the expression of *DEC1* and *DEC2* in both PDA cell lines, whereas it up-regulated the expression of *CRY1*. Consistently, we observed the opposite result upon *SMAD4*-KD in Panc1. Taken together, these data further corroborate the existence of a reciprocal interplay between the clock and the TGFβ canonical pathway via the modulation of *CRY1*, *DEC1* and *DEC2*.

4.2 Perturbation of core-clock elements and SMAD4 impacts on the cell cycle, proliferation and apoptosis in PDA cells

Refer to Figure. 3 - 4 in the publication.

Based on the literature suggesting that both SMAD4 loss and disrupting clock genes contribute to the cancer progress towards malignant phenotypes in PDA³²⁻³⁴, along with our observations of the interplay between the clock and the TGFβ canonical pathway, we hypothesized that their interaction likely affects cell-fate determination and further facilitates pancreatic cancer progression. Hence, we evaluated the effects of perturbing core-clock genes and *SMAD4* in terms of proliferation, cell cycle and apoptosis. Interestingly, SMAD4-proficient (Panc1) and SMAD4-deficient (AsPC1) cells had differing proliferating phenotypes upon the different clock gene KDs. Panc1 cells showed increased proliferative potential after *BMAL1* and *NR1D1* KDs, whereas this phenomenon was not observed upon the same KDs in AsPC1 cells.

To investigate with more details into the underlying mechanism, we analysed the cell cycle for all the conditions mentioned above. In Panc1 cells, we observed a significantly decreased number of cells in S phase and an increased portion of cells in G2/M phase upon *PER2*-KD ($p < 0.05$), whereas the number of cells in S phase increased after *NR1D1*-KD, which support the results of the observed proliferation phenotypes. For AsPC1 cells, S phase increased and G1 phase decreased significantly after *PER2*-KD ($p < 0.05$), which is likewise consistent with our proliferation results. Overall, our proliferation and cell cycle

analysis revealed a cell-type dependency upon the KDs of clock-genes. This might be attributed to their different genomic background (in particular for SMAD4 alteration) that likely impacts on the circadian pathway, resulting in the observed differential proliferative and cell cycle phenotypes.

Nevertheless, the apoptotic profiles of PDA cells exhibited a circadian- and a SMAD4-dependency. The KDs of *BMAL1*, *PER2* and *NR1D1* induced apoptotic properties as compared with *shCtrl*, and *SMAD4*-OE increased the apoptotic ability in both PDA cells. These results indicate that *SMAD4*-OE and the clock dysregulation induce the apoptotic ability in these PDA cells.

4.3 Clock disruption and modifications of the TGF β pathway impact on cell-fate decisions in PDA cells

Refer to Figure. 4 and Figure. S5 – S6 in the publication.

To dissect the putative impacts of the TGF β canonical- and non-canonical pathways in cell-fate decisions, we stimulated *SMAD4*-KD or -OE cells with additional TGF β 1 and analysed the cell cycle, apoptosis, and proliferation. The activation of the TGF β /SMAD4 pathway (*SMAD4*-OE \pm TGF β 1) had no impact on proliferation in Panc1, while its inactivation (*SMAD4*-KD \pm TGF β 1) accelerated proliferative speed. Remarkably, we also observed increased proliferative properties in AsPC1-oeCtrl (*SMAD4*-Del) cells when stimulated with TGF β 1, as compared to *SMAD4*-OE cells. Collectively, these results indicate that inhibiting *SMAD4* may activate the non-canonical pathway (e.g., RAS, PI3K, JNK), bringing out hyperproliferative potentials in PDA cells. To validate our assumption, we analysed the protein expression of RAS and phosphorylated-ERK (p-ERK) in Panc1-*shSMAD4* cells stimulated with 10ng/ml TGF β 1 or its corresponding solvent for 24 hours. We found that TGF β 1 stimulation triggers the phosphorylation of ERK significantly in both Panc1-*shCtrl* and -*shSMAD4* cells ($p < 0.05$). Furthermore, we observed a significant overexpression of RAS and p-ERK upon *SMAD4*-KD (particularly for cells stimulated with TGF β 1), in comparison to *shCtrl* cells ($p < 0.05$). Consistently, these data indicate the activation of the RAS-mediated TGF β (non-canonical) pathway upon *SMAD4* downregulation.

We then verified our above results by cell cycle analysis. *SMAD4* overexpression coupled with TGF β 1 stimulation was found to cause cell cycle arrest at G1/S phase in both PDA cell lines ($p < 0.05$). However, the impairment of the TGF β canonical pathway (Panc1-*shSMAD4*) increased the number of cells in S phase and decreased the number of cells in G1 phase as compared with *shCtrl* cells ($p < 0.05$). In AsPC1 oeCtrl (*SMAD4*-Del) cells, TGF β 1 stimulation led to an increase of cells in S phase, and consistently we observed a hyperproliferative potential in these cells. Altogether, these findings indicate that the active TGF β non-canonical pathway (termed the RAS-ERK pathway) without intact SMAD4 affects cell cycle dynamics and proliferative phenotypes in our PDA cellular model system.

Subsequently, we investigated the impact of TGF β stimulation on the cell cycle upon clock dysregulations. Overall, we observed the cell cycle arrest in G1/S phase in Panc1 cells (*shCtrl* and KDs of the clock genes)

after TGF β 1 stimulation. Unlike in other clock-gene KDs and *shCtrl* conditions, TGF β 1 stimulation increased the percentage of cells in G2/M phase in Panc1-*shNR1D1* condition, implying an altered effect of TGF β on the cell cycle after *NR1D1*-KD. In AsPC1 (SMAD4-deficient) cells, we instead observed increased amounts of cells in G2/M or S phase in *shBMAL1*, *shPER2*, *shNR1D1* and *shCtrl* cells after TGF β stimulation, which is distinct from Panc1 (G1/S phase arrest). Collectively, our findings highlight the importance of the TGF β pathway and core-clock genes in affecting cell-fate decisions of PDA cells and provide novel insights into the role of the interplay affecting the cell cycle, proliferation, and apoptosis.

4.4 Perturbing core-clock elements impacts on metastatic potential in a SMAD4-dependent manner

Refer to Figure. 5 - 6 and Figure. S7 - S8 in the publication.

Next, we examined whether modifications of the TGF β pathway or an aberrant clock may facilitate the formation of tumour metastasis. Hence, we carried out migration and invasion assays, then analysed known EMT markers as well as cellular morphological changes. The migration properties of both PDA cells were accelerated when stimulated with TGF β 1, in particular for *SMAD4*-OE cells. TGF β 1 stimulation alone was not able to enhance the migrative potential in SMAD4-silencing cells (e.g., Panc1-*shSMAD4* and AsPC1-oeCtrl), suggesting the indispensable role of SMAD4 in accelerating metastatic potentials via the TGF β pathway. In agreement with this hypothesis, invasion assays showed that *SMAD4*-OE or adding TGF β 1 enhanced the invasiveness of the cells. Vice versa, the impairment of the TGF β canonical pathway (*SMAD4*-KD) reduced metastatic abilities. Based on these results, we conclude that the intrinsic SMAD4 and sufficient amounts of TGF β in a favourable microenvironment are vital for the acquisition of invasiveness and cellular motility in PDA cells. Given that cancer cells undergoing EMT tend to invade, we verified the above results by measuring EMT makers and observing cell morphological alterations. In order to do this, we selected five known EMT markers (including *E-cadherin*, *N-cadherin*, *Vimentin*, *SNAIL* and *SLUG*) and one maker for cancer stemness (*CD133*). *CD133* and *E-cadherin* expression significantly increased and *Vimentin* and *SLUG* decreased after *SMAD4*-KD in Panc1 cells compared to the Ctrl condition ($p < 0.05$). In contrast, we observed a significant downregulation of *E-cadherin* and overexpression of *N-cadherin*, *Vimentin*, *SNAIL* and *SLUG* upon *SMAD4*-OE for both PDA cell lines ($p < 0.05$). These observations suggest that cells initiate the EMT process and gain cellular motility after *SMAD4*-OE. In line with the above described findings, we observed the alteration of cellular morphology from cuboidal to spindle shape after the activation of the TGF β pathway (*SMAD4*-OE + TGF β 1). The morphological cellular alternation may assist cells to traverse the cellular matrix and the basement membrane, eventually enabling cancer cells to metastasize through intercellular space to a favourable tumour microenvironment. Overall, these data reinforce that intact SMAD4 and adequate TGF β in the tumour vicinity are of importance in initiating EMT and enhancing cancer metastasis.

Next, we analysed the putative role of this interplay in the development of cancer metastasis. In Panc1 cells, the migrative potential is diminished upon *PER2*-KD, whereas it is increased after *NR1D1*-KD ($p < 0.05$),

this phenomenon was not observed in AsPC1 cells. After TGF β 1 stimulation, we observed a significant enhancement of migration properties in Panc1 cells for clock-gene KDs and *shCtrl* conditions. Interestingly, TGF β 1 did not alter migration potentials in AsPC1-*shCtrl* cells. However, TGF β 1 repressed the migration in AsPC1-*shBMAL1* and -*shPER2* conditions and enhanced it in *shNR1D1* cells, implying that SMAD4 loss modifies the crosstalk of the TGF β pathway and the clock, ultimately altering migration properties. To mimic the *in vivo* scenario using our cellular model, we further performed trans-well invasion assays and drew a conclusion that is consistent with the findings on basis of the migration assays. When quantifying EMT makers, we observed a significant downregulation of *N-cadherin*, *Vimentin* and *SLUG* upon *PER2*-KD in Panc1 cells ($p < 0.05$), hinting towards the initiation of mesenchymal-epithelial transition (MET), the reverse process of EMT, in these cells. The significant overexpression of *SNAIL* and *SLUG* in Panc1-*shNR1D1* cells indicated that these cells underwent EMT which further supports the migration and invasion results ($p < 0.05$). For AsPC1 cells, we observed increased *N-cadherin* after *PER2*-KD ($p < 0.05$), indicating that *PER2*-KD triggered EMT in SMAD4-Del (AsPC1) cells, which is in agreement with both the migration and invasion assays. Furthermore, the constant overexpression of *CD133* upon *PER2*-KD in both PDA cell lines indicates a role of *PER2* as a potential repressor of cancer stemness, regardless of SMAD4 status.

4.5 Crosstalk between the TGF β -circadian network influences drug response and patient outcome

Refer to Figure. 7 and Figure. S9 in the publication.

A major problem in PDA treatment is the rapid development of chemoresistance to gemcitabine. Gemcitabine is an analogue of deoxycytidine, it can lead to cell death by inhibiting DNA chain elongation and inducing DNA fragmentation³⁵. Therefore, we further verified whether clock dysfunction or SMAD4 status have an influence on the drug response of gemcitabine in PDA cells.

Remarkably, PDA cells were overall more sensitive to gemcitabine after SMAD4 restoration (*SMAD4*-OE), whereas *SMAD4*-KD cells were more resistant to treatment. Though the gemcitabine IC₅₀ of Panc1 (9.5 μ M) is lower than AsPC1 (23.9 μ M), more viable cells were detected in AsPC1-*shCtrl* condition than in Panc1-*shCtrl* condition after 72h treatment, further indicating that SMAD4 loss prompts chemoresistance of gemcitabine in PDA cells. Remarkably, clock-gene KDs (including *shBMAL1*, *shPER2* and *shNR1D1*) induced gemcitabine resistance only notably in Panc1, suggesting an important role of the circadian timing system in gemcitabine susceptibility in SMAD4-proficient cells. KDs of clock genes in Panc1 cells led to higher viability after treatment, as compared to clock-gene KDs in AsPC1 cells, hinting towards differential gene expression programs being involved in the clock and chemosensitivity in Panc1 cells line and its counterpart, AsPC1 cells.

To assess the optimal timing of gemcitabine administration, the time points 17h, 20h and 23h after synchronization of the cells were selected based on circadian profiles of PDA cells, showing peak, intermediate and trough expression of *BMAL1*. After *BMAL1*, *PER2* and *NR1D1* KDs, the time-dependent profile of drug response was diminished in comparison to the normal scenario in Panc1 cells. Interestingly,

this effect was not observed for the SMAD4-deficient AsPC1 cells. While, upon SMAD4-silencing in Panc1 cells, the time-dependent variation of drug response was significantly impaired. Taken together, these data indicate an alteration of the circadian timing system in drug response of gemcitabine with defect SMAD4.

To study the putative consequences of our genes of interest on patient survival, we analysed patient survival with different expression levels for our candidate genes as described in *Materials and Methods*. We analysed the mutation frequencies of 10 candidate genes (including *BMAL1*, *PER2*, *NR1D1*, *CRY1*, *DEC1*, *DEC2*, *SMAD3*, *SMAD4*, *SMAD7* and *TGF β 1*) from a cohort of 184 PDA patients (from the PanCancer study)³⁶. Among these genes, *SMAD4* exhibited the highest mutation rate of 34%, and its mutation (mostly Del) is strongly associated with worse progression-free survival (PFS).

Next, we performed a cox-regression survival analysis in regard to clinical indexes (e.g., age, tumour grade and gender) in addition to gene expression levels using 177 accessible mRNA data sets (RNA-Seq v.2). Among the 10 candidate genes, *CRY1*, *DEC1*, *SMAD3* and *SMAD4* showed significant influences in PFS for PDA patients (log-rank test, $p < 0.05$). These findings highlight a potential clinical value of the link between the clock and the TGF β pathway and their effect on tumour malignancy which might contribute to patient prognosis of PDA.

5. Discussion:

PDA is one of the deadliest cancers and is notorious for its late presentation of symptoms, high metastatic potential, and poor prognosis. Clock dysregulations in cancer patients were shown to be strongly correlated with pancreatic cancer development^{20,37}. The TGF β signalling pathway plays a critical role in the maintenance of cellular homeostasis. As cancers progress, the inactivation of the TGF β canonical components (e.g., mutations) often occurs. These genetic alterations subsequently override the growth inhibition of the pathway and finally facilitate tumourigenesis. Despite a few studies having identified the regulatory role of the clock in canonical TGF β elements^{10,14,16}, the molecular mechanisms underlying this interplay in cancers remain largely unexplored.

5.1 Conclusions and perspectives

In this study, we aimed to elucidate the underlying mechanism between the clock and cancer progression with an emphasis on the gene SMAD4, since it is under circadian regulation¹⁷ and also highly mutated in PDA cells³⁸. SMAD4 has been known as the key mediator of the TGF β pathway and SMAD4 loss usually facilitates the acquisition of a malignant phenotype in PDA cells. We assume that as tumours grow and progress, the interaction between the TGF β pathway and the cellular clock alters and further affects cell-fate determination, ultimately allowing the cancer to acquire aggressive features. In order to test our hypothesis, we established an *in vitro* PDA model system comprised of SMAD4-proficient (Panc1) and -deficient (AsPC1) cell lines to study this interplay by genetic modifications of core clock genes, SMAD4, and TGF β .

It has been reported that the *Tgfb1* transcript oscillates in a circadian fashion in mouse embryonic fibroblasts, while the oscillation is abolished in *Clock*-knockout mice¹⁶. Furthermore, *Bmal1* regulates the expression of *Tgfb1* and *Smad3* by binding to their promoter regions in mouse brown adipocytes¹³. These results hint at a regulatory role of the internal clock in the TGF β canonical pathway in healthy subjects. However, whether the TGF β pathway is also under the control of the circadian clock in human neoplasms is still unclear. Of note, our data show that *TGFB1*, *SMAD3*, *SMAD4* and *SMAD7* transcripts oscillate in a circadian fashion (with a period of circa 24 h) in SMAD4-proficient Panc1 cells. The oscillation of these genes was only detectable in SMAD4-proficient cell but not in SMAD4-deficient cell. Furthermore, the oscillatory profile of *BMAL1* in SMAD4-proficient cells resembled that of *SMAD3* and *TGFB* in terms of phases and periods. Furthermore, we showed that clock perturbations by knockdown of *BMAL1* and *NR1D1* resulted in disrupted oscillations of *TGFB1*, *SMAD3*, *SMAD4*, and *SMAD7*, confirming the existence of the hypothesized connection linking the clock to the TGF β pathway in PDA cells with SMAD4 acting as a mediator. Moreover, the clock-regulated genes *DEC1* and *DEC2* are known to be downstream targets of the TGF β canonical pathway^{18,19}. Hence, we further analysed the expression of *DEC1* and *DEC2* upon genetic modifications of SMAD4, and our results showed that *DEC1/2* were overexpressed upon SMAD4 down-regulation and vice versa. These findings further reinforced the mediating role of *DEC1/2* in bridging the TGF β pathway and the clock in PDA cells.

We further investigated whether extrinsic TGF β and SMAD4 alterations may affect circadian phenotypes of PDA cells using live-cells bioluminescence recordings. TGF β stimulation alone did not alter the periods of both cell lines. Surprisingly, circadian periods were significantly shortened in *SMAD4*-OE cells after TGF β 1 stimulation, indicating that the sufficient TGF β can affect circadian patterns depending on *SMAD4* expression level.

Our study further revealed that KDs of core-clock elements led to an overall higher proliferative and apoptotic phenotype in SMAD4-proficient cells. In SMAD4-deficient cells, the apoptotic properties were also increased after these clock gene KDs. However, proliferation was only notably increased upon *PER2*-KD in SMAD4-Del cells. These findings were further supported by cell cycle analysis.

Of note, *SMAD4* downregulation only enhanced cell proliferation and did not affect apoptosis in these cells. We assume that SMAD4 loss might result in the activation of the TGF β non-canonical pathway, such as the RAS-ERK pathway, subsequently affecting cell growth³⁹. Further experiments validated the activation of the RAS-ERK pathway by revealing an upregulation of RAS and p-ERK proteins upon *SMAD4*-KD after TGF β 1 stimulation. SMAD4 overexpression caused remarkable hyperapoptotic phenotypes for both PDA cell lines. This effect is more manifest in SMAD4-deficient cells, where a significantly increased apoptosis was observed in AsPC1 *SMAD4*-OE cells treated with TGF β 1. This confirms the apoptotic role of the TGF β canonical pathway mediated by SMAD4, as described in previous studies^{40,41}.

Previous studies further illustrate a prominent role for the TGF β pathway in regulating cell cycle progression^{10,42}. In line with these findings, we observed that *SMAD4*-OE cells with added TGF β 1 result in cell cycle arrest at G1/S phase. Additionally, TGF β 1 repressed G1/S cell cycle propagation only in SMAD4-positive cells (Panc1: *shCtrl*, *oeCtrl* and *SMAD4*-OE; AsPC1: *SMAD4*-OE). In contrast, an increased S phase and hyperproliferative properties were observed in SMAD4-silencing cells (AsPC1-*oeCtrl* and Panc1-*shSMAD4*) when stimulated with TGF β 1. These data highlight an indispensable role of SMAD4 in regulating cell-fate decisions via downstream targets (e.g., P21, c-MYC, and RAS) of the TGF β pathway^{43,44}.

Modulating EMT and cellular metastasis ability is one of the key functions of the TGF β pathway in cancers⁴⁵. Cells initiating EMT lose epithelial cellular junctions and produce a mesenchymal cellular cytoskeleton, in order to acquire cellular motility and metastatic abilities⁴⁶. The reverse process of EMT, MET suppresses cancer metastatic potential⁴⁶. To explore whether the TGF β -clock interplay impacts on tumour invasiveness and EMT, we analysed metastatic properties in the conditions described above. TGF β 1 stimulation alone was adequate to enhance the metastatic potential in SMAD4-positive cells. In SMAD4-deficient cells, both *SMAD4*-OE and sufficient TGF β 1 levels were needed to prompt metastatic abilities. These results indicate a determinant role of SMAD4 in cancer metastasis via the TGF β pathway. These findings were further confirmed when observing no significant change of migration in *SMAD4*-KD cells upon TGF β 1 stimulation, and by measuring the expression of EMT markers (e.g., *E-Cad*, *N-Cad*, *SNAIL*, *SLUG*). Our results showed consistently that SMAD4 overexpression is positively associated with the

enhancement of the EMT process, whereas the downregulation of SMAD4 initiates the MET process. Moreover, the up-regulation of *CD133* upon *SMAD4*-KD implies the acquisition of cancer stem-like hallmarks with defect SMAD4 in our cellular model system⁴⁷. We hypothesise that the RAS-mediated non-canonical pathway is active upon *SMAD4* silencing, which may further initiate cancer stemness.

Metastasis is a multistep process involving alterations of both the tumour itself and its microenvironment. Our *SMAD4*-proficient and -deficient cells showed differential migration properties upon *PER2*- and *NR1D1*-KDs. Cell migration was found to be enhanced after *PER2*-KD and diminished after *NR1D1*-KD in Panc1 cells, in contrast to AsPC1 cells. Interestingly, TGF β 1 stimulation induced migrative properties in *SMAD4*-proficient cells after clock dysregulations, which is also distinct from *SMAD4*-deficient cells. Collectively, these data indicate that effects of the clock on metastatic properties seem to be *SMAD4*-dependent in pancreatic cancer. Of note, the repression of *PER2* results in overexpression of *CD133* in both PDA cells, pointing to a modulatory role of *PER2* in cancer stemness regardless of the *SMAD4* status⁴⁸. Accordingly, our results (e.g., cell cycle, proliferation and metastatic properties) hint towards a differential regulation of the core-clock via the TGF β canonical (Panc1) and non-canonical (AsPC1) pathways (*Figure 3*).

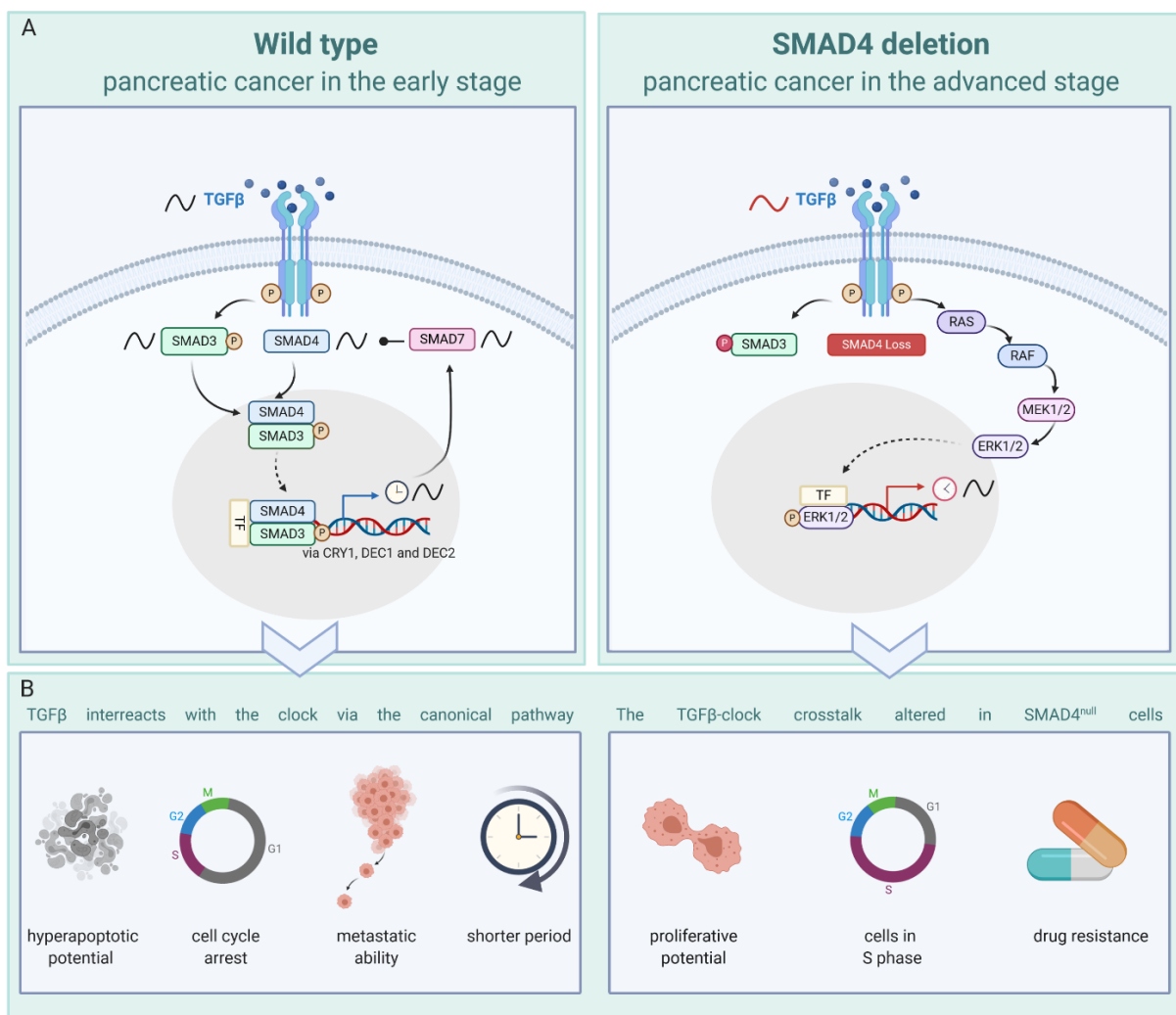
Clinical studies have reported that *SMAD4* loss is a negative indicator of patients' prognosis which is strongly correlated with resistance to chemotherapy^{12,49}. The drug gemcitabine, which is used for the first-line standard treatment of PDA, induces DNA damage by inhibiting DNA chain elongation⁵⁰. Genomic instability imposed by such an extrinsic DNA damage hazards cellular homeostasis related to modulations of the TGF β signalling transduction⁵¹ and the circadian pathway⁵². To explicate the molecular mechanisms for this, we speculated that the clock and TGF β components have implications in DNA damage and repair, as well as to genomic stability. We observed that *SMAD4*-silencing (including *SMAD4*-KD and *SMAD4*-Del) cells are more resistant to gemcitabine, and that clock perturbations via KDs exacerbate chemoresistance only detectably in *SMAD4*-proficient cells. Furthermore, a time-dependent variation of drug response was also only notable in *SMAD4*-proficient cells (including Ctrl and KDs). Since genetic alteration of *SMAD4* (mostly deletion) in PDA usually occurs in the advanced stage of the tumour, we hypothesise that the circadian clock acts as a chemoresistance suppressor for gemcitabine treatment while *SMAD4* is intact (e.g., PDA in the early stage). After *SMAD4* loss (e.g., PDA in the advanced stage), the high level of TGF β primarily released from tumour triggers the non-canonical (RAS/ERK) pathway, further leading to an acquisition of cancer stemness feature (increased level of *CD133*) and chemoresistance, and a malfunctional clock. Our results enforce the importance of *SMAD4* in gene expression programs involving the clock and chemosensitivity in *SMAD4*-positive cells, which differs from *SMAD4*-deficient cells (*Figure 3*).

The evidence that we obtained in our *vitro* model provides a profound understanding of the impact of *SMAD4* in the TGF β -clock networks and its effect on cell-fate decisions. Additionally, we carried out a computational analysis using public data sets of PDA patients to find out whether the expression level of

genes involved in this interplay affect patient survival. In agreement with our experimental work, *SMAD4* upregulation was correlated with increased expression levels of the core clock gene *CRY1* and downregulated levels of the clock-controlled gene *DEC1* and vice versa. We observed a significantly better PFS for patients with high-*CRY1*, low-*DEC1* and high-*SMAD4* gene expression. Remarkably, *SMAD4* mutations (mostly deletions) result in a worse PFS, which is aggravated along with mutations of other genes involved in this interplay. This information might be valuable for PDA patients suffering from the resistance of chemotherapy and could be applied to optimise the drug efficacy on basis of circadian rhythms and *SMAD4* status.

Taken together, these findings indicate that the *SMAD4* status, the circadian clock and its crosstalk with the TGFβ pathway affect the treatment efficacy and the determination of cell-fate in a pancreatic cancer context (Figure 3). This study highlights the pertinent role of the cellular clock as well as the TGFβ pathway in contributing to the cancer progression and patient prognosis.

Figure 3. Schematic representation of the interplay between the circadian clock and the TGFβ signalling transduction in pancreatic adenocarcinoma cells, and its impacts on cell-fate determination, metastatic properties, chemosensitivity (Created by Biorender.com).



5.2 limitations of the study

The main limitation of this study is the lack of *in vivo* experimental data (e.g., experiments in mice). Such limitation can eventually be circumvented, since mice are nocturnal animals, they have different circadian rhythms in contrast to humans. Experiments in mice cannot properly translate our finding concerning drug timing, toxicity and therapeutic efficiency to clinics. In addition, previous studies indicate that the clock phenotype of human cancer cells altered when transplanted into the host-animals using xenografts (e.g., rat and zebrafish)^{53,54}. These results suggest the clock of the host may perturb the circadian machinery in the xenograft, which might add complexity to the comprehension of the results in the present study. To better show the potential of our results beyond the *in vitro* experiments presented above, we performed a computational analysis with publicly available data sets for PDA patients as compensation.

Considering this thesis work is mainly based on cell populations, a further investigation at the single-cell level would be valuable for dissecting cellular heterogeneity in the TGF β -clock complex systems. Although primary cells or organoids that derived from pancreatic cancer patients are not easily accessible, a further study in primary cells harbouring diverse genomic background may assist to properly interpret the clock-TGF β interaction in pancreatic cancer cells and its further effects on cancer features.

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Statutory Declaration

“I, Yin Li, by personally signing this document in lieu of an oath, hereby affirm that I prepared the submitted dissertation on the topic “*Analysis of circadian regulation in a cellular model of pancreatic cancer*” independently and without the support of third parties, and that I used no other sources and aids than those stated.

All parts which are based on the publications or presentations of other authors, either in letter or in spirit, are specified as such in accordance with the citing guidelines. The sections on methodology (in particular regarding practical work, laboratory regulations, statistical processing) and results (in particular regarding figures, charts and tables) are exclusively my responsibility.

In the case of having conducted your doctoral research project completely or in part within a working group. Furthermore, I declare that I have correctly marked all of the data, the analyses, and the conclusions generated from data obtained in collaboration with other persons, and that I have correctly marked my own contribution and the contributions of other persons (cf. declaration of contribution). I have correctly marked all texts or parts of texts that were generated in collaboration with other persons.

My contributions to any publications to this dissertation correspond to those stated in the below joint declaration made together with the supervisor. All publications created within the scope of the dissertation comply with the guidelines of the ICMJE (International Committee of Medical Journal Editors; www.icmje.org) on authorship. In addition, I declare that I shall comply with the regulations of Charité – Universitätsmedizin Berlin on ensuring good scientific practice.

I declare that I have not yet submitted this dissertation in identical or similar form to another Faculty.

The significance of this statutory declaration and the consequences of a false statutory declaration under criminal law (Sections 156, 161 of the German Criminal Code) are known to me.”

Date

Signature

Declaration of your own contribution to the publications

Yin Li contributed the following to the below listed publications:

Publication 1: Li Y, Basti A, Yalçin M, Relógio A., *Circadian dysregulation of the TGF β /SMAD4 pathway modulates cell fate decisions, metastatic properties and drug response in pancreatic cancer*, iScience (cell press), 2020.

Contribution in detail:

Performance of the experiments and analysis:

Li Y performed most of the experiments and data analysis in this paper (Figure.1 - Figure.6, Figure.7A – 7E, Figure.S1 – S5, Figure. S7 – S9 and Table 1 - 4), including lumicycle measurement, time-course/single-timepoint RT-PCR, over-expression (OE) and knockdown (KD) assay, western blot for examining KD and OE efficiency, Incucyte real-time alive-cell recording assays (e.g., proliferation, apoptosis, migration and trans-well invasion), cell cycle analysis, cellular morphological analysis, time administrative treatment.

Basti A performed the supplementary experiment: western blot for examining phosphorylated-ERK and RAS in SMAD4-KD cells (Figure. S6).

Yalçin M performed survival analysis of pancreatic cancer patients using open-access database TCGA (Figure.7F - 7H).

Manuscript writing and submission:

Li Y illustrated the most of manuscript figures and the graphic abstract of this paper with the exception of Figure.7F – 7H (illustrated by Yalçin M).

Li Y and Basti A and drafted the manuscript with details as following: Li Y drafted abstract, introduction, methods, results and part of conclusion. Basti A mainly drafted conclusion of the manuscript.

Li Y, Basti A, Yalçin M and Relógio A critically read and contributed to writing and refining the manuscript.

Supervision:

Relógio A supervised the work and contributed with reagents/materials/analysis tools.

Signature, date and stamp of first supervising university professor / lecturer

Signature of doctoral candidate

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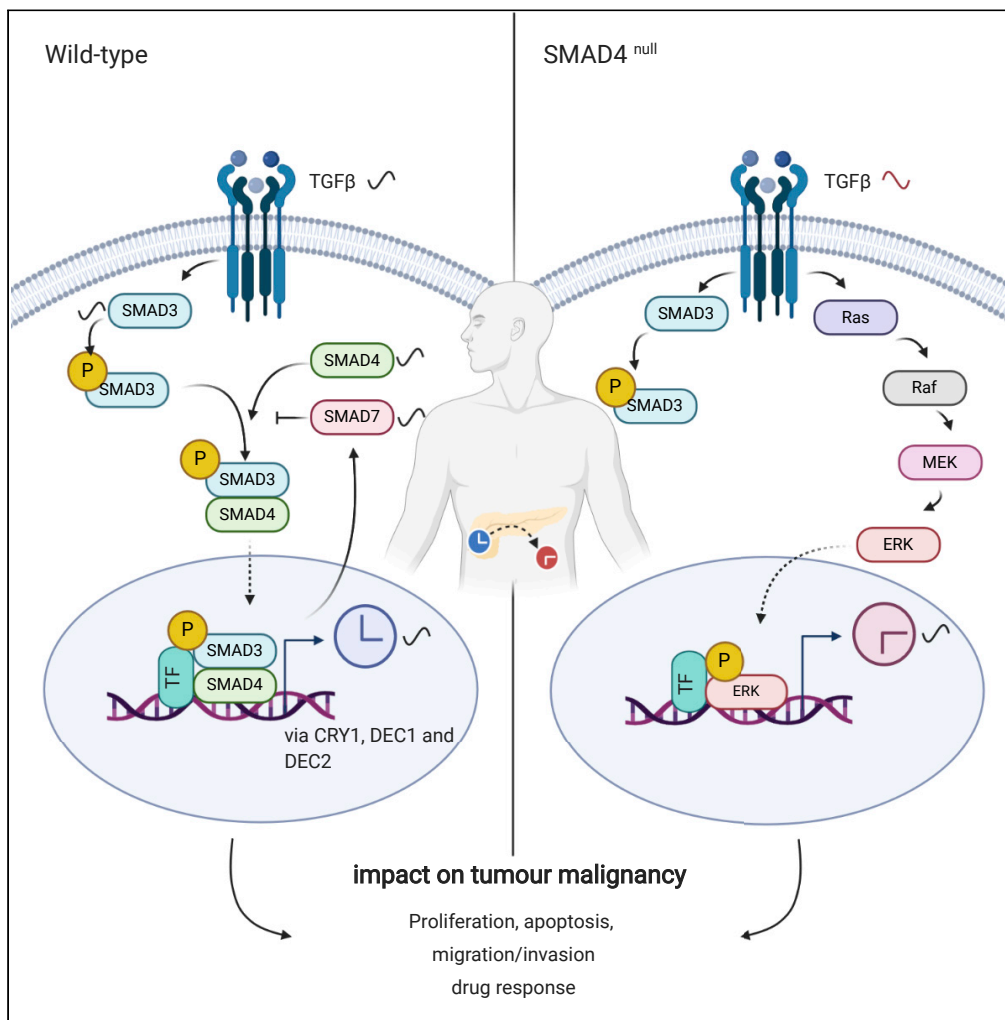
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4	Science Advances	36,380	13.116	0.172060
5	Nature Human Behaviour	2,457	12.282	0.014190
6	Nature Communications	312,599	12.121	1.259510
7	Science Bulletin	5,172	9.511	0.014150
8	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA	676,425	9.412	0.931890
9	Journal of Advanced Research	3,564	6.992	0.005470
10	GigaScience	4,068	5.993	0.016410
11	Scientific Data	5,761	5.541	0.028720
12	Research Synthesis Methods	2,572	5.299	0.006440
13	ANNALS OF THE NEW YORK ACADEMY OF SCIENCES	45,596	4.728	0.026370
14	FRACTALS-COMPLEX GEOMETRY PATTERNS AND SCALING IN NATURE AND SOCIETY	2,156	4.536	0.002210
15	iScience	1,410	4.447	0.004140
16	GLOBAL CHALLENGES	481	4.306	0.001440
17	Scientific Reports	386,848	3.998	1.231180
18	JOURNAL OF KING SAUD UNIVERSITY SCIENCE	1,640	3.819	0.002020
19	Journal of the Royal Society Interface	13,762	3.748	0.027670

Article

Circadian Dysregulation of the TGFβ/SMAD4 Pathway Modulates Metastatic Properties and Cell Fate Decisions in Pancreatic Cancer Cells



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HIGHLIGHTS

Transcripts of the canonical TGFβ pathway are rhythmically expressed in SMAD4^{+/+} PDA

A reciprocal interplay exists between the TGFβ pathway and the circadian clock in SMAD4^{+/+} PDA

SMAD4-WT and SMAD4-Null cells exhibit differential circadian regulation of cell-fate decisions

Drug administration in PDA cells shows time- and SMAD4-dependent effects

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Article

Circadian Dysregulation of the TGF β /SMAD4 Pathway Modulates Metastatic Properties and Cell Fate Decisions in Pancreatic Cancer CellsYin Li,^{1,2} Alireza Basti,^{1,2} Müge Yalçın,^{1,2} and Angela Relógio^{1,2,3,4,*}

SUMMARY

Impairment of circadian rhythms impacts carcinogenesis. SMAD4, a clock-controlled gene and central component of the TGF β canonical pathway, is frequently mutated in pancreatic ductal adenocarcinoma (PDA), leading to decreased survival. Here, we used an *in vitro* PDA model of SMAD4-positive and SMAD4-negative cells to investigate the interplay between circadian rhythms, the TGF β canonical signaling pathway, and its impact on tumor malignancy. Our data show that TGF β 1, SMAD3, SMAD4, and SMAD7 oscillate in a circadian fashion in SMAD4-positive PDA cells, whereas altering the clock impairs the mRNA dynamics of these genes. Furthermore, the expression of the clock genes DEC1, DEC2, and CRY1 varied depending on SMAD4 status. TGF β pathway activation resulted in an altered clock, cell-cycle arrest, accelerated apoptosis rate, enhanced invasiveness, and chemosensitivity. Our data suggest that the impact of TGF β on the clock is SMAD4-dependent, and SMAD3, SMAD4, DEC1, and CRY1 involved in this cross-talk affect PDA patient survival.

INTRODUCTION

In mammals, an internal biological timing system, the circadian clock coordinates the time of behavioral activities and physiological processes. At the molecular level, the circadian clock is composed of a set of genes and their protein products, interconnected by transcriptional/translational feedback loops (Fuhr et al., 2015). This core-clock network (CCN) generates endogenous 24-h oscillations in the expression of genes and proteins and is involved in the circadian regulation of various cellular processes, including the cell cycle (El-Athman et al., 2017), apoptosis (Gery et al., 2005; Wang et al., 2016), DNA repair (Di Micco et al., 2011), the epithelial-to-mesenchymal transition (EMT) (Mao et al., 2012), metabolism (Fuhr et al., 2018; Reinke and Asher, 2019), and immunity (Abreu et al., 2018). Its aberrant function impacts cell functioning and can lead to the development and progression of several diseases including cancer (Davis et al., 2019; Sulli et al., 2019; Yalçın et al., 2020). Genes involved in cell cycle regulation (e.g., MYC, WEE1, and INK4A), immune function (e.g., TNF), and metabolism (e.g., SIRT3, CPT1, and PDH) show a rhythmic pattern of expression and are known clock-controlled genes (CCGs).

The transforming growth factor β (TGF β) transduction pathway is among the clock-controlled pathways involved in oncogenic transformation. The TGF β pathway is implicated in the maintenance of tissue homeostasis, regulation of fetal development, immune system control, wound repair, and EMT (Massague, 2008). The basic elements of the canonical TGF β pathway include TGF β cytokines, receptors, and Smads (Smad4, receptor-Smads, and inhibitory-Smads). TGF β activates downstream pathways by binding to two pairs of receptors (type I and type II receptors). Once the receptors are activated, receptor-Smads (R-Smads) undergo phosphorylation, which results in signal propagation. The activated R-Smads (Smad2 and Smad3) translocate to the nucleus and form a complex with Smad4. Activated Smad complexes regulate gene expression by DNA-binding activity, and inhibitory-Smads (Smad7) prevent this complex formation (Massague, 2008; Prunier et al., 2019).

In normal and premalignant cells, TGF β functions as tumor suppressor via the regulation of cytoskeleton, differentiation, cell cycle, apoptosis, and suppression of inflammation, and malfunctions in the TGF β signaling pathway can result in tumorigenesis (Cheng et al., 2001; Massague, 2008; Principe et al., 2017; Scandura et al., 2004; Siegel and Massague, 2003).

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Pancreatic ductal adenocarcinoma (PDA) is a malignant disease with poor prognosis and low overall survival rate, and it is the fourth leading cause of cancer death in the European Union and the United States (Coveler et al., 2016). More than half of the patients with PDA harbor mutations in *SMAD4*. The inactivation of *SMAD4* in tumors is a common event in advanced-stage PDA and is linked to poorer prognosis (Singh et al., 2012).

Interestingly, several components of the TGF β canonical pathway are circadian regulated in different organisms (Akagi et al., 2017; Chen et al., 2015; Sato et al., 2019). Previous studies reported circadian expression of TGF β 1 and Smad3 (transcripts or proteins) in mouse brown adipocyte (Nam et al., 2015), mouse kidney (Sato et al., 2019), and mouse heart (Sato et al., 2017). In addition, the oscillating pattern of *TGF β 1* was altered after the disruption of *Clock* (Chen et al., 2015). However, it remains unclear whether components of the TGF β canonical signaling (including *TGF β 1*, *SMAD4*, *SMAD3*, and *SMAD7*) are clock regulated in human cancer cells and whether circadian disruption affects these elements in cancer cells with consequences on tumor malignancy. Work from our group indicates that *Smad4*, the core mediator of the TGF β canonical pathway, is regulated indirectly by the circadian clock (Lehmann et al., 2015). Wu et al. reported the binding of Smad3 or Smad4 to the Smad-binding elements in the *DEC1* promoter in pancreatic cancer cells, further contributing to their circadian regulation (Wu et al., 2012). These studies pointed to a link bridging the circadian and TGF β pathway.

Despite current findings regarding rhythmicity in elements of the TGF β pathway and the functionality of this pathway, the reciprocal interplay between the TGF β /SMAD4 pathway, the circadian clock, and its impact on tumor progression remains unclear in PDA.

Here, we investigated the influence of a dysregulated biological clock on PDA progression using an *in vitro* cellular model system. For this, we used SMAD4 wild-type and mutant PDA cell lines, derived respectively, from the primary tumor and the metastatic lesions of patients with PDA. We further explored the impact of clock dysregulation on the TGF β /SMAD4 canonical pathway. Our results show that elements of the TGF β canonical pathway (including *SMAD3*, *SMAD4*, *SMAD7*, and *TGF β 1*) are expressed in a circadian manner in SMAD4 wild-type PDA cells. In addition, we found that the rhythmic expression of the above-mentioned transcripts was altered upon the dysregulation of the circadian clock, suggesting that these TGF β canonical elements are under circadian modulation. Our data point to a modulation of the TGF β canonical pathway via the clock through interactions with the transcription factors *DEC1*, *DEC2*, and the core-clock gene *CRY1*. Also, we explored the influence of the canonical TGF β pathway on the clock phenotype in these cells. Our results indicated that the activation of the TGF β canonical pathway through *SMAD4* overexpression and TGF β induction results in a faster clock in PDA cells. Also, genetic modifications of *SMAD4* (knockdown or overexpression) altered the expression of the core-clock genes *BMAL1*, *PER2*, *NR1D1*, and *CRY1*, and of the clock- and TGF β -controlled genes, *DEC1* and *DEC2*.

Furthermore, we investigated proliferation, apoptosis, migration, and invasion in clock-disrupted (*shBMAL1*, *shPER2*, and *shNR1D1* knockdown) and *SMAD4* up- or downregulated PDA cells, as well as the effects of a dysregulated clock on drug sensitivity in both SMAD4-proficient and SMAD4-deficient PDA cell lines. Our data provide evidence for SMAD4- and clock-dependent drug response in PDA cells, and highlight the role of the bidirectional interaction between the biological clock and the TGF β /SMAD4 canonical pathway in cell cycle, apoptosis, and cancer metastasis in pancreatic cancer cells, which may further affect patient survival.

RESULTS

Bidirectional Interplay between the Circadian Clock and TGF β Canonical Pathway

To investigate the impact of a dysregulated clock in cancer metastasis and cell fate decisions in a pancreatic cancer cellular model, we used an established *in vitro* model of SMAD4-proficient (Panc1) and SMAD4-deficient (AsPC1) pancreatic adenocarcinoma cells (PDA), derived from different anatomical patient lesions (primary tumor and metastasis ascites, respectively) representing PDA tumors at different stages. Panc1 (ATCC: CRL-1469) is derived from the primary tumor of a male patient. The cell line AsPC1 (ATCC: CRL-1682) was established from ascites of a female patient with PDA. The doubling time of both cell lines is very similar and close to 52 h (Lieber et al., 1975; Watanabe et al., 2012). In addition, we analyzed cell growth of wild-type Panc1 and AsPC1 in our work using cell nucleus fluorescence labeling, which shows similar growth curves within 72 h for both cell lines ($n \pm$ SEM, $n = 8$, Figure S1D). Hence, both cell lines show similar cell cycle dynamics, making them suitable for our study. Of note, both cell lines carry mutated forms of *KRAS*, *p16*, and *TP53* (Berrozpe et al., 1994; Kita et al., 1999; Sun et al., 2001). Furthermore, our preliminary

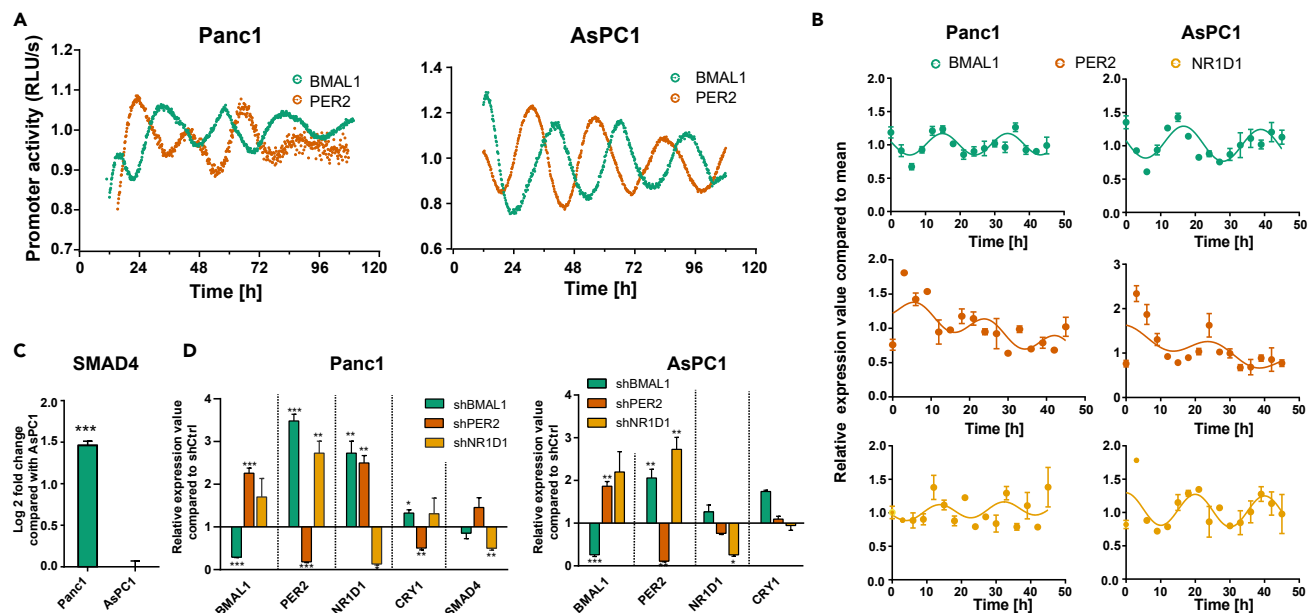


Figure 1. Panc1 and AsPC1 Cell Lines Harbor Different Clock Phenotypes

(A) Panc1 and AsPC1 cells were lentivirally transduced with a *BMAL1* promoter (green) or *PER2* promoter (orange)-driven luciferase construct. Bioluminescence was measured for 5 consecutive days. Depicted is one representative replicate for each condition.

(B) The 48 h time course RT-qPCR measurements of selected core-clock genes (*BMAL1*, *PER2*, and *NR1D1*) in Panc1 and AsPC1 WT cells.

(C) The relative mRNA levels of *SMAD4* compared with AsPC1.

(D) RT-qPCR measurements after knockdown of core-clock genes (*shBMAL1*, *shPER2*, and *shNR1D1*) in Panc1 and AsPC1 cells.

Data are expressed as mean \pm SEM, $n = 3$, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. See also Figures S1 and S2.

work for this study (via computational network analysis) showed that, among the highly mutated genes in PDA (above 5% mutation rate), *SMAD4* is tightly correlated with the CCN and has an impact on patient outcome (Cancer Genome Atlas Research Network, 2017; Lehmann et al., 2015).

Both cell lines showed oscillations, but with smaller amplitudes and shorter period for the Panc1 cells (*BMAL1*: 26.1 ± 0.3 h, $n = 3$) when compared with the AsPC1 cells (*BMAL1*: 27.4 ± 0.6 h, $n = 3$, Figure 1A). The oscillation parameters of *PER2*:Luc are provided in Table 1. We performed a 48 h time course RT-qPCR analysis, which confirmed the phenotypes observed in our luminescence data for *BMAL1* and *PER2* with an anti-phasic oscillation in both PDA cells (Figures 1A and 1B, Tables 1 and 2). Thus, according to our data, the endogenous time machinery operates differentially in these PDA cell lines.

Next, to explore the impact of clock disruption in the TGF β pathway, we produced knockdown PDA cell lines for the core-clock genes *BMAL1*, *PER2*, and *NR1D1* and evaluated the output in terms of gene expression (Figures 1D, S1B, and S1C). *SMAD4* expression in Panc1 cells was significantly higher when compared with that of AsPC1 (Figure 1C, *** $p < 0.001$). We confirmed that AsPC1 is a *SMAD4*-deficient cell line at the protein level (Figure S1A), as previously reported (Schutte et al., 1996; Sun et al., 2001). Furthermore, *SMAD4* expression was downregulated in Panc1-*shBMAL1* and Panc1-*shNR1D1* cells at 3 h after cell synchronization (Figure 1D, Panc1, ** $p < 0.01$, $n = 3$). Interestingly, the downregulation of *BMAL1* and *NR1D1* impacts the rhythmic expression of *SMAD4* in the *SMAD4*-proficient PDA cells (Figure 2A).

We further evaluated the consequences of these perturbations on the clock phenotype (Figure S2). The downregulation of *BMAL1* and *PER2* in Panc1 cells resulted in an almost complete loss of oscillations, whereas *NR1D1* KD (knockdown) showed no significant effect on the rhythmicity of *BMAL1*. The downregulation of *BMAL1* in AsPC1 cells led to a complete loss of oscillations, and AsPC1-*shNR1D1* cells depicted a significant shorter period.

Our results point to a connection between core-clock elements and *SMAD4*. To further investigate this interplay, we quantified the expression of *SMAD3*, *SMAD4*, *SMAD7*, and *TGF β 1* in our *in vitro* model (Figure S3).

	Panc1	AsPC1
Period (h)	26.6 ± 2.7	26.4 ± 0.4
Phase (h)	22.1 ± 2.7	5.2 ± 0.5
Amplitude	0.2 ± 0.0	0.2 ± 0.1
CC	0.9 ± 0.1	0.9 ± 0.1
Phase shift relative to BMAL1 (h)	15.0	6.8

Table 1. Circadian Parameters of *PER2* Promoter Activity in PDA Cells (Chronostar Analysis)

According to previous studies in other model systems (Chen et al., 2015; Nam et al., 2015), Clock-Bmal1 heterodimers or Bmal1 activate the expression of *Tgfb*, *Smad3* by binding to their promoter regions. Particularly, the robust circadian rhythmicity of *mTgfb1* is abolished in *mClock*-KO mice (Chen et al., 2015). Such findings suggest the existence of a circadian regulation of these TGFβ signaling components at the transcriptome level. Thereby, we hypothesized that this phenomenon might also exist in human PDA cancer cells. We found rhythmic expression of *TGFβ1* in both the SMAD4-proficient and SMAD4-deficient PDA cells (Figures S3A and S3E). Surprisingly, we also observed circadian oscillations in the expression of *SMAD3*, *SMAD4*, and *SMAD7* in SMAD4 WT cells (Panc1, Figures S3B–S3D and Table 3). Interestingly, *SMAD3* and *TGFβ1* transcripts oscillated with slightly different phases and similar periods as *BMAL1* in SMAD4-proficient cells (Panc1, Figure S3, Tables 2 and 3). However, the oscillation of *TGFβ1* exhibited longer periods (~27 h) when compared with *BMAL1* (22.3 ± 0.9 h) in SMAD4-deficient cells (AsPC1, Figure S3E), implying that the correlation between the rhythmic expression of *TGFβ1* and *BMAL1* is likely SMAD4 dependent. Furthermore, we compared the expression level of these components for the PDA cell lines in a 39 h time course (Figures S3F–S3H). The mRNA levels of *SMAD3* and *SMAD7* (Figures S3G and S3H) were much reduced in AsPC1 when compared with Panc1, whereas *TGFβ1* was highly expressed in AsPC1 when compared with Panc1 (Figure S3F). These data point to the inactivation of the TGFβ canonical pathway in SMAD4-deficient PDA cells, which may result in altered interaction with the clock machinery and ultimately support further progression towards malignant phenotypes.

We further explored the reciprocal interplay between the core-clock and the TGFβ canonical pathway and analyzed the effect of perturbing the core-clock elements on the expression of several components of the TGFβ canonical pathway (*SMAD3*, *SMAD7*, and *TGFβ1*).

A former study suggested *Bmal1* and *Nr1d1* to be key clock elements bridging the clock and the TGFβ canonical pathway in mouse adipocytes (Nam et al., 2015). Hence, we performed a 24 h time course RT-qPCR for *BMAL1* and *NR1D1* KDs and *shCtrl* in Panc1 cells. The expression of *TGFβ1*, *SMAD3*, *SMAD4*, and *SMAD7* exhibited a large variation after the *BMAL1* and *NR1D1* KDs when compared with *shCtrl* (Figure 2A). In particular, in Panc1-*shBMAL1* and Panc1-*shNR1D1* cells, the expression of *SMAD4* reached its peak at 18 h after synchronization. As previously reported, Bmal1 binding to the promoter region of *Smad3* (resulting in activation of *Smad3*) occurred at a specific time point (CT8 in mice) (Nam et al., 2015). Our results show that clock dysregulation (*BMAL1* KD) repressed *SMAD3* and *SMAD7* transcripts at 21 h after synchronization, suggesting that the inactivation of the TGFβ canonical pathway (particularly *SMAD7* as an indicator of the TGFβ pathway activation) occurs at a specific time point after the clock disruption (Figure 2A). The *TGFβ1* transcript was overexpressed upon *BMAL1* KD over the time of the measurements (Figure 2A). These data indicated that the disruption of *BMAL1* and *NR1D1* modified the time-dependent variations of elements of the TGFβ pathway (Figures 2A and S3). We observed a similar expression pattern of *SMAD3* and *SMAD7* upon *BMAL1* and *NR1D1* KDs, indicating that these elements may assist to set up a rapid reciprocal cross-talk between the TGFβ canonical pathway and the circadian clock (Figure 2A).

We then measured *BMAL1*- and *PER2*-promoter activity in *SMAD4*-KD and overexpression (*SMAD4*-OE) cells when compared with the corresponding control conditions (*shCtrl* or *oeCtrl*) and with additional TGFβ1 stimulation, to explore the impact of the TGFβ pathway on the clock phenotype. Overexpression efficiency was analyzed at the transcript and protein levels (Figure S5A and S5B). The activation of the TGFβ canonical pathway by *SMAD4*-OE and additional TGFβ1 stimulation significantly shortened the period of the oscillations (Figures 2E, 2F, 2H, 2I, and S4A–S4C, **p* < 0.05, *n* = 3). In addition, *SMAD4*-KD

Cosinor Analysis			
	Panc1		
	BMAL1	PER2	NR1D1
Phase (h)	17.0 ± 0.5	4.1 ± 0.7	14.4 ± 0.5
Period (h)	19.0 ± 1.0	18.3 ± 1.5	18.6 ± 0
Amplitude	0.2 ± 0.1	0.2 ± 0.1	0.1 ± 0.1
p Value	<0.0001	<0.0001	0.045
	AsPC1		
	BMAL1	PER2	NR1D1
Phase (h)	14.4 ± 0.3	0 ± 3.6	20 ± 0.0
Period (h)	22.3 ± 0.9	24.8 ± 0.0	20.0 ± 1.3
Amplitude	0.3 ± 0.0	0.2 ± 0.1	0.2 ± 0.1
p Value	<0.0001	<0.0001	0.0003

Table 2. Circadian Parameters Retrieved with Cosinor Analysis for a 48 h Time Course RT-qPCR Data (BMAL1, PER2, and NR1D1).

in Panc1 led to a shorter period when compared with *shCtrl* (Figures 2B and 2C, ** $p < 0.01$), pointing to a putative role of *SMAD4* in the regulation of the circadian clock via *BMAL1*.

In addition, we evaluated the impact of *SMAD4* in the regulation of core-clock elements *BMAL1*, *PER2*, *NR1D1*, and *CRY1* and further analyzed the expression of the clock genes *DEC1* and *DEC2* (Figures 2D, 2G, and 2J), reported as mediators in the above cross-talk (Kon et al., 2008; Sato et al., 2016, 2019). Interestingly, most of the core-clock genes showed significant alterations for Panc1 *SMAD4*-OE and *SMAD4*-KD (Figures 2D and 2G). Overall, *CRY1* was upregulated, whereas *DEC1* and *DEC2* were downregulated in *SMAD4*-OE PDA cells (Figures 2D and 2J, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, $n = 3$). In agreement, we observed the opposite results in Panc1-*shSMAD4* (Figure 2G, ** $p < 0.01$, *** $p < 0.001$, $n = 3$). These results further reinforce the existence of a bidirectional connection between the core-clock and the *SMAD4*-dependent pathways via the regulation of *CRY1*, *DEC1*, and *DEC2*.

Dysregulation of the Core-Clock Genes *BMAL1*, *PER2*, and *NR1D1*, and Perturbations in *SMAD4* Impact Cell Proliferation and Apoptosis in PDA Cells

We further evaluated the effects of disrupting core-clock genes and *SMAD4* in cell fate decisions by analyzing cell proliferation and apoptosis. Interestingly, *SMAD4*-proficient (Panc1) and *SMAD4*-deficient (AsPC1) cells showed different effects on proliferation upon the different knockdowns (Figure 3A). Proliferation increased in Panc1 cells after *BMAL1* and *NR1D1* KDs, whereas this was not observed in AsPC1 knockdown cells (Figure 3A). Panc1-*shSMAD4* cells showed increased proliferation when compared with the *shCtrl*. However, *SMAD4*-OE in both PDA cells showed no significant difference in the proliferative ability compared with *oeCtrl*. These results indicate that the non-canonical pathway (which includes RAS, MAPK, JNK) might be activated after *SMAD4* KD, leading to an increase in proliferation. To verify our assumption, we measured RAS and phosphorylated-ERK (p-ERK) proteins in Panc1-*shCtrl* and Panc1-*shSMAD4* cells with and without a 24-h TGF β 1 stimulation. Our results show that the TGF β 1 stimulation activates the phosphorylation of ERK for both Panc1-*shCtrl* and Panc1-*shSMAD4* (Figures S6A and S6C). In addition, *SMAD4*-KD (particularly stimulated with TGF β 1) indeed upregulated the expression of RAS and p-ERK, when compared with control cells (Figures S6A–S6C). These data suggest the activation of the Ras pathway after the downregulation of *SMAD4*. In addition, the apoptotic profiles of PDA cells were altered upon core-clock dysregulation. The downregulation of *BMAL1*, *PER2*, and *NR1D1* increased apoptosis when compared with *shCtrl* (Figures 3B, 3C, and 3E). *SMAD4* OE promoted apoptosis in both PDA cells (Figures 3B, 3D, and 3F). These results implied that the upregulation of *SMAD4* and the disruption of core-clock genes induces apoptosis in our *in vitro* model.

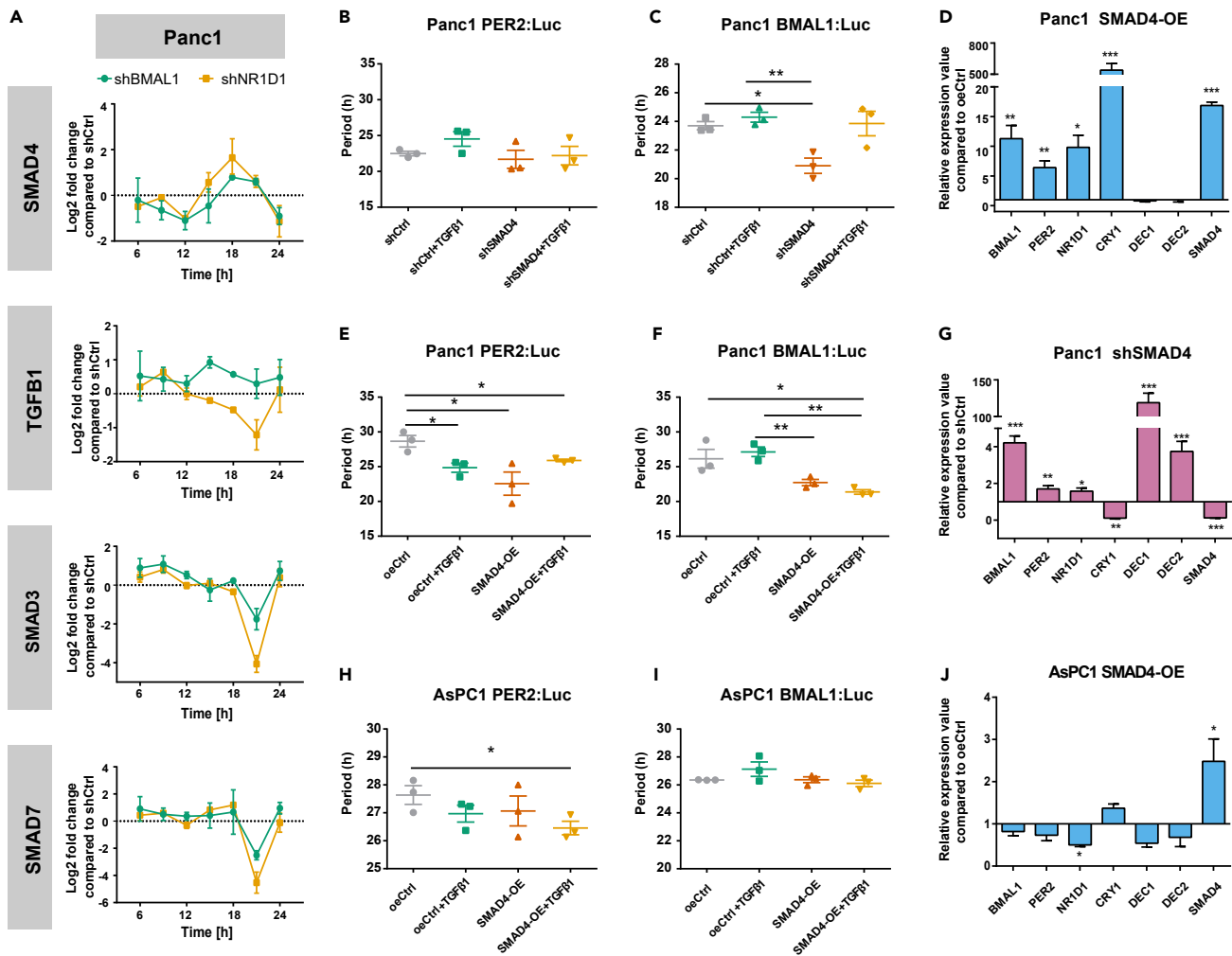


Figure 2. Panc1 and AsPC1 Cells as a Model for Investigating the Cross-Talk between the Circadian Clock and the TGFβ Canonical Pathway

(A) The 24 h time course RT-qPCR was carried out in Panc1 cells (A) containing *shCtrl* empty vector, *shBMAL1*, and *shNR1D1* constructs. Relative expression value of TGFβ signaling-associated genes (*SMAD4*, *TGFβ1*, *SMAD3*, and *SMAD7*) is shown compared with *shCtrl* cells at each time point. (B, C, E, F, H, and I) *SMAD4*-KD or *SMAD4*-OE cells were lentivirally transduced with a *BMAL1*- or a *PER2*-promoter-driven luciferase construct. Bioluminescence was measured for 5 consecutive days with TGFβ1 or corresponding empty vehicle (0.1% BSA). Depicted are the periods for Panc1 (B, C, E, and F) and for AsPC1 (H and I) of *BMAL1* or *PER2* promoter activities, as indicated. One representative replicate for each condition is provided in Figure S4. (D, G, and J) Effect of *SMAD4*-KD or *SMAD4*-OE on the expression of clock genes in Panc1 (D and G) and AsPC1 (J) cells. Data are expressed as mean ± SEM, n = 3, one-way ANOVA (B, C, E, F, H, and I) or multiple t test (D, G, and J); *p < 0.05, **p < 0.01, ***p < 0.001. See also Figures S3, S4, and S5A–S5B.

Clock Dysregulation and the Activation of the TGFβ/SMAD4 Pathway Impacts Apoptosis and Cell Cycle in PDA Cells

To further characterize the putative effects of dysregulating the TGFβ/SMAD4 signal transduction in our model, we stimulated the pathway with TGFβ1 in addition to *SMAD4*-KD or *SMAD4*-OE and analyzed cell proliferation and apoptosis. The activation of the pathway (*SMAD4*-OE with TGFβ1 stimulation) did not alter proliferation in Panc1 cells, and its inactivation (*SMAD4*-KD with or without TGFβ1) promoted proliferation (Figures 4A and 4B). Interestingly, we observed increased proliferation in *SMAD4*-deficient cells (AsPC1) with TGFβ1 stimulations compared with *SMAD4*-OE cells (Figure 4C). Thus, we hypothesized that TGFβ1 triggers the downstream elements of the TGFβ non-canonical signaling pathway (e.g., RAS, PI3K) leading to increased proliferation in *SMAD4*-deficient cells.

The stimulation of TGFβ1 induced apoptosis particularly in *SMAD4*-positive PDA cells (including *SMAD4*-OE and wild-type, Figures 4E–4G).

Cosinor Analysis				
	Panc1			
	TGFβ1	SMAD3	SMAD7	SMAD4
Phase (h)	1.7 ± 1.5	19.1 ± 0.8	11.85 ± 1.3	12.6 ± 1.1
Period (h)	20.0 ± 3.8	21.8 ± 2.6	22.8 ± 4.7	21.7 ± 3.4
Amplitude	0.1 ± 0.1	0.3 ± 0.1	0.2 ± 0.1	0.3 ± 0.2
p Value	0.0015	0.0004	0.0001	0.0256
	AsPC1			
	TGFβ1			
Phase (h)	4.6 ± 0.3			
Period (h)	27.0			
Amplitude	0.2 ± 0.0			
p Value	<0.0001			

Table 3. Circadian Parameters Retrieved with Cosinor Analysis for a 33 h Time Course RT-qPCR Data (TGFβ1, SMAD3, SMAD4, and SMAD7).

We analyzed the cell cycle of the PDA cells in greater detail in all the aforementioned conditions. Our analysis showed significant cell-type-specific alterations upon KD of clock genes when compared with control cells. For the SMAD4-proficient cell line (Panc1), the percentage of cells in S phase decreased significantly and G2/M phase increased after *PER2* KD (Figure 4I, **p < 0.01, ***p < 0.001, n = 3), whereas the percentage of cells in S phase increased after *NR1D1*, in agreement with the proliferation results. In AsPC1 cells, we observed a significant increase of S phase and decrease of G1 phase in *PER2* KD cells (Figure 4K, **p < 0.01, ***p < 0.001, n = 3), and no significant alterations upon the KD of *BMAL1* and *NR1D1*, in agreement with our proliferation results (Figure 3A). The differential phenotypes observed might result from the different genomic background of both cell lines (in particular the *SMAD4* alteration) that subsequently impacts the circadian pathway, leading to an overall differential proliferative phenotype.

Next, we investigated the impact of TGFβ on the cell cycle. Panc1 cells depicted increased G1/S arrest upon TGFβ1 stimulation (Figures 4D and S5C). Interestingly, unlike the impact of TGFβ1 that has been reported in previous studies for other model systems (Alexandrow and Moses, 1995; Mukherjee et al., 2010), and also found in SMAD4-proficient cells, a 24-h TGFβ1 stimulation increased the percentage of cells in G2/M phase in *shNR1D1* cells (Figure S5C), pointing towards differential regulation of the cell cycle by TGFβ upon *NR1D1* downregulation. Additional TGFβ1 did not cause G1/S arrest in SMAD4-deficient cells (AsPC1, Figures 4H and S5D); this is distinct from the observations in SMAD4-proficient cells (Panc1). Instead, we observed an increase in G2/M or S phase in all KD conditions (*shBMAL1*, *shPER2*, and *shNR1D1*) and *shCtrl* cells upon TGFβ stimulation when compared with non-stimulated cells (Figures 4H and S5D). These results point to a SMAD4 dependency regarding the effects of TGFβ on cell cycle distribution. We further analyzed the cell cycle in SMAD4-KD and SMAD4-OE conditions with or without additional TGFβ1 stimulation (Figures 4I–4K). For Panc1, the additional TGFβ1 and upregulation of SMAD4 led to increased number of cells in G1/S phase (Figures 4I and 4J). However, the impairment of the TGFβ canonical pathway (SMAD4 KD) increased the number of cells in S phase particularly when compared with the activation of TGFβ canonical pathway (*shCtrl* with TGFβ1): G1 decreased and S phase increased (Figure 4J). In SMAD4-deficient cells (AsPC1), SMAD4 OE with additional TGFβ1 stimulation resulted in an increased G1 and decreased S phase when compared with oeCtrl cells (Figure 4K). However, in AsPC1 oeCtrl cells, TGFβ1 stimulation led to an increase in the percentage of cells in S phase (Figure 4K) and consistently a higher proliferative potential (Figure 4C) when compared to non-stimulation oeCtrl. This finding further supports the activation of the non-canonical TGFβ pathway in the absence of SMAD4, which triggers the activation of the oncogene RAS (Figure S6) in the downstream pathway and subsequently affects cell cycle and proliferation.

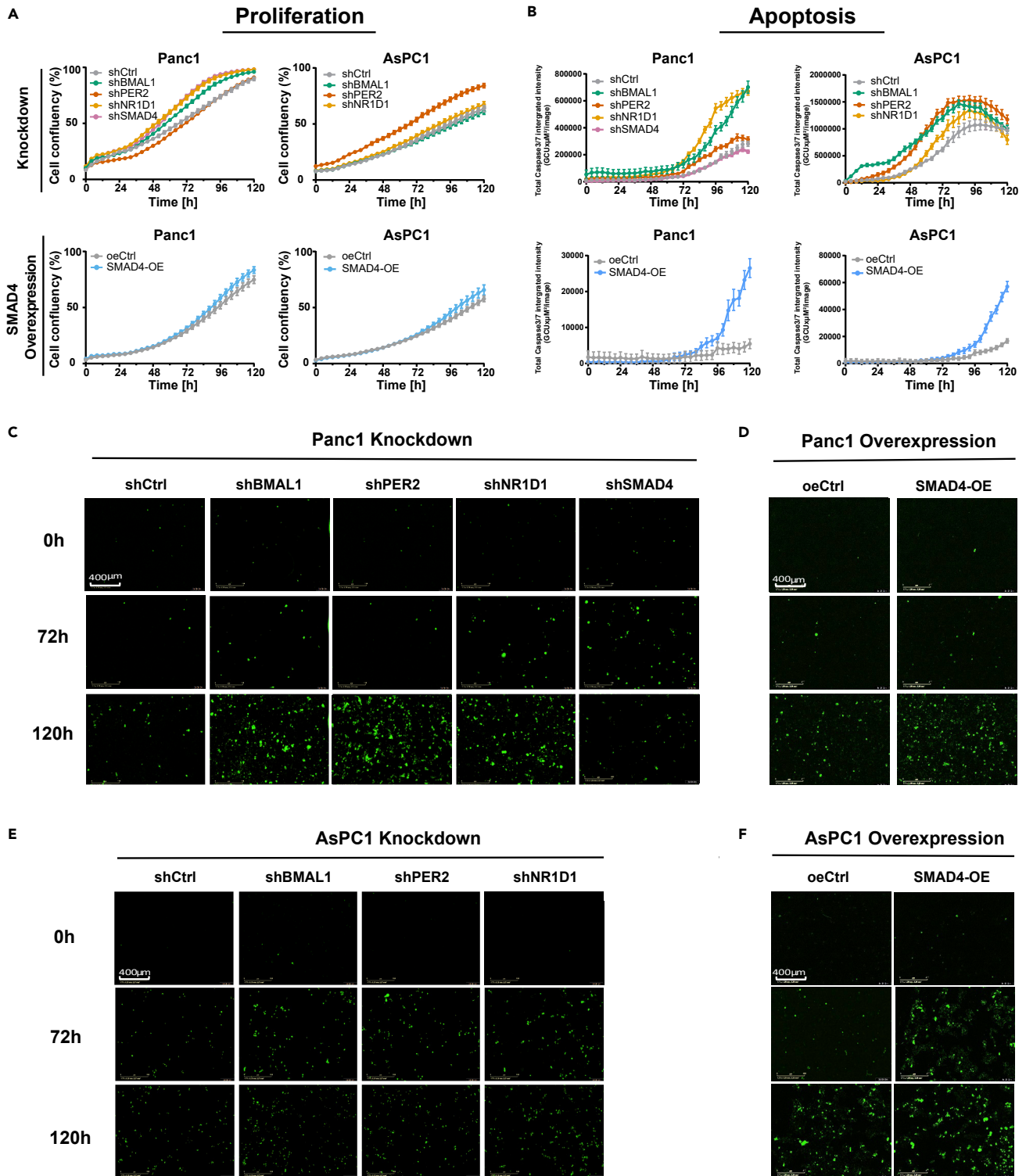


Figure 3. Dysregulation of the Core-Clock Genes (*BMAL1*, *PER2*, and *NR1D1*) and *SMAD4* Leads to Differential Cell Proliferation and Apoptosis in *Panc1* and *AsPC1* Cells

(A) Proliferation analyses of PDA cell lines for KD conditions (*shBMAL1*, *shPER2*, *shNR1D1*, and *shSMAD4*), *SMAD4*-OEs, and corresponding empty vectors (*shCtrl* and *oeCtrl*, respectively).

Figure 3. Continued

(B) Apoptosis analysis of PDA cell lines after KDs or OEs. Data are expressed as mean \pm SEM, $n \geq 6$ (A and B).

(C–F) Representative images of apoptosis assays for Panc1 *shCtrl* and knockdown cells *shBMAL1*, *shPER2*, *shNR1D1*, *shSMAD4* (C) or Panc1 oeCtrl and *SMAD4*-OE cells (D) and AsPC1 *shCtrl* and knockdown cells *shBMAL1*, *shPER2*, *shNR1D1* (E) or AsPC1 oeCtrl and *SMAD4*-OE cells (F), with fluorescently labeled caspase3/7 with (objective 20 \times) at time points 0, 72, and 120 h, respectively. Data are expressed as mean \pm SEM, $n \geq 6$ (A and B).

These results demonstrate that TGF β canonical and non-canonical pathways regulate the cell cycle, proliferation, and apoptosis in a SMAD4-dependent manner.

The Dysregulation of the Core Clock Impacts Cell Migration in a SMAD4-Dependent Manner

Next, we aimed to examine if the activation of TGF β /SMAD4 pathway may contribute to the formation of tumor metastasis. We used a real-time cell recording approach to measure the invasive and migration properties of these PDA cells, analyzed known EMT markers, and investigated morphological cellular alterations (Figure 5). TGF β 1 stimulation significantly increased the migration speed in both PDA cells, particularly in *SMAD4*-OE cells (Figures 5B, 5C, 5E, and 5F, $*p < 0.05$, $***p < 0.001$, $n = 8$). For AsPC1 oeCtrl cells, TGF β 1 stimulation did not significantly promote migration likely due to its intrinsic *SMAD4* deficiency. In contrast, Panc1 cells showed a significantly slower migration speed after *SMAD4* KD (Figure 5D, $**p < 0.01$, $n = 8$) and TGF β stimulation was not able to induce the migrative potential in *SMAD4* KD cells (Figures 5A and 5D), in agreement with previous data by Takano and colleagues who reported a role for SMAD4 in the expression of EMT marker genes in pancreatic cancer (Takano et al., 2007). In addition, the resembled phenomenon was found in invasion assays as well; TGF β 1 stimulation or *SMAD4* overexpression promoted the invasiveness of PDA cells (Figures 5H and 5I), whereas *SMAD4*-KD without additional TGF β 1 impaired invasive ability (Figure 5G). Altogether, these data suggest that the presence of intrinsic SMAD4 and TGF β in the tumor microenvironment is crucial for tumor invasiveness and cell motility. Cells that undergo EMT have a greater tendency to invade and metastasize (Yang et al., 2020), thus we verified our results by quantifying EMT biological markers and examining alterations in cell morphology. The cadherins are major adhesion molecules anchoring in the cytomembrane. Epithelial cells express E-cadherin, whereas cells that show mesenchymal features express N-cadherin and R-cadherin (Wheelock et al., 2008). Cancer cells can enhance or reduce their metastatic potential through cadherin switching, which is one characteristic of the EMT. Also Vimentin, a cytoskeletal molecule responsible for maintaining cell integrity and resistance against stress (Satelli and Li, 2011), has been described as an EMT biomarker. Additionally, we also analyzed the transcription factors *SNAIL* and *SLUG* that are sensitive to microenvironmental stimuli and function as EMT switchers (Lamouille et al., 2014).

CD133 has been commonly used as an important biomarker to identify cancer stem cells (Glumac and LeBeau, 2018). We found a significant overexpression of *CD133* and *E-cadherin* and a downregulation of *Vimentin* and *SLUG* in Panc1 *SMAD4*-KD cells (Figure 5J, $**p < 0.01$, $***p < 0.001$, $n = 3$). In contrast, *E-cadherin* expression decreased, whereas *N-cadherin*, *Vimentin*, *SNAIL*, and *SLUG* were significantly increased in both PDA cells after *SMAD4*-OE (Figures 5K and 5L, $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $n = 3$), pointing to the initiation of the EMT process and gain of motility in *SMAD4*-OE cells, increasing the invasiveness potential of these cells. Furthermore, the decrease in the expression level of *CD133* after *SMAD4*-OE indicated a reduction of CSCs (cancer stemness cells) along with the increased levels of *SMAD4*. Interestingly, we observed morphological changes in the cells (from cuboidal shaped to spindle shaped), after the activation of the TGF β canonical pathway (Figure S7). The morphological cellular change may facilitate cells to traverse the cellular matrix into intercellular spaces. Consistently, the upregulation of *Vimentin* pointed to an alteration of the cytoskeleton in *SMAD4*-OE cells (Figures 5K and 5L). However, this morphological change was not observed in the *SMAD4*-deficient or *SMAD4*-KD cells.

Altogether, these results reinforce the important role of *SMAD4* and TGF β in the EMT process and PDA cancer metastasis; on the other hand, the absence of SMAD4 enhanced tumor stemness in our PDA model system.

We then further analyzed the possible role of the interplay between the TGF β pathway and the biological clock in the formation of cancer metastasis. Interestingly, cell migration decreased upon *PER2* KD, but increased after *NR1D1* KD in *SMAD4*-proficient cells (Panc1, Figures 6A and 6C, $***p < 0.001$, $n = 3$), in contrast to the results in *SMAD4*-deficient cells (AsPC1, Figures 6B and 6D, $***p < 0.001$, $n = 3$). The TGF β stimulation promoted the migration properties in clock genes KDs Panc1 cells (Figure 6E,

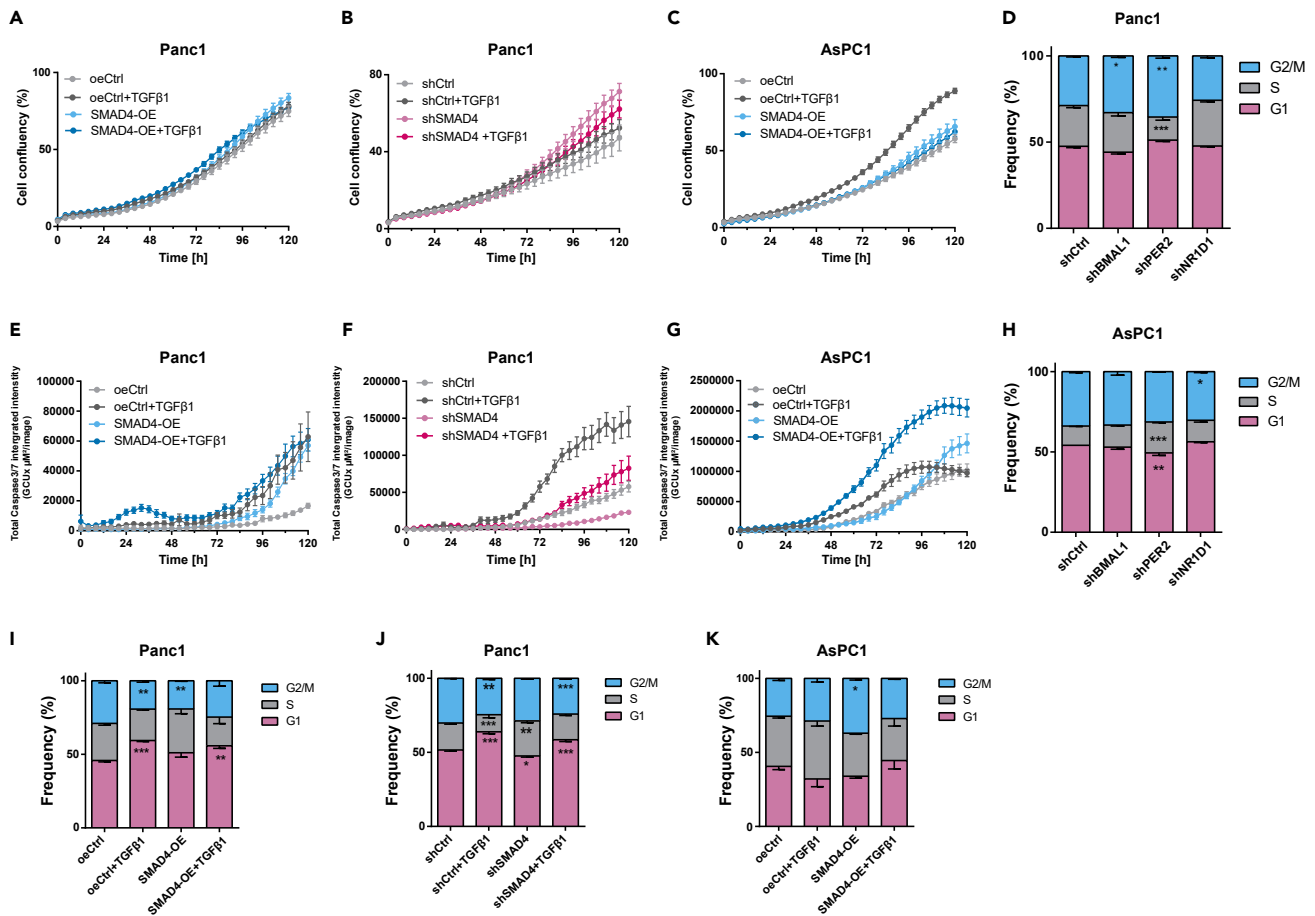


Figure 4. Clock Disruption and the Activation of the TGFβ/SMAD4 Pathway Affects Apoptosis and Cell Cycle in PDA Cells

(A–C) Proliferation analysis of PDA cells containing *SMAD4*-OE (A, C) or *SMAD4*-KD (B) constructs and their corresponding empty vectors (*shCtrl* or *oeCtrl*) stimulated with additional TGFβ1 (10ng/ml) or its solvent. (n = 8; mean ± SEM).

(E–G) Apoptosis analysis of PDA cell lines after *SMAD4*-OE (E, G) or *SMAD4*-KD (F) and their corresponding empty vectors (*shCtrl* or *oeCtrl*) with 24-h stimulation with TGFβ1 or its solvent (n = 3, mean ± SEM).

(D and H) Cell cycle measurements after clock gene KDs (*shBMAL1*, *shPER2*, *shNR1D1*) and its empty control (*shCtrl*) in Panc1 (D) and AsPC1 (H) cells.

(I–K) Cell cycle measurements of *SMAD4*-KD and *SMAD4*-OE and corresponding control conditions (*shCtrl* and *oeCtrl*) in Panc1 (I, J) and AsPC1 (K) cells after a 24-h stimulation with TGFβ1 (10 ng/mL) or its solvent. (D and H–K) Phase distributions were compared with their respective control conditions (n = 3, mean ± SEM, two-way ANOVA, *p < 0.05, **p < 0.01, ***p < 0.001).

See also Figures S5C, S5D, and S6.

*p < 0.05, **p < 0.01, ***p < 0.001, n = 3). TGFβ stimulation did not alter the migration ability of AsPC1 cells containing empty vectors (Figures 5F and 6F). On the other hand, TGFβ stimulation repressed migration in *shBMAL1* and *shPER2* and induced it in *shNR1D1* cells (Figure 6F, *p < 0.05, **p < 0.01, ***p < 0.001, n = 3), indicating that the interactions of the clock and the TGFβ non-canonical pathway may modify migration properties in *SMAD4*-deficient cells (AsPC1).

Therefore, we examined the expression level of clock genes after a 24-h TGFβ stimulation compared to Ctrl. We found that TGFβ stimulation upregulated *NR1D1* expression in AsPC1 (*SMAD4*-deficient) *NR1D1* KD cells (Figure S8D, ***p < 0.001, n = 3). Considering the decreased migration potential observed upon *NR1D1* KD (Figure 6B), the overexpression of *NR1D1* resulting from TGFβ stimulation (Figure S8D) might be the cause of the increase in migration in *NR1D1* KD cells (Figure 6F).

We further carried out trans-well invasion assays, which are more similar to the *in vivo* scenario. The results supported the conclusion from the migration assays (Figures 6G, 6H, 6K, and 6L).

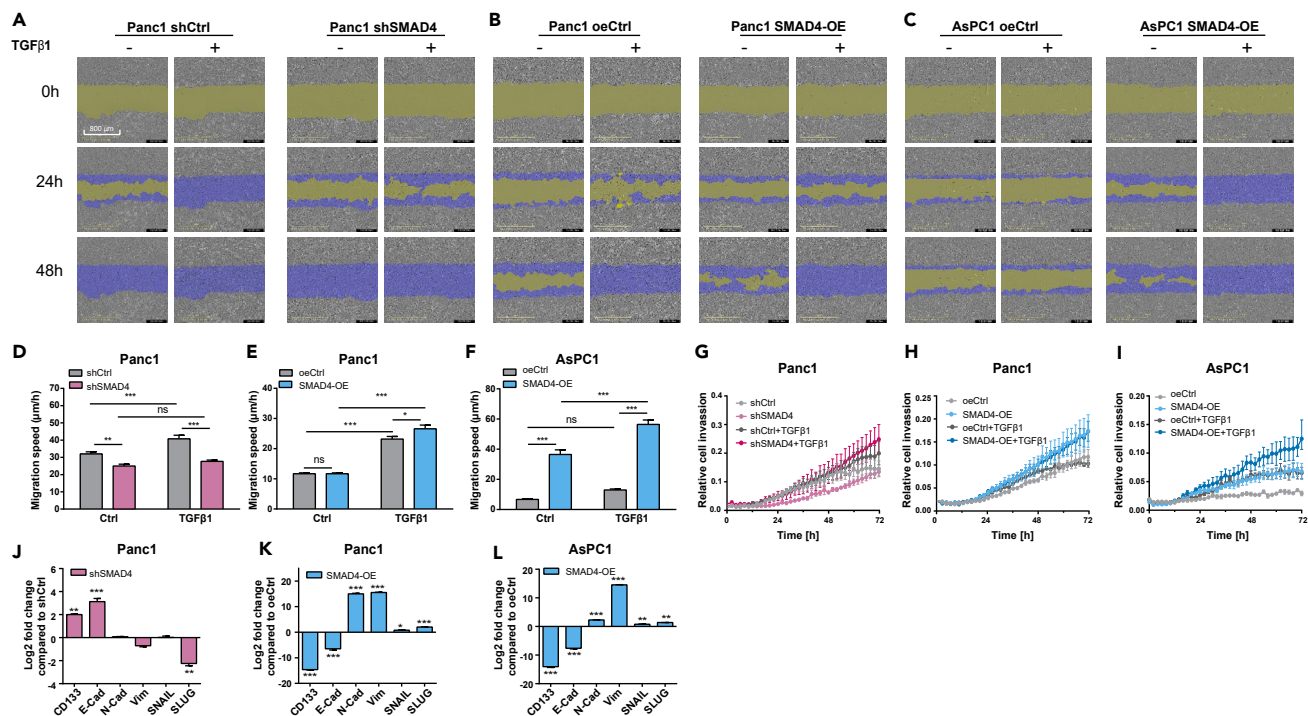


Figure 5. Migration and Invasion Analysis of SMAD4-KD and SMAD4-OE PDA Cells With or Without TGFβ1 Stimulations and Corresponding Expression Levels of EMT Markers

(A–C) Migration assays were performed with the IncuCyte S3 Live Cell System Analysis using a scratch wound assay for SMAD4-KD (A) or SMAD4-OE (B, C) and their control (shCtrl and oeCtrl) conditions in PDA cells with additional TGFβ1 or its solvent stimulation at 0, 24, 48 h. Images were obtained with the IncuCyte S3 Software. Yellow mask indicates the wound boundaries. Blue mask indicates the initial scratch wound area.

(D–F) Average cell migration speed distribution in Panc1 (D, E) and AsPC1 (F) cells containing SMAD4-KD or SMAD4-OE constructs and their empty vectors (shCtrl and oeCtrl) with additional TGFβ1 or its solvent stimulation, (n ≥ 8, mean ± SEM; two-way ANOVA, *p < 0.05, **p < 0.01, ***p < 0.001).

(G–I) Invasion assays were carried out using a chemotaxis cell invasion assay for the IncuCyte S3 Live Cell System Analysis. Trans-well invasion assays for SMAD4-KD (G) or SMAD4-OE (H, I) and their control (shCtrl and oeCtrl) conditions in PDA cells were measured every 2h. Quantification was performed by measuring the total phase area of the bottom layer of the inner chamber within 72 h. Data were normalized for the initial value (n ≥ 6, mean ± SEM).

(J–L) Expression levels of EMT and cancer stemness-related genes (*E-cadherin*, *N-cadherin*, *Vimentin*, *SNAIL*, *SLUG*, and *CD133*) in SMAD4-KD (J) or SMAD4-OE (K, L) conditions compared with their control conditions, shCtrl and oeCtrl respectively (n = 3, mean ± SEM, t test, *p < 0.05, **p < 0.01, ***p < 0.001). See also Figure S7.

We quantified the expression of *N-cadherin*, *E-cadherin*, *Vimentin*, *SNAIL*, and *SLUG*. Although the expression of *E-cadherin* was not significantly altered in *PER2* KD Panc1 cells, the expression of key MET (mesenchymal-epithelial transition, the reverse process of EMT) markers (*N-cadherin*, *Vimentin*, and *SLUG*) were significantly reduced, which hints toward initiation of MET in these cells, compared to the control cell line (Figures 6I and S8A, *p < 0.05, **p < 0.01, ***p < 0.001).

Although *N-cadherin* expression was not significantly altered (Figure 6I), the significant overexpression of *SNAIL* and *SLUG* in Panc1 cells upon *NR1D1* KD (Figure S8A) suggested that *NR1D1* KD initiated the EMT process in Panc1 cells, which is further supported by our results on migration and invasion. In AsPC1 cells, *N-cadherin* expression increased significantly upon *PER2* KD, whereas *NR1D1* KD led to the downregulation of *SLUG* (Figures 6J and S8B, *p < 0.05, ***p < 0.001, n = 3). Thus, *PER2* KD triggered the EMT process in AsPC1 (SMAD4 deficient) cells, as supported by our results from the migration and invasion assays. Interestingly, *N-cadherin* was significantly increased, but *SLUG* was suppressed in AsPC1 shBMAL1 cells (Figures 6J and S8, ***p < 0.001). However, there was no significant increase of the migration ability of shBMAL1 when compared with shCtrl (Figure 6B). Furthermore, *CD133* was overexpressed in *PER2* KD for both PDA cell lines (Figures 6I and 6J, *p < 0.05), pointing to a role of *PER2* as a potential suppressor of tumor stemness in these cells.

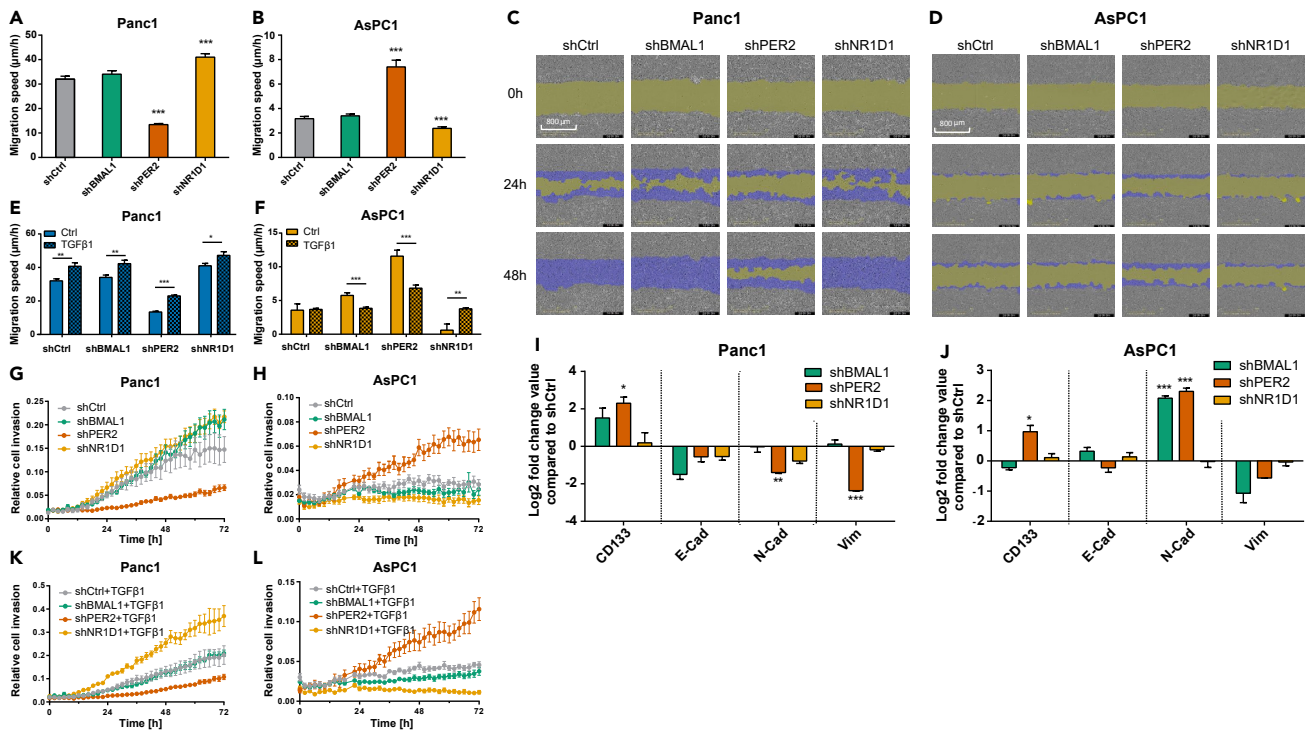


Figure 6. Dysregulation of Core-Clock Genes Affects Migration of Panc1 and AsPC1

(A, B, E, and F) Migration properties of *shCtrl* and knockdown cells (*shBMAL1*, *shPER2*, and *shNR1D1*) of Panc1 and AsPC1 with stimulation of TGFβ1 (10 ng/mL) or its solvent. Migration assays were performed using a scratch wound assay for the IncuCyte S3 Live Cell System Analysis. Average cell migration speed distribution from Panc1 and AsPC1 cells ($n \geq 8$, mean \pm SEM; (A and B): one-way ANOVA; (E and F): t test, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

(C and D) Partial representation of the scratch wound assay for Panc1 (C) and AsPC1 (D) knockdown (*shBMAL1*, *shPER2* and *shNR1D1*) and control (*shCtrl*) cells at 0, 24, and 48 h. Images were obtained with the IncuCyte S3 Software. Yellow mask indicates the wound boundaries. Blue mask indicates the initial scratch wound area.

(G, H, K, and L) Invasion assays were carried out using a chemotaxis cell invasion assay for the IncuCyte S3 Live Cell System Analysis. Invasion assay for *shCtrl* and knockdown (*shBMAL1*, *shPER2* and *shNR1D1*) conditions in Panc1 (G, K) and AsPC1 (H, L) cells with or without TGFβ1 stimulation (10 ng/mL).

Quantification was performed by measuring the total phase area of the bottom layer of the inner chamber within 72 h. Data were normalized to the initial value and presented as mean \pm SEM, $n \geq 6$.

(I and J) mRNA levels of *CD133*, *Vimentin*, *E-cadherin*, and *N-cadherin* in PDA cells were analyzed after knockdown of core-clock genes (*shBMAL1*, *shPER2*, *shNR1D1*). Data shown as comparison to the *shCtrl* (mean \pm SEM, $n = 3$, t test, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

See also [Figure S8](#).

In addition, TGFβ impacts the expression of clock genes in a SMAD4-dependent manner ([Figures S8C and S8D](#)). *BMAL1* and *NR1D1* were upregulated in SMAD4-proficient cells (Panc1), and *PER2* was upregulated in SMAD4-deficient cells (AsPC1). These alterations on clock gene expression observed in *shCtrl* cells were not present upon *BMAL1* and *NR1D1* KDs in Panc1 and *PER2* KD in AsPC1. The expression of clock genes in AsPC1 *shBMAL1* revealed no significant difference with or without additional TGFβ. These results indicated that TGFβ upregulated the expression of core-clock genes differentially via the canonical and non-canonical pathway in our PDA cell model system.

The Knockdown of Core-Clock Genes and Modifications of the TGFβ Canonical Pathway Impact Treatment Response and Patient Survival

The main problem in current PDA standard therapy with gemcitabine is the rapid development of chemoresistance. Gemcitabine, an analog of deoxycytidine, leads to DNA fragmentation and cell death by inhibiting DNA chain elongation ([Noble and Goa, 1997](#)). We further investigated whether SMAD4 or clock dysfunction impacts the response of gemcitabine in our *in vitro* model system. Our results showed that SMAD4-OE PDA cells were remarkably more sensitive to gemcitabine compared with oeCtrl, whereas *shSMAD4* cells were resistant to gemcitabine ([Figures 7A–7C](#)). Next, we explored the differential drug response of these two cell lines after core-clock gene KD. Although the gemcitabine IC₅₀ of

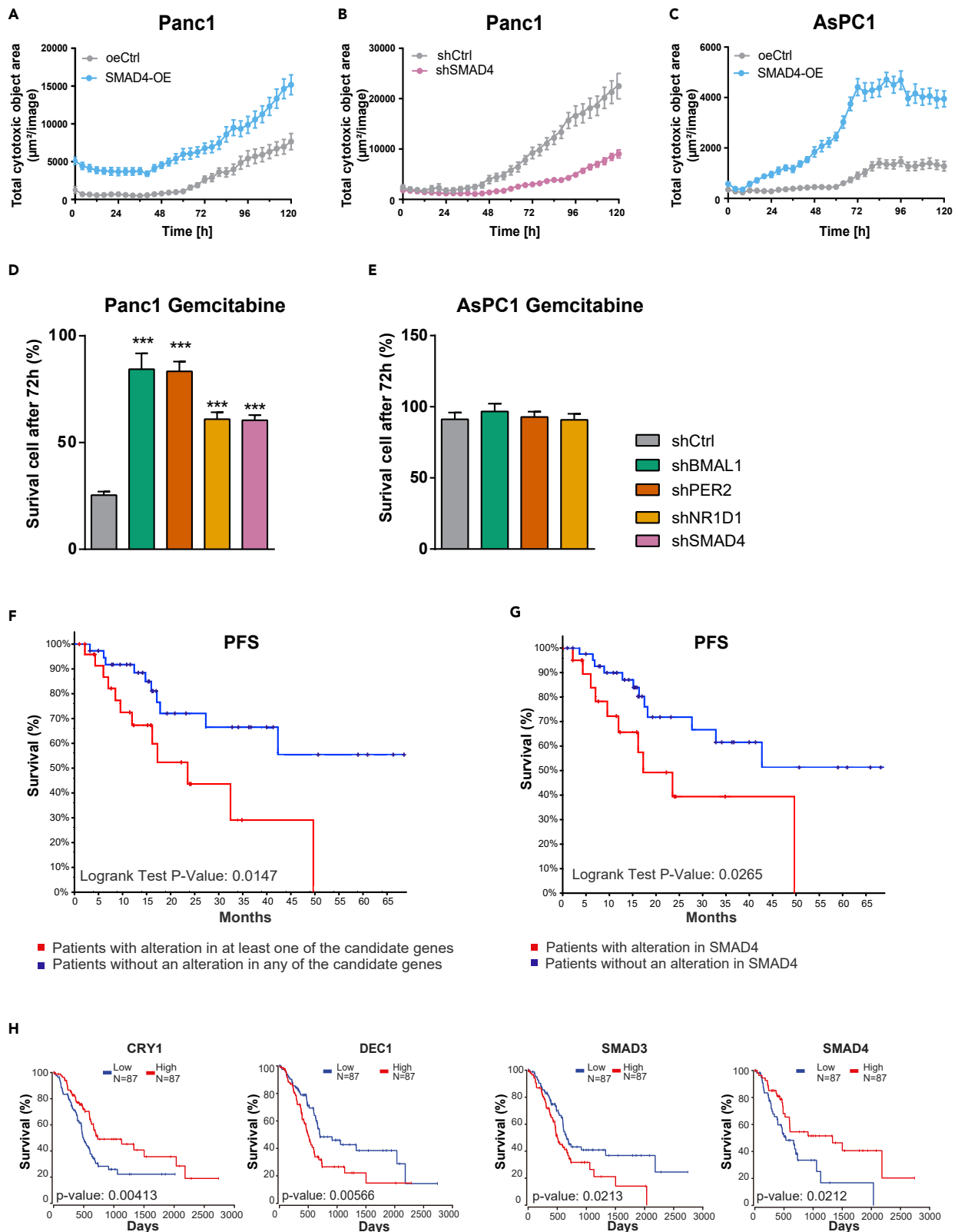


Figure 7. The Downregulation of Core-Clock Genes and the Alteration of SMAD4 Expression Affects Drug Response in Panc1 and AsPC1 Cells

Cytotoxicity assays were performed using either an IncuCyte Red Cytotoxicity Reagent or NucLight Rapid Red Reagent for the IncuCyte S3 Live Cell System Analysis

(A–C) Cytotoxicity analysis for Panc1 (A, B) and AsPC1 (C) cells containing *SMAD4*-KD or *SMAD4*-OE constructs, in comparison with the corresponding empty controls (*shCtrl* and *oeCtrl*). 0 h after cell synchronization, gemcitabine was dissolved in IncuCyte Red Cytotoxicity Reagent and added to PDA cells (IC50: Panc1, 9.5 μ M, and AsPC1, 23.9 μ M). A cytotoxic index was calculated on IncuCyte S3 Live-Cell Analysis System in red phases. Data are expressed as mean \pm SEM, $n \geq 6$.

(D and E) Cytotoxicity analysis for Panc1 (D) and AsPC1 (E) cells containing knockdown constructs (*shBMAL1*, *shPER2* and *shNR1D1*) or its empty vector (*shCtrl*). Cell nuclei were labeled with NucLight Rapid Red Reagent. At 0 h after cell synchronization, gemcitabine (IC50: Panc1, 9.5 μ M, and AsPC1, 23.9 μ M) was added into the cells. 72 h after treatment, the number of viable cells per well was quantified with IncuCyte S3 Live-Cell Analysis System. Compared with the *shCtrl* (mean \pm SEM, $n = 6$, one-way ANOVA, *** $p < 0.001$). See also [Figure S9](#).

(F) Impact of alterations in our 10 candidate genes on progression-free survival (PFS) in a TCGA cohort of patients with pancreatic adenocarcinoma.

(G) Impact of *SMAD4* mutation on PFS in a TCGA cohort of patients with pancreatic adenocarcinoma when compared with patients who do not have *SMAD4* mutation (log rank $p < 0.05$).

(H) Impact of variation in candidate gene expression on overall survival in a TCGA cohort of patients with pancreatic adenocarcinoma. Survival curves were plotted using a Cox model that includes $\text{coxph}(\text{Surv}(\text{times}, \text{died}) \sim \text{gene} + \text{grade1} + \text{grade2} + \text{grade3} + \text{age})$. Statistically significant results ($p < 0.05$) are shown in the figure. The project ID used for Kaplan Meier survival analysis (F and H) is retrieved from TCGA PAAD, dbGaP Study Accession No: phs000178 (<https://portal.gdc.cancer.gov/projects/TCGA-PAAD>).

AsPC1(23.9 μ M) is much higher than that of Panc1 (9.5 μ M), AsPC1 *shCtrl* cells revealed higher viability after 72-h treatment when compared with Panc1 *shCtrl*. This further confirms an increased resistance to gemcitabine in the absence of *SMAD4*, in PDA cells. Unlike AsPC1, Panc1 clock gene KD cells showed significant resistance to gemcitabine treatment compared with *shCtrl* cells ([Figures 7D and 7E](#), *** $p < 0.001$). These results emphasize the importance of circadian dysfunction in gemcitabine resistance in *SMAD4*-proficient PDA cells. The dysregulation of the circadian clock in Panc1 cells increased the resistant to gemcitabine, when compared with *SMAD4*-deficient cells (AsPC1), suggesting that *SMAD4* impacts gene expression programs associated with the circadian clock and drug response in Panc1, which are distinct from AsPC1. These data highlight a novel role of the circadian clock in fine-tuning drug effectiveness in PDA with an emphasis on *SMAD4*. Moreover, to test whether drug administration at different times had different effects, we selected the time points 17, 20, and 23 h based on the time course RT-qPCR and bioluminescence data for the two cell lines, which show different expression of the core-clock genes measured ([Figure S9A](#)). Our data show that the timing of treatment administration has different effects in cell survival depending also on the additional perturbations generated to the cells. At particular times, the *SMAD4*-proficient PDA cells are more resistant to treatment, whereas for the *SMAD4*-deficient AsPC1 cells this effect was not observed ([Figures S9B and S9C](#)). After downregulation of *SMAD4* in Panc1 ([Figure S9B](#)), the differential drug response to different treatment time points is significantly impaired. These results point to a role of *SMAD4* in the time-dependent effect of treatment administration.

We then analyzed the impact of alterations in the clock genes *BMAL1*, *PER2*, *NR1D1*, *CRY1*, *DEC1*, and *DEC2*, as well as elements of the TGF β pathway, *TGF β 1*, *SMAD3*, *SMAD4*, and *SMAD7* in patient survival. For that we quantified the mutational frequencies of these 10 genes from a cohort of patients with pancreatic adenocarcinoma (184 samples from the PanCancer study, Study Accession No: phs000178, <https://portal.gdc.cancer.gov/projects/TCGA-PAAD>) ([Cancer Genome Atlas Research Network, 2017](#)) curated from The Cancer Genome Atlas (TCGA) database. Among these candidate genes, *SMAD4* showed the highest mutation rate in the population (34%).

Patients with *SMAD4* mutation (mostly deletion) had a significant worse progression-free survival (PFS, $p < 0.05$) ([Figure 7G](#)). This suggested that *SMAD4* mutation in the advanced stage of the disease facilitates cancer progression. Interestingly if we compare the survival between the group of patients having no mutations for any of the candidate genes with the patients having mutations in at least one of the candidate genes, our results show a statistically significant influence on PFS ($p < 0.05$, [Figure 7F](#)). These results suggest that *SMAD4* mutation alone had a significant impact on the PFS, which is likely to be increased with the influence of additional mutations in our other candidate genes ([Figures 7F and 7G](#)).

To study the influence of alterations in gene expression for the set of genes described earlier in survival of patients, we performed a cox-regression-based survival analysis based on clinical parameters that include age, tumor grade, and gender in addition to the gene expression levels ([Figure 7H](#)). To evaluate high- and low-risk groups based on gene expression changes, we applied OncoLnc to 177 available mRNA datasets (RNA-Seq v.2) from the TCGA, Pancreatic Adenocarcinoma, patient cohort, which we divided into two

equal cohorts (N = 87 low, N = 87 high) representing high- and low-expression groups, respectively (Figure 7H). The clock genes *CRY1* and *DEC1*, and TGF β signaling family members *SMAD3* and *SMAD4*, showed significant impact on survival (Figure 7H, log rank test $p < 0.05$) for PDA patients suggesting a potential clinical value for targeting these genes in a therapeutic context. Together with the results from our *in vitro* model, the expression of the clock genes *DEC1* and *CRY1* also revealed a *SMAD4* dependency. These data highlight an important role for the cross-talk between the endogenous molecular clock and the TGF β canonical pathway and its likely contribution to the progression and prognosis of PDA.

DISCUSSION

A dysregulated clock in patients with cancer was shown to be associated with poorer prognosis and a shorter lifespan. Pancreatic cancer is one of the major causes of cancer mortality worldwide. Several studies have identified disruptions in clock genes, which are correlated with cancer progression in pancreatic cancer (Jiang et al., 2016; Relles et al., 2013; Tavano et al., 2015; Wu et al., 2012). Among these genes are members of the core-clock machinery (*BMAL1* and *PER2*), as well as clock-regulated genes (*SIRT1* and *DEC1*), which either show abnormal expression or altered rhythmic pattern resulting in cancer progression and EMT (Jiang et al., 2016; Relles et al., 2013; Tavano et al., 2015; Wu et al., 2012). However, the detailed mechanism of circadian clock regulation in pancreatic cancer is still unclear. TGF β is involved in oncogenic transformation and cancer progression, and it plays a vital role in cancer homeostasis. As tumors grow and progress, genetic alterations often occur on TGF β canonical signaling components (including *SMAD4* mutations), leading to the activation of pro-oncogenic pathways such as RAS, PI3K, and MAPK (Principe et al., 2017). These genetic modifications eventually override the growth inhibitory effects of the TGF β canonical pathway, further contributing to tumor development. Although it is known that elements of TGF β canonical pathway are involved in circadian regulation (Akagi et al., 2017; Chen et al., 2015; Sato et al., 2019), the molecular mechanisms underlying this cross-talk in human cancers remain largely uncharacterized.

In the present study, we first characterized the circadian phenotype of pancreatic cancer cells, with similar proliferation profiles, originated from a primary tumor (Panc1) and metastasis ascites (AsPC1). The cells derived from the primary tumor show a differential clock phenotype when compared with the cells derived from the metastasis ascites, pointing to a differential regulation of the clock machinery in different types, genomic background, and stages of cancer, in agreement with previous reports for other cancer types (Fuhr et al., 2018; Relogio et al., 2014).

To explore the possible mechanisms connecting the circadian clock and tumor progression in pancreatic cancer, we focused on the CCG *SMAD4*. As the core mediator of the TGF β canonical pathway, *SMAD4* is known to assist the modulation of cancer progression (reviewed in Xu et al., (2009)). We hypothesized that *SMAD4* could affect the circadian phenotype and subsequently malignant phenotypes of PDA cells. Hence, we established a pancreatic cancer *in vitro* model consisting of *SMAD4*-positive (Panc1) and *SMAD4*-negative (AsPC1) cell lines and investigated this interplay through gene knockdown and overexpression of core-clock elements, TGF β and *SMAD4*. Our data show that *TGF β 1*, *SMAD3*, *SMAD4*, and *SMAD7* exhibit circadian oscillation at the transcript level in Panc1 cells, pointing to the circadian regulation of the TGF β pathway in *SMAD4*-proficient PDA cells. Chen et al. reported that the transcript of *TGF β 1* oscillates in a circadian fashion in mouse embryonic fibroblasts, whereas the oscillation is perturbed in *Clock*-deficient mice (Chen et al., 2015). Furthermore, the authors showed that binding of the Bmal1-Clock heterodimer to *mTGF β 1* exhibits a circadian rhythmicity in mouse renal cells (Chen et al., 2015). Another study showed enriched Bmal1 binding on promoter regions of *TGF β 1* and *Smad3*, which occurred at the similar time as Bmal1 E-box binding to Nr1d1 (at CT8) in mouse brown adipocytes (Nam et al., 2015). These results indicate that Bmal1 activates the expression of components of the TGF β canonical pathway (via *TGF β 1* and *Smad3*) in parallel with the activation of Nr1d1. However, whether mRNA dynamics of TGF β signaling elements are under the circadian modulation in human cancers is still largely uncharacterized. Interestingly, our results show that the circadian oscillation (period of circa 24 h) of elements of the TGF β pathway is only detectable in *SMAD4*-positive cells and not in *SMAD4*-deficient cells. In the absence of extrinsic TGF β , transcription of *SMAD7* can be induced by the intrinsic TGF β following a circadian pattern. *TGF β 1* transcript also shows a similar period with a different phase than *SMAD7*. This further suggests that autocrine TGF β may activate the transcription of *SMAD7* in a circadian fashion. We also detected circadian rhythms in *BMAL1* mRNA of *SMAD4*-positive cells, resembling our observation in transcripts of

TGF β canonical elements (*SMAD3* and *TGFB1*). This supported our hypothesis that *SMAD4* may serve as a mediator element bridging the clock and the TGF β signaling pathway.

It has been previously shown that the core-clock genes *Bmal1* and *Nr1d1* are involved in the TGF β canonical pathway in mouse brown adipose (Nam et al., 2015). In agreement, we show that clock perturbation via small hairpin RNA knockdown of core-clock elements (*BMAL1* and *NR1D1*) resulted in abolished oscillations of *TGF β 1*, *SMAD3*, *SMAD4*, and *SMAD7*, confirming the existence of bidirectional connection between core-clock elements and the TGF β canonical pathway in human PDA cells. In addition, the transcription factors, *DEC1* and *DEC2*, inhibit *PER* via protein-protein interactions with *BMAL1* and/or competition for E-box elements (Honma et al., 2002). Of note, *DEC1/2* is a downstream element of TGF β canonical pathway as well (Adorno et al., 2009; Kon et al., 2008; Prunier et al., 2019; Zewel et al., 2002). To identify the specific bridging elements between the core-clock and the TGF β signaling, we further analyzed the expression of the clock genes *DEC1* and *DEC2* (Figures 2D, 2G, and 2J). We observed a negative correlation between *SMAD4* and *DEC1/2* expression through *SMAD4* downregulation and overexpression assays, which reinforced the mediating role of *DEC1/2* via TGF β pathway in regulating the circadian clock.

We further investigated whether TGF β activation and *SMAD4* expression could affect the oscillatory phenotype of *BMAL1* and *PER2* promoter activity in both *SMAD4*-positive and *SMAD4*-deficient pancreatic cancer cell lines using live bioluminescence recordings. Surprisingly, TGF β stimulation alone did not cause major changes in the period of oscillations for both cell lines. However, the period was significantly shorter when we combined TGF β stimulation with *SMAD4* overexpression in both cell lines, indicating that the TGF β -clock interplay might be *SMAD4* dependent.

Downregulation of core-clock genes resulted in an overall higher proliferative and apoptotic activity in *SMAD4*-positive cells. Of note, *SMAD4* downregulation only affected cell proliferation and not apoptosis in these cells. We speculate that reduced expression of *SMAD4* might activate the non-*SMAD* TGF β signaling pathway, including the MAPK/ERK, resulting in higher cell proliferation and growth (reviewed in Zhang, 2017). We confirmed the activation of the Ras-mediated TGF β non-canonical pathway by measuring the expression of RAS and p-ERK, and particularly after stimulation with TGF β , further pointing to the activation of the RAS/ERK pathway.

In *SMAD4*-deficient cells, the apoptotic rate was also increased upon knockdown of clock genes. However, cell proliferation was only notably increased upon *PER2* downregulation in AsPC1. Our cell cycle analysis also confirmed this finding showing higher percentage of *shPER2* cells in the S phase. The overall differential proliferative properties and cell cycle distributions upon the KD of clock genes in both PDA cells suggest that cell fate determination via the clock is altered in *SMAD4* mutant (AsPC1) cells. *SMAD4* overexpression, on the other hand, resulted in remarkably higher cellular apoptosis in both cell lines. This confirms the apoptotic role of the canonical TGF β signaling pathway mediated by *SMAD4*, as described in previous studies, and hints to the central role of *SMAD4* in regulating the canonical TGF β signaling pathway (Du et al., 2018; Pang et al., 2011). This effect is more evident in our *SMAD4*-deficient cells, with a notable increase in apoptosis upon *SMAD4* overexpression with additional TGF β 1 stimulation.

Previous reports indicate a prominent role for the TGF β signaling pathway in regulating cell cycle progression (Buenemann et al., 2001; Mukherjee et al., 2010; Voss et al., 1999). Indeed, we showed in our PDA model that cell-cycle arrest was triggered when cells were stimulated with TGF β and *SMAD4* was overexpressed. We observed an opposite effect after *SMAD4* downregulation resulting in more S-phase cells and proliferation. Furthermore, TGF β stimulation alone inhibited G1/S cell cycle propagation only in *SMAD4*-positive cells. These results highlight the determinant role of *SMAD4* in regulating cell cycle proliferation and apoptosis via downstream genes of TGF β canonical and non-canonical signaling pathway (e.g., *P21*, *c-MYC*, and *RAS*) (Alexandrow and Moses, 1995; Mukherjee et al., 2010; Principe et al., 2017; Voss et al., 1999), further pointing to a differential regulation of TGF β pathway in different stages of pancreatic cancer, as reported in the present or former studies in a *SMAD4*-dependent manner.

Regulating EMT and cell invasion is one of the key functions of TGF β signaling pathway in cancer cells (Lee et al., 2013; Xu et al., 2009). Cells undergoing EMT lose expression of E-cadherin and other components needed for epithelial cell junction stability and are able to produce a mesenchymal cell cytoskeleton acquiring motility and invasive properties (Massague, 2008). The reverse process of EMT, MET, involves

the activation of E-cadherin and suppression of N-cadherin (Yao et al., 2011). Hence, we analyzed migration/invasion properties upon *SMAD4* expression and TGF β stimulation in both cell models. TGF β stimulation alone was sufficient to enhance cell migration in *SMAD4*-positive cells, whereas in *SMAD4*-deficient cells, both *SMAD4* overexpression and TGF β stimulation resulted in the highest migratory and invasion activities, suggesting that *SMAD4* expression is necessary for enhancing cancer metastasis. We confirmed this finding through *SMAD4* downregulation and showed that cell migration was not affected upon TGF β stimulation. After measuring the expression of EMT marker genes (e.g., *E-Cad*, *N-Cad*, *SNAIL*, *SLUG*) in pancreatic cancer (Takano et al., 2007), we found that *SMAD4* overexpression reduced the expression of epithelial marker genes (*E-Cad*) and enhanced the expression of genes involved in mesenchymal transition (*N-Cad*, *Vim*, *SNAIL*, and *SLUG*) in both cell lines, indicating that *SMAD4* mediates invasion by regulating the expression of key marker genes involved in EMT. We observed the opposite effect in EMT gene expression after *SMAD4* knockdown, which reinforces the role of *SMAD4* in cancer invasion. In addition, we sought to explore another cancer hallmark, tumor stemness via the analysis of *CD133* (Tabu et al., 2010). In our model system, we observed a downregulation of *CD133* in PDA cells with *SMAD4* overexpression. More interestingly, increased *CD133* expression after *SMAD4* KD implied the acquisition of cancer stem-like hallmark in our study, in agreement with previous studies (Chen et al., 2014).

Cancer metastasis is the cumulative result of multiple changes in tumor cells and their microenvironment. Cell migration was differentially regulated in *SMAD4*-positive and *SMAD4*-deficient cells upon *PER2* and *NR1D1* downregulation (Figure 6). In *SMAD4*-positive cells, cell migration was decreased upon *PER2* knockdown and increased after *NR1D1* downregulation, whereas we observed an opposite effect in the cell line deficient for *SMAD4*. Interestingly, TGF β activation also implied an overall opposite effect in the core-clock knockdown cells from *SMAD4*-positive and *SMAD4*-negative PDA: promoting migration in Panc1 cells and inhibiting it in AsPC1 cells. These results show that cancer cell properties seem to be *SMAD4*-dependent upon clock dysregulation, highlighting the reciprocal role of the circadian clock and *SMAD4* in pancreatic cancer. Notably, the downregulation of *PER2* results in the increased expression of *CD133* in both PDA cells, hinting at the crucial role of *PER2* in cancer stemness independent of *SMAD4* (Kamtamune et al., 2019). Hence, based on our results on proliferation, apoptosis, cell cycle, and cellular metastatic properties, we speculated that TGF β might alter the circadian clock differently via the canonical (in Panc1) and non-canonical (in AsPC1) pathways.

Finally, we tested whether treatment response in pancreatic cancer is clock and/or *SMAD4* dependent. Results from previous clinical trials concluded that the loss of *SMAD4* is a negative prognostic indicator, which is strongly associated with poor chemosensitivity (Shin et al., 2017; Singh et al., 2012; Yamada et al., 2015). Extrinsic DNA damage due to gemcitabine administration imposes threats to cellular homeostasis involving the regulation of both the TGF β signaling pathway (Li et al., 2019; Liu et al., 2019) and clock components (Jiang et al., 2018; Ka et al., 2017; Mazzoccoli et al., 2016; Sulli et al., 2018). To elucidate the molecular mechanisms that drive chemoresistance in this PDA model, we hypothesized that during the exposure to gemcitabine, clock genes and TGF β canonical components participate in the regulation of DNA repair, as well as in the maintenance of genomic stability.

A previous study showed that patients with PDA with *SMAD4* loss have poorer PFS in the gemcitabine-based treatment subgroup (Ormanns et al., 2017). Consistently, we observed that *SMAD4*-deficient cells are resistant to the chemotherapy with gemcitabine. Although the intrinsic mechanism has not been fully understood yet, based on our apoptosis and cell cycle data, we assume that it relates to the effect in the cell cycle due to the anti-apoptotic role of *SMAD4*.

Clock perturbation via the knockdown of core-clock genes aggravates chemoresistance, notably only in *SMAD4*-proficient pancreatic cancer cells. Associated with the fact that genetic alterations (mostly inactivation) of *SMAD4* often occur in the advanced stage of pancreatic cancers, we concluded that the molecular clock functions as a repressor of chemoresistance of gemcitabine while *SMAD4* is not mutated (e.g., cancers in the early stage). Hence, loss of *Smad4* function along with TGF β stimulation (as observed for AsPC1, *SMAD4*-deficient cells) activates the non-canonical pathway (RAS) and increases CSCs (*CD133* upregulation), further contributing to the acquisition of malignant properties and drug resistance. These findings highlight the important role of *SMAD4* in affecting gene expression programs associated with the circadian clock and drug response in *SMAD4*-proficient cells, which are distinct from those in *SMAD4*-deficient cells. Furthermore, our results emphasize the importance of circadian clock dysfunction in gemcitabine resistance in *SMAD4*-proficient PDA cells. Our

data indicate that drug response and cell fate determination in pancreatic cancer cells with WT or mutated SMAD4, upon the dysregulation of the circadian clock, resulted in a significant differential change in cell survival rate and invasiveness, highlighting the importance of the associations between the TGF β canonical pathway, biological clock, and drug timing affecting chemosensitivity in a cancer context.

The information that we obtained from our *in vitro* model system aids to the understanding of the impact of the clock in the SMAD4 network and consequently in cell fate decisions. In addition, and to better show the potential of our results beyond the *in vitro* experiments presented, we performed a computational analysis with publicly available datasets for patients with pancreatic cancer. In our PDA model system, the overexpression of SMAD4 resulted in upregulation of CRY1 and downregulation of DEC1; the downregulation of SMAD4 led to suppression of CRY1 and overexpression of DEC1. These results agree with our survival analysis for a cohort of patients with PDA that indicated a better prognosis (PFS, $p < 0.05$) for the groups of patients with high expression of CRY1, low expression of DEC1, and high expression of SMAD4. In addition, the genomic alteration of SMAD4 (mostly deletion) alone led to a worse PFS ($p = 0.0265$), which is aggravated when combined with alterations of other genes bridging the clock and the TGF β canonical pathway ($p = 0.0147$). This points to a relevant role of the molecular clock, together with the TGF β pathway, in contributing to the progression and prognosis of PDA. Altogether, our data show that the circadian clock regulates the TGF β /SMAD4 pathway in PDA cells with likely consequences on cancer progression (invasion and EMT) and patient survival and suggest a profound role for SMAD4 as an intermediate component linking the clock machinery to the TGF β pathway. This information may be relevant for patients with pancreatic cancer undergoing chemotherapy to increase the effectiveness of the therapy based on SMAD4 mutation and the circadian clock.

Limitations of the Study

We consider the lack of *in vivo* data as a limitation of our study, with the caveat that mice (as nocturnal animals) have a different clock compared with humans (as diurnal animals) and hence results from an *in vivo* mouse model regarding alteration of the circadian clock may not be directly relevant or properly translated to human disease models. This is particularly relevant when comparing drug timing, drug toxicity, and drug efficacy between nocturnal and diurnal models (reviewed in Dallmann et al., 2016). In addition, we have previously shown that in circadian studies, the host-cancer interaction in *in vivo* models (using xenografts) has an impact on the circadian phenotype of the xenograft, which adds complexity to the interpretation of the results with regards to the circadian machinery (Basti et al., 2020).

Resource Availability

Lead Contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Dr. Angela Relógio (angela.relogio@charite.de).

Materials Availability

This study did not generate new unique reagents.

Data and Code Availability

This study did not generate datasets/code.

METHODS

All methods can be found in the accompanying [Transparent Methods supplemental file](#).

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.isci.2020.101551>.

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AUTHOR CONTRIBUTIONS

Conceptualization, A.R.; Methodology, A.R. and Y.L.; Investigation, Y.L., A.B., and M.Y.; Validation, Y.L., A.B., and A.R.; Writing – Original Draft, Y.L., A.B., and A.R.; Writing – Review & Editing, Y.L., A.B., M.Y., and A.R.; Funding Acquisition, A.R.; Resources, A.R.; Supervision, A.R.

DECLARATION OF INTERESTS

The authors declare that they have no conflict of interest.

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Supplemental Information

**Circadian Dysregulation of the TGF β /SMAD4
Pathway Modulates Metastatic Properties and Cell
Fate Decisions in Pancreatic Cancer Cells**

Yin Li, Alireza Basti, Müge Yalçın, and Angela Relógio

Supplemental Data Items

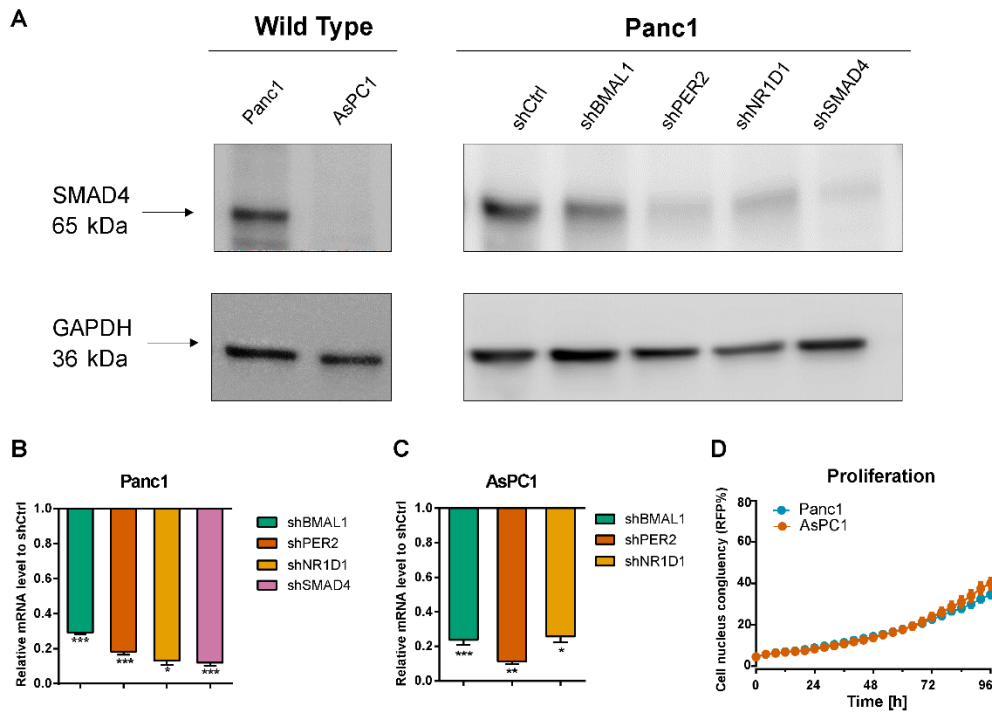


Figure S1. Western blot analysis of SMAD4 protein expression for KDs and OE cells. Related to Figure 1. (A) Western blot analysis of SMAD4 (65kDa) for wild type PDA cells and Panc1 KD cells (*shCtrl*, *shBMAL1*, *shPER2*, *shNR1D1* and *shSMAD4*). Depicted is one representative replicate, GAPDH is provided as loading control. (B - C) KD efficiency for *shBMAL1*, *shPER2*, *shNR1D1* and *shSMAD4*. Gene expression analysis of corresponding KD genes in Panc1 (B) and AsPC1 (C) cells. Relative gene expression is shown compared to the corresponding *shCtrl* (pLKO.1) (mean ± SEM, n = 3, t-test, **p* < 0.05, ***p* < 0.01, ****p* < 0.001). KD efficiency in Panc1 *shBMAL1*: 70.8% (0.29 ± 0.01), *shPER2*: 81.7% (0.18 ± 0.02), *shNR1D1*: 86.1% (0.13 ± 0.02) and *shSMAD4*: 88.5% (0.12 ± 0.02). KD efficiency in AsPC1 *shBMAL1*: 76.2% (0.24 ± 0.03), *shPER2*: 88.7% (0.11 ± 0.02) and *shNR1D1*: 74.2% (0.26 ± 0.03). (D) Proliferation assays for pancreatic cell lines (Panc1 and AsPC1) were performed using NuLight Rapid Red Reagent for the IncuCyte S3 Live Cell System Analysis (mean ± SEM, n = 8).

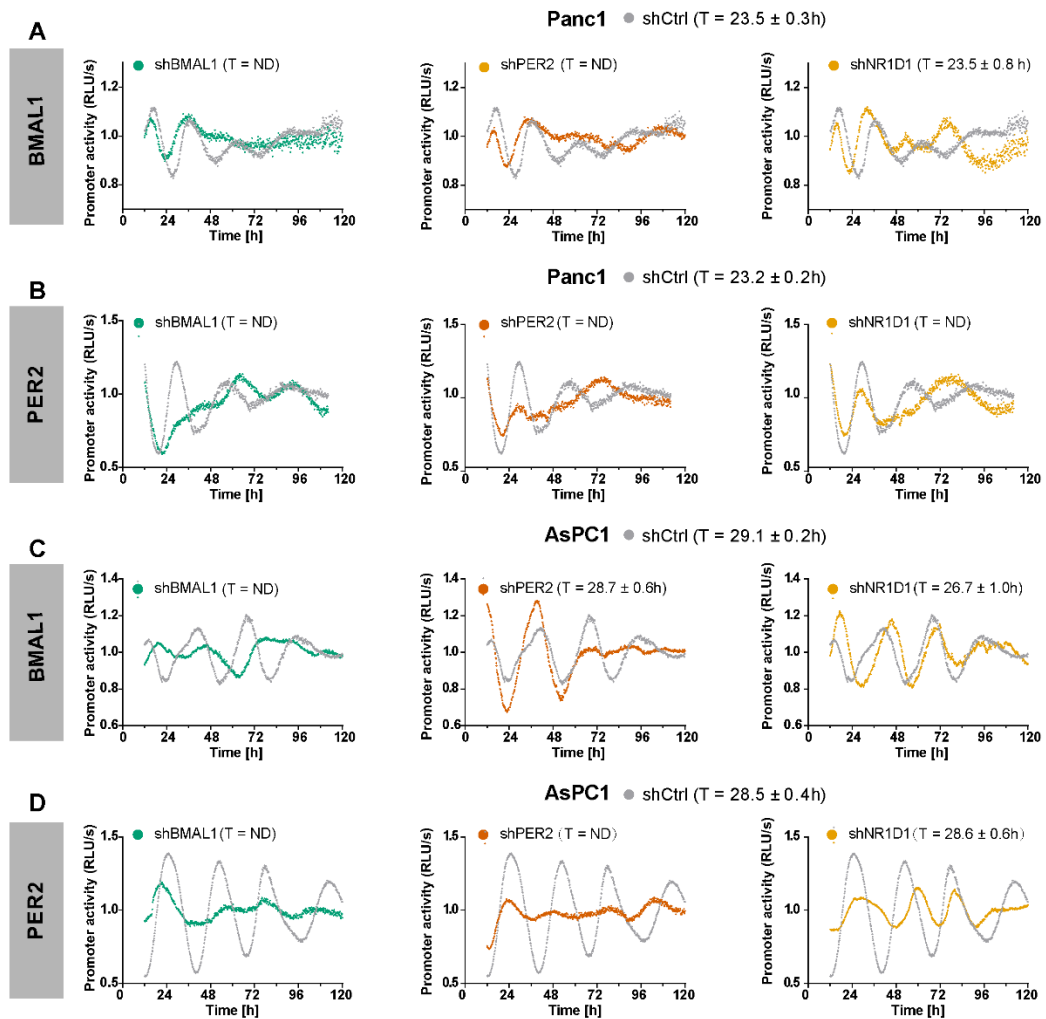


Figure S2. The promoter activity of BMAL1 and PER2 after clock genes KD. Related to Figure 2. Bioluminescence recordings for the promoter activity of *BMAL1* and *PER2* for *shCtrl* (pLKO.1) and KDs (*shBMAL1*, *shPER2* and *shNR1D1*) in Panc1 (A - B) and AsPC1 (C - D). Depicted is one representative replicate (mean \pm SEM, n = 3).

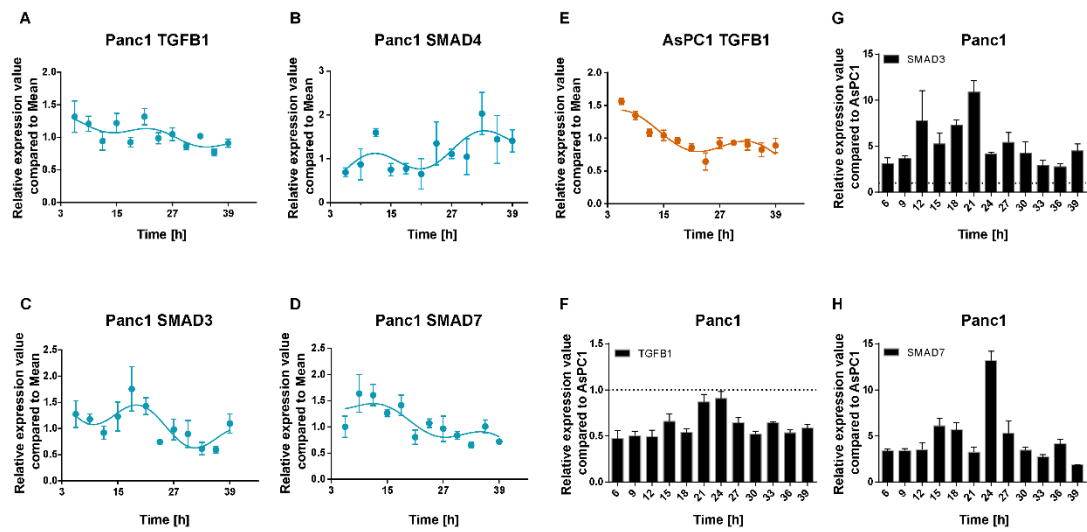


Figure S3. Panc1 (SMAD4 proficient) cells show circadian oscillations in expression for elements of the TGFβ pathway. Related to Figure 2. (A - E) 33h time-course gene expression analysis for *TGFβ1*, *SMAD4*, *SMAD3* and *SMAD7* in Panc1 and AsPC1 wild type cells (n = 3, mean ± SEM, a cosine curve was fitted to all data sets, Table. 3). (F - H) Comparisons of gene expression (*SMAD3*, *SMAD7* and *TGFβ1*) for each time point over 33 h (mean ± SEM, n = 3).

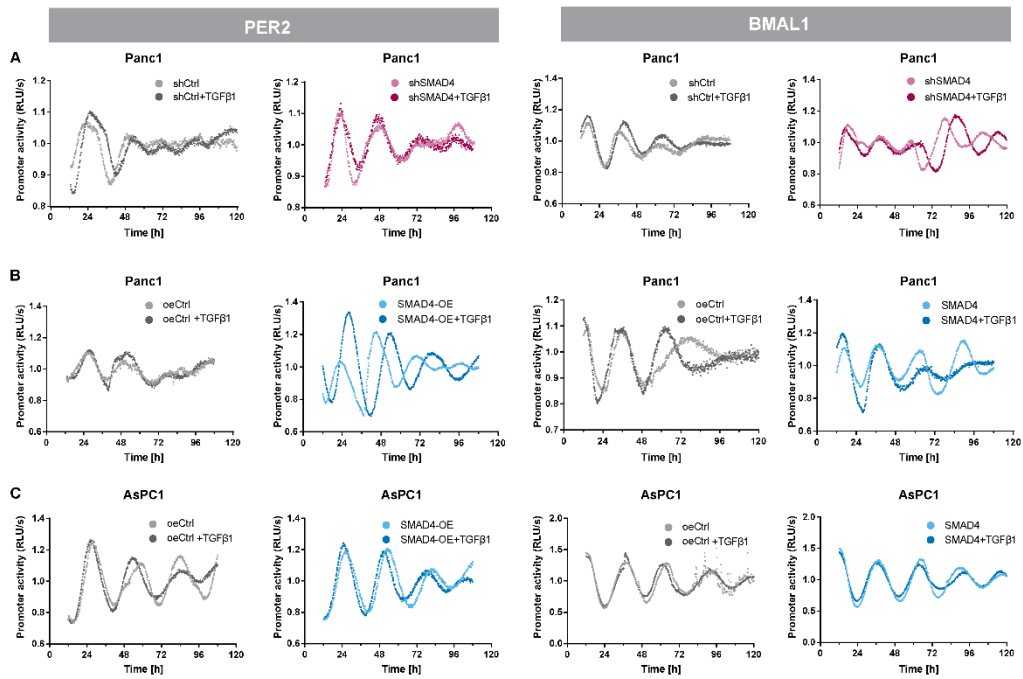


Figure S4. The real-time bioluminescence recording of a *BMAL1* and *PER2* promoter activity for activation or inactivation of the canonical TGFβ pathway. Related to Figure 2.

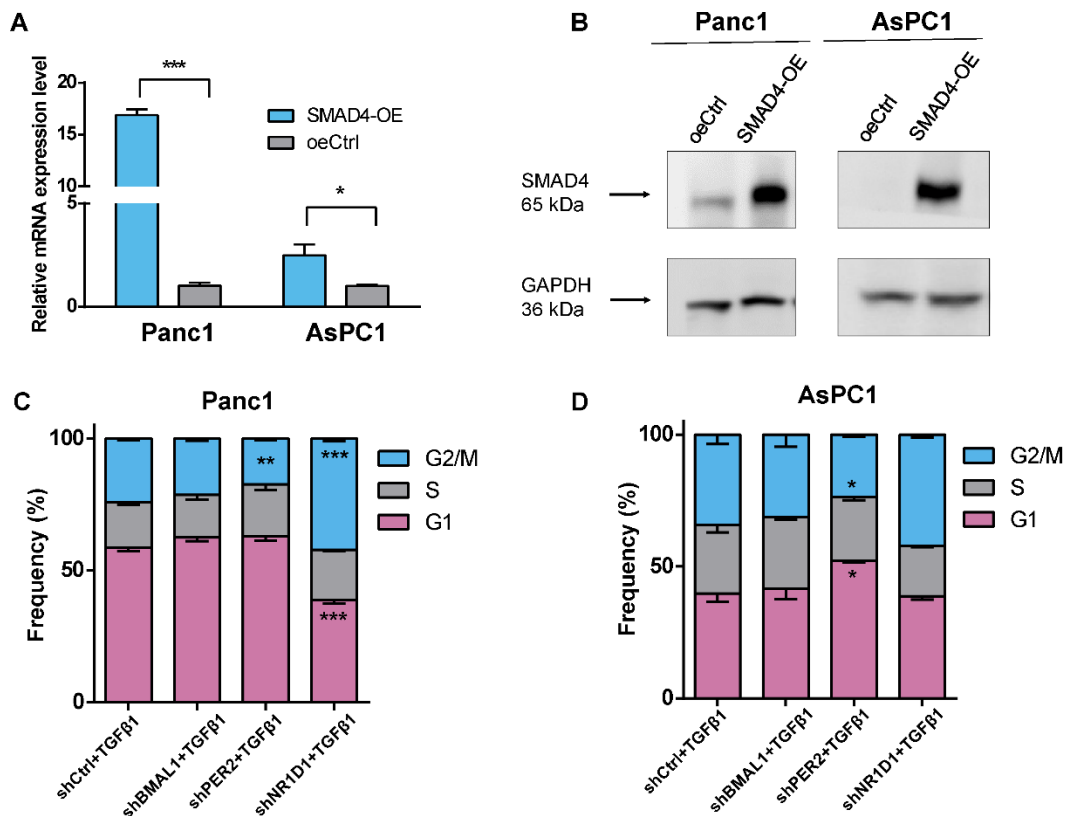


Figure S5. Clock disruption stimulated with TGFβ impacts on cell cycle in PDA cells.

Related to Figures 3 and 4. (A) *SMAD4* overexpressing efficiency after γ -retroviruses transduction. Gene expression analysis of *SMAD4* in Panc1 and AsPC1 cells. Relative gene expression value is shown compared to the corresponding empty vector oeCtrl (Flag-puro). (B) Shown is one representative replicate for the Western blot analysis of SMAD4 (65kDa) for PDA cells containing overexpression construct and respective control (*SMAD4*-OE and oeCtrl). GAPDH was used as loading control. (mean \pm SEM, n = 3). (C-D) Cell cycle measurements after KDs of BMAL1, PER2 and NR1D1 with or without a 24h-TGF β 1 stimulation. Cell cycle phase distributions were compared with their respective control conditions (n = 3, mean \pm SEM, two-way ANOVA, * p < 0.05, ** p < 0.01, *** p < 0.001).

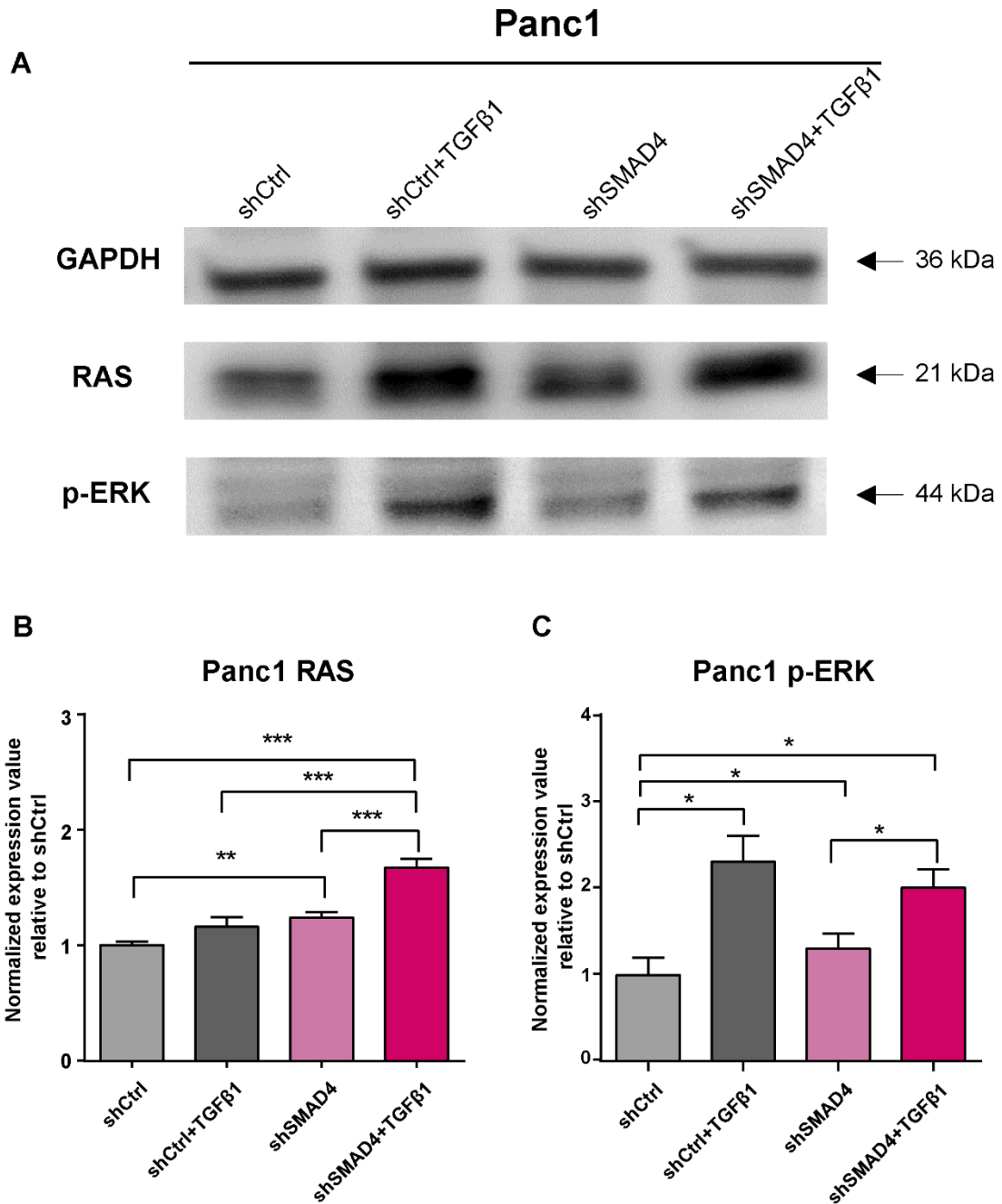


Figure S6. Loss of SMAD4 and TGFβ stimulation promote the overexpression of p-ERK and RAS. Related to Figures 3 and 4. (A) Shown is one representative replicate for the Western blot analysis of RAS (21kDa) and phosphorylated-ERK (p-ERK, 44.42kDa) for Panc1 cells containing *shSMAD4* construct and respective control (*SMAD4*-KD and *shCtrl*) with or without a 24h-TGFβ-stimulation. GAPDH (36kDa) was used as loading control. (B-C) Relative protein expression level of RAS, p-ERK for each condition as compared to *shCtrl* (one-way ANOVA, mean ± SEM, n ≥ 3, **p* < 0.05, ***p* < 0.01, ****p* < 0.001).

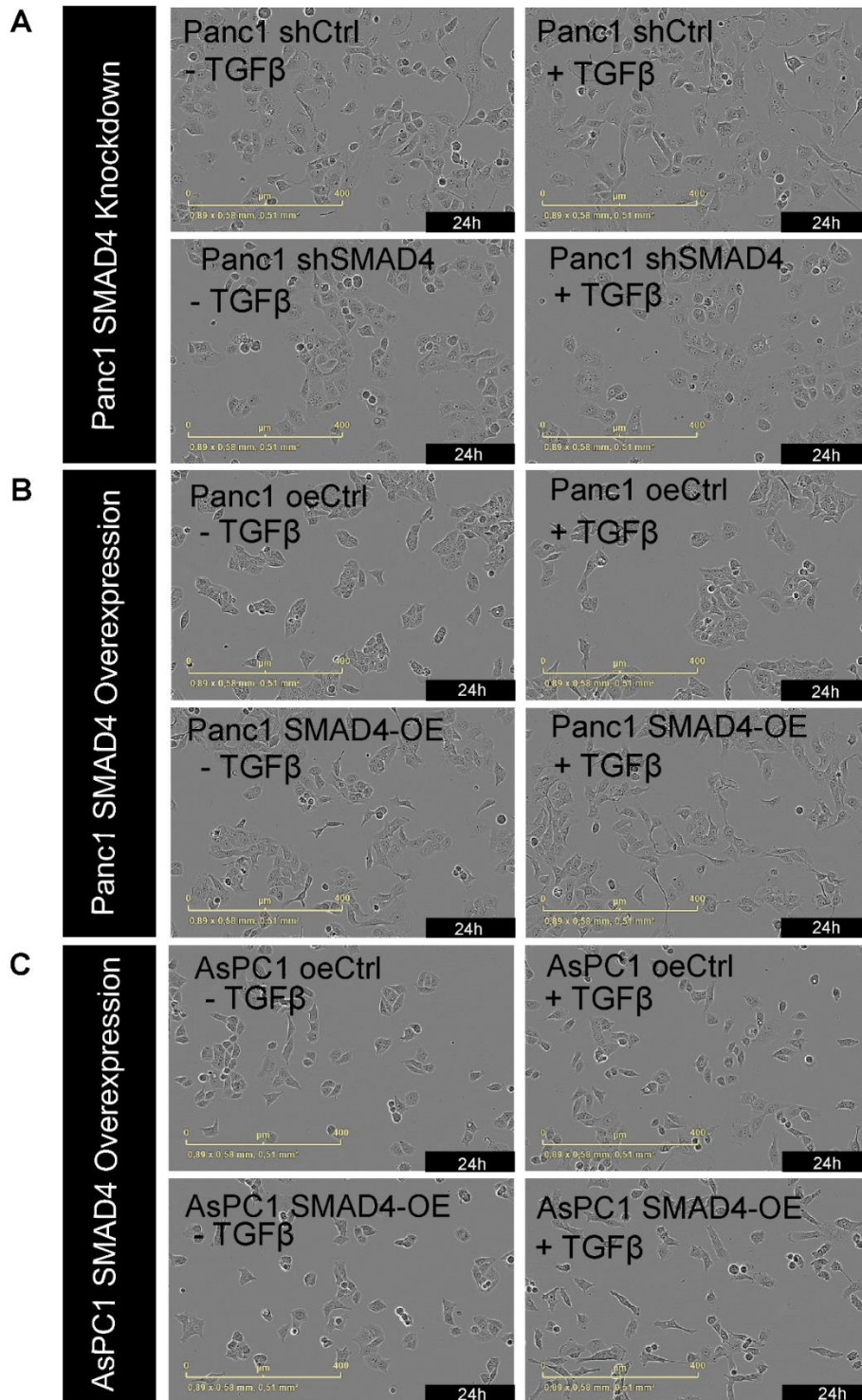


Figure S7. Morphology changes after activation and inactivation of the canonical TGFβ pathway. Related to Figure 5. *SMAD4*-KD and -OE cells were stimulated with 10ng/ml TGFβ1 or the corresponding solvent. Changes in cell morphology were observed 24h after stimulation (20x objective, scale bar = 400 μm).

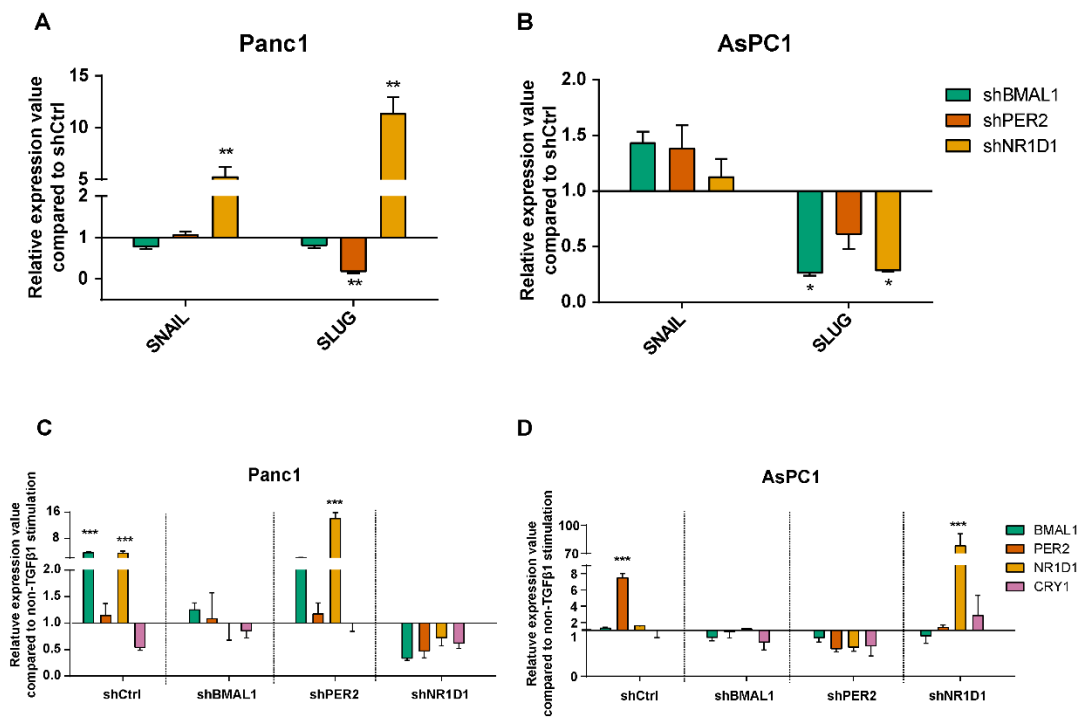


Figure S8. TGF β stimulation impacts the clock gene expression differentially in SMAD4-proficient and -deficient PDA cells. Related to Figure 6. (A - B) mRNA levels of EMT markers (*SNAIL* and *SLUG*) in PDA cells were altered after knockdown of core-clock genes (*shBMAL1*, *shPER2* and *shNR1D1*). Depicted are RT-qPCR results for KD PDA cells compared to the *shCtrl* (mean \pm SEM, n = 3, t-test, * p < 0.05, ** p < 0.01, *** p < 0.001). (C - D) The comparison of clock genes (*BMAL1*, *PER2*, *NR1D1* and *CRY1*) expression with stimulation of TGF β 1 (10ng/ml) or its solvent. Data shown as comparison to the non-TGF β 1 stimulation (mean \pm SEM, n = 3, t-test * p < 0.05, ** p < 0.01, *** p < 0.001).

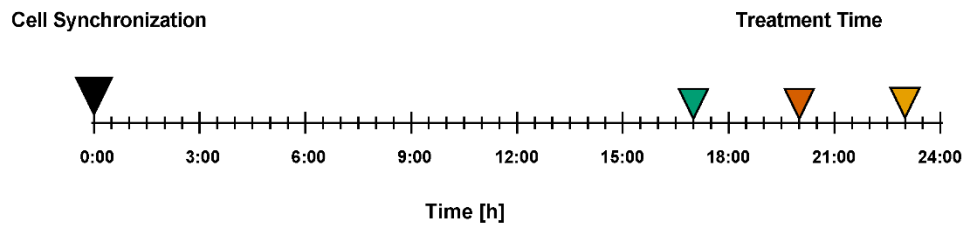
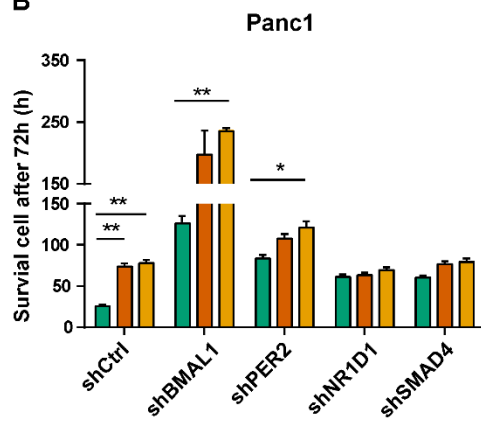
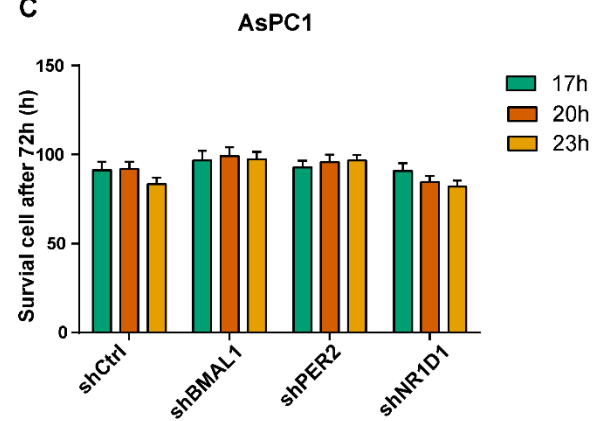
A**B****C**

Figure S9. Cytotoxicity assays were performed using NuLight Rapid Red Reagent for the IncuCyte S3 Live Cell System Analysis. Related to Figure 7. (A) At 17h, 20h, 23h after cell synchronization respectively, gemcitabine was added to the cell culture medium. (B - C) 72h after treatment, the number of living cells per well was quantified using the IncuCyte S3 Live-Cell Analysis System. Depicted are the comparisons to the 17h time point. (means \pm SEM, $n = 6$, two-way ANOVA, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

Table S1. Primer sequences.

Gene	Primer sequence	
	Forward	Reverse
SMAD3	F:5'-CCCCAGAGCAATATTCCAGA-3'	R:5'-GGCTCGCAGTAGGTAAGTGG-3'
SMAD4	F:5'-TGTGCCTGGTTTGATGGTAA-3'	R:5'-GCCATTTTCCCAATCTGCTA-3'
SMAD7	F:5'-TACCGTGCAGATCAGCTTTG-3'	R:5'-AGTTTGAAGTGTGGCCTGCT-3'
DEC1	F:5'-GTCTGTGAGTCACTCTTCAG-3'	R:5'-GAGTCTAGTTCTGTTTGAAGG-3'
DEC2	F:5'-CACCTTTGACGTCTTTGGAG-3'	R:5'-GAGAGTGGGAATAGATGCAC-3'
E-cadherin	F:5'-ATTGCAAATTCCTGCCATTC-3'	R:5'-CTCTTCTCCGCCTCCTTCTT-3'
N-cadherin	F:5'-CTCCTATGAGTGGAACAGGAACG-3'	R:5'-TTGGATCAATGTCATAATCAAGTGCTGTA-3'
Vimentin	F:5'-GGGAGAAATTGCAGGAGGAG-3'	R:5'-ATTCCACTTTGCGTTCAAGG-3'
CD133	F:5'-CCCCAGGAAATTTGAGGAAC-3'	R:5'-TCCAACAATCCATTCCCTGT-3'
SNAIL	F: 5'-GAGGCGGTGGCAGACTAG-3'	R: 5'-GACACATCGGTGAGACCAG-3'
SLUG	F: 5'-CATGCCTGTCATACCACAAC-3'	R: 5'-GGTGTGTCAGATGGAGGAGGG-3'

Transparent Methods

Cell culture

The PDA cell lines Panc1 and AsPC1 were used as an *in vitro* model system for our study. Panc1 (ATCC: CRL-1469) was derived from the primary tumor of a male patient with a doubling time of 52h (Lieber et al., 1975). AsPC1 (ATCC: CRL-1682) was established from ascites of a female patient with similar doubling time as Panc1 (Watanabe et al., 2012). Both cell lines were maintained in RPMI 1640 (Gibco, CA, USA) supplemented with 1% penicillin-streptomycin (Gibco) and 10% fetal bovine serum (Gibco). For lumicycle measurements and IncuCyte S3 analysis, RPMI 1640 (Gibco) was supplemented with 10 μ M HEPES (Gibco) to avoid pH variation. All cells were incubated at 37°C in a humidified atmosphere with 5% CO₂.

Lentivirus production of *Bmal1*: Luc, *Per2*: Luc reporters and shRNA-mediated knockdown

Lentiviral elements containing a *BMAL1*-promoter-driven luciferase (BLH) or a *PER2*-promoter-driven-Luciferase (PLB) were generated as previously described (Brown et al., 2005). For the knockdown of *BMAL1*, *PER2*, *NR1D1* and *SMAD4*, a TRC lentiviral shRNA glycerol set (Dharmacon Inc., Lafayette, CO, USA) specific for each gene was used consisting of 5 - 6 individual shRNAs. The construct with best knockdown efficiency was determined by RT-qPCR or Western-blot analysis and used for further experiments.

For lentiviral production, HEK293T (ATCC: CRL-11268) cells were seeded in a 75 cm² cell culture flask and co-transfected with 4.2 μ g packaging plasmid psPAX, 2.5 μ g envelope plasmid pMD2G and 5.8 μ g expression plasmid (*Bmal1*:luc-hygromycin, *PER2*:luc-Blasticidin, pLKO.1 empty vector or specific knockdown plasmids) using the CalPhos mammalian transfection kit (Clontech Fremont, CA, USA) according to the manufacturer's instruction. Virus particles were harvested and centrifuged at 4000xg for 15 min to remove cell debris. The supernatant was filtered (0.45 μ m filter, Sarstedt, Nümbrecht, DE) and used for lentiviral transduction.

Retrovirus production for *SMAD4* overexpression

pBabe-puro-Smad4-Flag was a gift from Sam Thiagalingam (Addgene plasmid # 37041; <http://n2t.net/addgene:37041>; RRID: Addgene_37041). To generate retrovirus, HEK293T (human, kidney, ATCC: CRL-11268) cells were seeded in 75 cm² culture flasks and co-transfected by 6 μ g pBabe-puro empty vector or pBabe-Smad4-Flag along with 0.3 μ g PMD2.G envelope and 2.7 μ g pUMVC packaging plasmids using FuGENE HD Transfection Reagent (Promega, WI, USA) according to manufacturer's introduction. The supernatant was replaced after 12 h, subsequently, retroviral particles were collected at 24h and 36h after incubation. The retroviral particles were centrifuged at 4100xg for 15 min to remove cell debris filtered (45 μ m filter, Sarstedt, Nümbrecht, DE), and stored at -80°C for further usage.

Lentivirus and retrovirus transduction

Cells were transduced with 1.5 ml virus filtrate including 8 µg/µl protamine sulphate (Sigma, MO, USA) and 4 µg/µl polybrene (Sigma) in 6-well plates. To enhance transduction efficiency, plates were centrifuged at 800xg for 90 minutes at 35°C. Subsequently, the supernatant was replaced after 6 - 8 hours. Stably-transduced cells were selected using the corresponding antibiotics (BMAL1: Luc hygromycin, PER2: Luc blasticidin; *shBMAL1*, *shPER2*, *shNR1D1*, *shSMAD4* and pLKO.1 empty vector puromycin; pBabe-puro empty vector and pBabe-Smad4-Flag puromycin). Untransduced cells were used as control. pLKO.1 empty vector and pBabe-puro empty vector are referred as *shCtrl* and *oeCtrl* respectively.

Cell synchronisation

For all experiments, cells were synchronized by medium change. For the cytotoxicity analysis, time point 0 h is defined as the time point of medium change. Untreated control cells were prepared in the same way, but treated with the corresponding vehicle control (H₂O for gemcitabine).

Bioluminescence measurement

For live-cell bioluminescence measurements, cells were seeded onto 35mm dishes (Thermo scientific MA, USA) and maintained in phenol red-free RPMI1640 (Gibco) containing 10% FBS, 1% penicillin-streptomycin, 10µM HEPES supplemented with 250 µM D-Luciferin (PJK, Kleinblittersdorf, DE). Prior to the measurement, cells were synchronized by medium change and washed with 1xPBS twice to avoid the influence of phenol red. Subsequently, the live-cell bioluminescence was recorded by a LumiCycle instrument (Actimetrics, Wilmette, IL, USA) for five consecutive days. For live-cell bioluminescence measurements of *SMAD4* knockdown or overexpression with TGFβ1 stimulation, cells were treated and maintained with 10ng/ml TGFβ1 (Stem Cell Technologies, Vancouver, CA) for five consecutive days. The concentration of TGFβ1 was retrieved from a previous publication (Ellenrieder et al., 2001). Chronostar software was used for data analysis (Sporl et al., 2011). The data of the first 12 hours was automatically excluded to avoid the influence of intrinsic noise of the device. Bioluminescence measurements were performed at least three times, as indicated.

RNA extraction and gene expression analysis by RT-qPCR

Total RNA was isolated with the plus RNeasy Mini kit (Qiagen, Venlo, NL) following the manufacturer's instructions. For a single time-point RT-qPCR, cell medium was replaced by fresh medium 3 hours before RNA extraction. Subsequently, the medium was discarded and cell pellets were washed twice with 1xPBS. To digest genomic DNA, homogenized cell lysates were passed through gDNA eliminator spin column with a 30s centrifugation at 17000xg. RNA was eluted in 20-30 µl Rnase-free water. The final RNA concentration was measured using a Nanodrop 1000 (Thermo Fisher Scientific) and stored at -80 °C for further usage. For RT-qPCR analysis, the extracted RNA was reverse transcribed into cDNA by using random hexamers

(Eurofins MWG Operon) and Reverse Transcriptase (Life technologies). RT-qPCR was performed using SsoAdvanced Universal SYBR Green Supermix (Bio-Rad Laboratories, Hercules, CA, USA) in 96-well plates. For the detection of human gene expression, primers were either custom designed (**Table. S1**) or a human Quantitect Primer assay (Qiagen) was used. Gene expression levels were normalised by Gapdh mRNA. The qPCR was performed in a CFX Connect Real-Time PCR Detection System (Biorad). Relative gene expression was calculated using the $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen, 2001). Mean and SEM were calculated including biological and technical replicates.

Proliferation assays

For the proliferation assay, 5000 cells/ well of each condition were seeded in a 96-well plate (Sarstedt). Cells were allowed to adhere. Subsequently, the medium was replaced with fresh medium containing TGF β 1 or its solvent. Plates were measured in the IncuCyte® S3 Live Cell System Analysis (Sartorius, Göttingen, Germany). Four images per well were recorded every 2 hours. The analysis was performed using the IncuCyte S3 Software (Sartorius).

For TGF β 1 stimulation, stimulated and control cells were treated with and maintained in 10ng/ml TGF β 1 (Stem Cell Technologies, Vancouver, CA) or its solvent (0.1% BSA, Sigma) for five consecutive days.

Apoptosis assays

Cells were seeded in a 96-well plate (Sarstedt) at a concentration of 5000 cells/ 100 μ L RPMI medium and incubated overnight at 37 °C with 5% CO₂. After incubation, cell media were replaced with fresh medium containing caspase 3/7 reagent (Sartorius, 1:2000) and TGF β 1 or its solvent. Cell apoptosis was measured using the IncuCyte® S3 Live Cell System Analysis (Sartorius). Cells were scanned every 2 hours with a 20x objective and by using the phase and green image channels.

Migration assays

60000 cells/ well of each condition were seeded in a 96-well Essen Image Lock TM microplate (Essen BioScience, Michigan, USA) and incubated overnight at 37 °C, 5% CO₂. In the next day, the WoundMaker™ (Essen BioScience) was used to create precise and reproducible wounds. Subsequently, the medium was replaced with a fresh medium containing TGF β 1 (10 ng/mL) or its solvent and the plate was placed in the IncuCyte® S3 Live Cell System Analysis (Essen BioScience). Image acquisition was performed by setting the “scan type” to Scratch Wound and Wide Mode, using the 10x objective. The plate was scanned every 2 hours. The analysis was performed in the IncuCyte S3 Software (Sartorius), the wound width for each well were exported and the migration speed were calculated using either the time of wound closed or the cut-off of 48 hours, which is shorter than the doubling-times of Panc1 and AsPC1 (48 - 52h). Biological triplicates and 8 technical replicates were carried out for each experiment.

Invasion assays

5000 cells/ well of each condition were mixed with 20µl 5mg/ml Basement Membrane Matrix (Trevigen Gaithersburg, MD, USA) seeded in the inner chamber of a 96-well IncuCyte Chemotaxis cell invasion clear view plates (Sartorius). Subsequently, the plate was centrifuged at 50x G to avoid the formation of bubbles. Basement membrane matrix was allowed to polymerize at 37°C for 45 minutes to form a reconstituted basement membrane. Cell invasion was measured using the IncuCyte® S3 Live Cell System Analysis. Cells were scanned every 2 h with a 20x objective and phase image channels. Biological triplicates and 8 technical replicates were carried out for each experiment.

Cytotoxicity assays

5000 cells/well were seeded in a 96-well plate (Sarstedt) containing 100 µL RPMI medium and incubated overnight at 37 °C with 5% CO₂. After incubation, the supernatant was replaced with fresh medium containing IncuCyte® Cytotox Reagents (Sartorius, (Red)) and appropriate concentrations of gemcitabine (Panc1, 9.5µM; AsPC1, 23.9µM (Awasthi et al., 2013)). For the time-dependent treatment assay, cells were synchronized by a medium change. At specific time points after synchronization (17h, 20h and 23h). Gemcitabine in a solution containing IncuCyte® Cytotox Reagents (Red) was added into each well with a micro-pipette. Cell cytotoxicity was measured using the IncuCyte® S3 Live Cell System Analysis (Sartorius). Cells were scanned every 2 hours with a 20x objective and using the phase and red image channels. Biological triplicates and 8 technical replicates were carried out for each experiment.

Cytotoxicity assays with live-cell nuclear labelling

Cells were labelled with IncuCyte® NuLight Rapid Red Reagent (Sartorius) 30 min before measurements. Cell survival after treatment was quantified using the IncuCyte® S3 Live Cell System Analysis (Sartorius). The plates were scanned every 2 hours with a 20x objective and using the phase and red image channels.

Treatment with Gemcitabine

Treatment concentrations for each PDA cell line were determined based on the experimentally determined IC₅₀ value in a previous study (Awasthi et al., 2013).

Western blot

Cells were synchronized by medium change, gently detached from the dish at 3h after synchronization, sedimented by low-speed centrifugation and resuspended in lysis buffer. Aliquots containing 20 mg of proteins from each cell lysate were subjected to SDS polyacrylamide gel electrophoresis and transferred to a Nitrocellulose Membranes (GE Healthcare Amersham™) using Trans-Blot Turbo Transfer System. Membranes were probed with the following primary antibodies: SMAD4 (1:5000; ab40759, Abcam, Cambridge, UK); GAPDH (1:20000; ab9485, Abcam); RAS (1:5000; ab52939, Abcam); p-ERK (1:2000, Cell

Signaling Technology, Frankfurt am Main, Germany). After incubation with corresponding secondary antibody (1:2000; ab205718, Abcam), signals were detected using the Amersham ECL Select Western Blotting Detection Reagent (GE Health care, Chicago, US), acquired by Image Quant LAS 4000 series (GE Health care). Data was analysed by image J v1.8 (developed by National Institutes of Health).

Cell cycle analysis

1×10^6 cells under the logarithmic growth phase were collected, washed with 1xPBS (Gibco) and fixed with ice cold 80% ethanol. Cells were maintained in medium containing 10ng/ml TGF β 1 stimulation (or the solvent) for 24 hours before the measurement. Subsequently, samples were washed with PBS and incubated in a 200ul of 1xPBS solution containing 0.5% Tween20 (Sigma), 1% BSA (Sigma), 2 N HCl/Triton x-100 (Sigma) and 10 mg/mL of Rnase (AppliChem, Cat. No. A2760) for 30 minutes at room temperature. For PI staining, supernatant was removed, the fixed cell pellets were resuspended and stained in 500 μ L of 1xPBS containing 50 μ M PI (Sigma) for 30 minutes at 37°C. Subsequently, supernatant containing PI solution was removed and the stained cells were resuspended in cold 500 μ L 1xPBS and read in FACS Cabilur (Becton Dickinson, NJ, USA). Cell cycle analysis was conducted by fitting a univariate cell cycle model using the Watson pragmatic algorithm as implemented in FlowJo v10.2 (FlowJo LLC).

Statistical Analysis

Experiments were carried out with at least three biological replicates per condition. Data are provided as mean \pm SEM. p -value < 0.05 was considered as statistically significant. The significance of differences between groups ($*p < 0.05$; $**p < 0.01$; $***p < 0.001$) was analysed by one-way or two-way ANOVA followed by Tukey's multiple comparisons test and the unpaired two-tailed t-test or multiple t-tests using the Prism software (version 6.0; GraphPad Prism).

Cosinor Analysis

To detect significant ($p < 0.05$) circadian rhythmic expression, the cosinor analysis was performed. The p -value was calculated using a QUICK CALCS (GraphPad, <https://www.graphpad.com/quickcalcs/pValue1/>). The oscillating transcripts were estimated by GrapdPad Prism. 6 software and fitting a non-linear equation as following:

$$Y(t) = B + A \cdot \left(\cos \frac{2\pi \cdot t}{P} + \varphi \right) + S \cdot t$$

t = Time, B = baseline, A = amplitude, S = slope, φ = acrophase, P = period.

Analysis of pancreatic adenocarcinoma data from a cohort of patients retrieved from the TCGA data base

Clinical information for pancreatic adenocarcinoma with overall patient survival was retrieved from The Cancer Genome Atlas (TCGA) (<https://portal.gdc.cancer.gov>). Mutational frequencies in the TCGA PDA patient population (184 pancreatic adenocarcinoma samples from PanCancer Atlas) were plotted using cBio Cancer Genomics Portal (<http://cbioportal.org>) (Cerami et al., 2012; Gao et al., 2013). OncoPrint functionality was used for graphical representation of mutation frequency for 10 candidate genes retrieved from our results. Survival curves were plotted using a Cox model that includes $\text{coxph}(\text{Surv}(\text{times}, \text{died}) \sim \text{gene} + \text{grade1} + \text{grade2} + \text{grade3} + \text{age})$ via OncoLnc (<http://www.oncolnc.org>), each tumour grade is represented as a separate term as 1 or 0 (Anaya, 2016). The survival data includes clinical data for patients with complete clinical information needed for the analysis and based on a follow up or days until death greater than zero. Previous studies revealed contribution of additional clinical parameters to the benefit provided by chemotherapy (i.e., age). Therefore, in our cox survival analysis we included patient age as an additional clinical parameter. The PDA cohort was divided into two equal groups (N1=87, N2=87 patients). based on the mean expression value of the candidate gene, the change in gene expression levels were categorized as high or low for equal number of patients in the cohort (N = 87 for high expression group and N = 87 for low expression group).

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Curriculum Vitae:

For reasons of data protection law, my curriculum vitae will not be published in the electronic version of my work.

List of Publications:

Research Publications:

- Circadian dysregulation of the TGF β /SMAD4 pathway modulates cell fate decisions, metastatic properties and drug response in a cellular model of pancreatic cancer.
Li Y, Basti A, Yalçın M, Relógio A.
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- Circadian regulation of physiology: relevance for space medicine.
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score: 3.2

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- Dysregulation of the circadian clock alters cellular processes and impacts on physiology and human health.

Li Y, Aretz Z, Basti A, Naderi J, El-Athman R, Relógio A

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