Hedgehog-EGFR cooperation response genes determine the oncogenic phenotype of basal cell carcinoma and tumour-initiating pancreatic cancer cells

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Keywords: cancer; epidermal growth factor receptor; Hedgehog signalling; signal transduction

DOI 10.1002/emmm.201100201

Received May 17, 2011
Revised December 09, 2011
Accepted December 12, 2011

Inhibition of Hedgehog (HH)/GLI signalling in cancer is a promising therapeutic approach. Interactions between HH/GLI and other oncogenic pathways affect the strength and tumourigenicity of HH/GLI. Cooperation of HH/GLI with epidermal growth factor receptor (EGFR) signalling promotes transformation and cancer cell proliferation in vitro. However, the in vivo relevance of HH-EGFR signal integration and the critical downstream mediators are largely undefined. In this report we show that genetic and pharmacologic inhibition of EGFR signalling reduces tumour growth in mouse models of HH/GLI driven basal cell carcinoma (BCC). We describe HH-EGFR cooperation response genes including SOX2, SOX9, JUN, CXCR4 and FGF19 that are synergistically activated by HH-EGFR signal integration and required for in vivo growth of BCC cells and tumour-initiating pancreatic cancer cells. The data validate EGFR signalling as drug target in HH/GLI driven cancers and shed light on the molecular processes controlled by HH-EGFR signal cooperation, providing new therapeutic strategies based on combined targeting of HH-EGFR signalling and selected downstream target genes.

INTRODUCTION

Malignant transformation is a multistep process that involves cooperation (i.e. synergistic interaction) of oncogenic signals to determine the malignant state of a cell (Hanahan & Weinberg, 2000). A detailed understanding of these interactions and the downstream processes induced by oncogene cooperation is important for the identification of novel drug targets and the development of rational-based combination therapies.

The Hedgehog (HH)/GLI signalling pathway has been implicated in a variety of human malignancies such as basal cell carcinoma (BCC), melanoma, medulloblastoma, glioblastoma, cancers of the prostate, lung, pancreas, breast as well as certain haematopoietic malignancies (reviewed in, Ng & Curran, 2011; Teglund & Toftgard, 2010). First clinical studies using selective HH/GLI pathway inhibitors have demonstrated a
remarkable therapeutic efficacy in advanced BCC and medulloblastoma, suggesting that targeted HH/GLI inhibition may hold promise also in other malignant diseases (Rudin et al, 2009; Skvara et al, 2011; Von Hoff et al, 2009). Furthermore, distinct tumour-initiating and metastatic cancer cells are sensitive to HH/GLI pathway inhibition, raising the hope that interfering with HH/GLI signalling may also improve relapse rates and metastasis (Clement et al, 2007; Dierks et al, 2008; Mueller et al, 2009; Peacock et al, 2007; Varnat et al, 2009, 2010; Zhao et al, 2009).

Activation of HH/GLI signalling is initiated by binding of HH proteins to the trans-membrane protein patched (PTCH), which in the absence of ligand represses the pathway by preventing the activation of the essential pathway effector smoothened (SMO). Binding of HH to PTCH allows activation of SMO, leading to the formation of activator forms of the GLI zinc finger transcription factors GLI2 and GLI3. Direct transcriptional activation of GLI1 by GLI2/3 enhances the level of GLI activators (Jiang & Hui, 2008; Rohatgi & Scott, 2007) and high-level expression of GLI1 is considered a reliable indicator of HH pathway activity. GLI1 and GLI2 act as main mediators of HH signalling in cancer by controlling the expression of target genes involved in proliferation, metastasis, survival and stemness (reviewed in, Kasper et al, 2006a; Ruiz i Altaba et al, 2007; Stecca & Ruiz, 2010).

Current therapeutic strategies are targeting the essential HH effector SMO. Despite first promising results in BCC and medulloblastoma (Rudin et al, 2009; Skvara et al, 2011; Von Hoff et al, 2009), limited therapeutic efficacy and drug resistance pose major challenges for targeting HH/GLI signalling by SMO-inhibition (Buonamici et al, 2010; Rudin et al, 2009; Von Hoff et al, 2009; Yauch et al, 2009). In addition, SMO-independent stimulation of GLI activity via interactions with RAS-MEK/ERK, PI3K/AKT (Riobo et al, 2006a; Riobo et al, 2006b; Stecca et al, 2007) or growth factor pathways such as TGFβ (Dennler et al, 2009; Nolan-Stevaux et al, 2009) and epidermal growth factor receptor (EGFR) signalling (Kasper et al, 2006a; Palma et al, 2005; Palma & Ruiz i Altaba, 2004; Schnidar et al, 2009) may bypass or attenuate the therapeutic efficacy of SMO antagonists in malignant diseases such as melanoma or pancreatic cancer.

In previous studies, our own group has analysed at a molecular level the cooperative interaction of the HH/GLI and EGFR pathway, which results in synergistic regulation of selected HH/GLI target genes and oncogenic transformation in vitro (Schnidar et al, 2009). Integration of EGFR and HH/GLI signalling involves activation of RAS/MEK/ERK and JUN/AP1 signalling in response to EGFR activation (Kasper et al, 2006b; Schnidar et al, 2009). In vivo evidence for the therapeutic relevance of HH/GLI and EGFR signal cooperation in HH-associated cancers is lacking and key mediators acting downstream of HH/GLI and EGFR signal cooperation are still unknown.

Here, we demonstrate an essential in vivo requirement of EGFR in HH/GLI-driven BCC and identify a set of HH/GLI-EGFR cooperation response genes critical for the determination of the oncogenic phenotype of BCC and tumour-initiating pancreatic cancer cells. The data shed light on the molecular mechanisms underlying in vivo tumour growth in response to HH-EGFR signal cooperation.

RESULTS

In vivo requirement of EGFR in Hh/Gli-driven skin cancer

Having shown that HH/GLI and EGFR cooperate in oncogenic transformation in vitro, we aimed to evaluate the in vivo role of EGFR in Hh/Gli driven cancers. To do so, we first tested genetically the requirement of EGFR in a mouse model of BCC. Using tamoxifen-regulated Cre/loxP technology to accomplish skin-specific expression of an oncogenic Smo variant (SmoM2) (Xie et al, 1998; Supporting Information Fig S1), we addressed whether concomitant epidermal deletion of EGFR affects SmoM2-driven BCC development. Activation of SmoM2 in K5creER;SmoM2;EGFRfl/fl mice resulted in focal epidermal hyperplasia and numerous BCC-like lesions that were most prominent on the ears (Fig 1A (right), B and B'). Of note, epidermal-specific deletion of EGFR in K5creER;SmoM2;EGFRfl/fl mice reduced both the number and size of tumours (Fig 1A, C and C'). Similarly, EGFR deletion reduced basaloid hyperplasia and basaloid hamartoma-like lesions in the dorsal skin of transgenic mice (Supporting Information Fig S3). Together, these data suggest a functional requirement of EGFR for tumour initiation and growth in SmoM2-driven skin cancer.

We next addressed whether systemic administration of afatinib (BIBW2992), a highly efficient irreversible EGFR/erbB family inhibitor (Li et al, 2008), is able to affect BCC development in vivo. Therefore, we established an allograft model that allows in vivo tumour growth of Pcth−/− mouse BCC cells (ASZ001) (Aszterbaum et al, 1999; So et al, 2006). Mice grafted with ASZ001 BCC cells were allowed to grow palpable tumours before the start of treatment with afatinib or solvent. Notably, afatinib at a dose of 15 mg/kg/day efficiently arrested tumour growth, while control treated mice (solvent only) showed a rapid increase in tumour volume (Fig 2A). To confirm the cell-autonomous requirement of EGFR in BCC cells, we performed knockdown of EGFR expression in Pcth−/− BCC cells. shRNA against EGFR (see Fig 2C) significantly reduced tumour growth (Fig 2B), confirming the cell-autonomous in vivo requirement of EGFR in BCC tumour cells.

HH/GLI-EGFR cooperation response genes as mediators of synergistic signal integration

Oncogenic signal cooperation has been shown to synergistically regulate so called cooperation response gene (CGR) sets enriched for determinants of the malignant phenotype (McMurray et al, 2008). We therefore set out to identify
HH-EGFR cooperation response genes that mediate HH/GLI and EGFR cooperation in tumourigenesis.

Given the potent mitogenic activity of combined HH/GLI and EGFR, e.g. in neural stem cells (Palma et al., 2005; Palma & Ruiz i Altaba, 2004), we first tested whether HH-EGFR cooperation promotes oncogenic transformation by cooperative induction of cell cycle regulators. As HH-EGFR signalling converges at the promoters of selected direct GLI target genes (Kasper et al., 2006b), we first screened for cell cycle regulators directly controlled by GLI and then tested whether these factors can be activated synergistically by GLI/EGFR (Supporting Information Tables S1 and S2). We identified CCND1, CDT1, FOXM1, KNTC1 and TOPBP1 as direct GLI targets (Supporting Information Fig S4A and B). However, none of these target genes was

Figure 1. Epidermal-specific deletion of EGFR inhibits SmoM2-driven growth of BCC-like lesions.

A. Genetic mouse BCC model testing EGFR function. To induce SmoM2 expression and delete EGFR, transgenic mice were injected with tamoxifen (TAM) 28 days after birth (P28) and analysed three months later at post-natal day P120. Left: ears of wild-type (WT), K5creER;SmoM2;EGFR+/+ and K5creER;SmoM2;EGFRfl/fl mice injected with tamoxifen (+TAM). In K5creER;SmoM2;EGFRfl/fl, but not in EGFR-deficient mice, pigmented BCC-like lesions are readily visible on ears.

B-B'. Phenotype of SmoM2 BCC mice. Histological analysis of ears from TAM injected K5creER;SmoM2;EGFR+/+ mice. Basaloid BCC-like lesions with pronounced downgrowths are clearly visible.

C-C'. Phenotype of BCC mice lacking EGFR. Histology of ears from TAM injected K5creER;SmoM2;EGFRfl/fl mice. Arrowheads point at small basaloid hyperproliferations.

D. Quantification of BCC lesions. Tumour multiplicity represented as mean number of lesions in TAM treated K5creER;SmoM2;EGFR+/+ (n = 10) and K5creER;SmoM2;EGFRfl/fl mice (n = 10). Error bars represent SEM.

E. Quantification of BCC tumour size. To quantify the effect of epidermal EGFR deletion on tumour size, lesions were categorized into small (<1000 μm²), medium (1000–2999 μm²) and large sized tumours (3000–15,000 μm²) (for details see Material and Methods) and plotted as percentage fraction of all tumours analysed per genotype (nWT = 602, nEGFRfl/fl = 255).
synergistically induced by combined GLI/EGFR activation (Supporting Information Fig S4C). In addition, deletion of EGFR did not promote apoptosis of SmoM2-expressing keratinocytes (Supporting Information Fig S4D), suggesting that enhanced proliferation and survival are not the main reason for the tumour promoting effect of HH-EGFR cooperation.

To shed light on the molecular processes controlled by HH-EGFR cooperation, we screened for downstream mediators of signal cooperation by genome-wide expression profiling of human HaCaT keratinocytes with either single activation of GLI1, EGFR or a combination of both signals. Synergistically induced GLI1-EGFR cooperation response genes were selected based on their synergy score (see Materials and Methods) and filtered for (i) early synergistic activation by HH/GLI-EGFR (i.e. within 4–18 h post stimulation), (ii) a documented role in the regulation of tumour growth, cancer stem cell activation and/or metastasis and (iii) the presence of putative GLI binding sites in their cis-regulatory region. This approach identified JUN, TGFA, FGF19 (criterion: tumour growth), SOX9, SOX2 (criterion: stemness), and SPP1/osteopontin and CXCR4 (criterion: metastasis) as putative candidate mediators of HH-EGFR signal cooperation. qPCR validation of chip data confirmed that GLI1 and EGFR stimulation (by EGF treatment (10 ng/ml)) synergistically activated transcription of JUN, FGF19 and CXCR4 already after 4.5 h. Activation of SOX9 and TGFA at the 4.5-h time point is mainly induced by EGF but at later time points becomes dependent on combined GLI1 and EGFR activation. Combined GLI1-EGFR signalling also induced synergistic activation of SOX2 and SPP1 transcription at the 9 and 18-h time points (Fig 3A).

To address if these genes represent immediate early HH/GLI-EGFR response genes, we tested them for direct regulation by GLI. All response genes, including the previously identified GLI targets JUN and SPP1 (Laner-Plamberger et al, 2009; Yoon et al, 2002) (data not shown), contained at least two clustered GLI binding sites within 5 kb of their upstream cis-regulatory sequences (Fig. 3B). Luciferase reporter assays in combination with site-directed mutagenesis of predicted GLI binding sites confirmed direct regulation of FGF19, TGFA, CXCR4 and SOX9 by GLI1 and dominant active GLI2 (GLI2deltaN) (Fig. 3C and Fig S5 of Supporting Information). GLI1 and GLI2deltaN also induced the promoter activity of the stemness transcription factor SOX2 (Fig 3C, and Fig S5 of Supporting Information), in line with a previous study (Takanaga et al, 2009). In summary, the data suggest that FGF19, TGFA, CXCR4, SOX9, SOX2—and the known GLI targets JUN and SPP1—represent immediate-early targets of HH/GLI-EGFR cooperation.

Activation of cooperation response genes requires the specific combination of GLI and EGFR signalling

SMO-independent signal inputs such as RAS-MEK/ERK have been shown to modify the transcriptional activity of GLI proteins (Riobo et al, 2006a; Stecca et al, 2007). We have previously
Figure 3. Identification of HH/GLI-EGFR cooperation response genes (CRG).

A. CRG regulation by GLI1 and EGFR signalling. qPCR analysis of CRG mRNA expression in response to GLI1 expression, EGFR signalling (EGF) or a combination of both stimuli (GLI1/EGF) after 4.5, 9 and 18 h of single or combined activation (three biological replicates measured in duplicate, values are fold change compared to untreated controls).

B. Location of GLI binding sites in CRG promoters. Genomic locus of CRG with in silico predicted GLI binding site clusters located in their 5’ upstream regulatory regions. Numbers indicate the position of binding sites relative to the transcriptional start site (TSS).

C. Direct transcriptional regulation of CRG by GLI. Luciferase reporter assays showing activation of CRG promoters in response to GLI1 expression. For FGF19, CXCR4, TGFA and SOX9 selected GLI binding sites were mutated (FGF19mut, CXCR4mut, TGFAmut, SOX9mut). The mutated GLI binding sites are indicated by asterisks in B. Error bars represent SEM. *p < 0.05, **p < 0.01.
shown that EGFR-dependent activation of RAS-MEK/ERK and JUN/AP1 activation is critical for mediating HH/GLI-EGFR signal cooperation (Schnidar et al., 2009). Since activation of RAS-MEK/ERK is a common event in response to receptor tyrosine kinase (RTK) activation, we addressed whether the activation of HH/GLI-EGFR response genes is specifically mediated by combined GLI and EGFR signalling, or whether other RTK pathways can also cooperate with GLI and induce a similar cooperation response gene profile. Therefore, we tested various RTK ligands including hepatocyte growth factor (HGF), vascular endothelial growth factor (VEGF), fibroblast growth factor 7 (FGF7) and basic FGF (bFGF) for their ability to induce RAS/RAF/MEK/ERK and JUN/AP1 activation in human HaCaT keratinocytes. As shown in Fig 4A, EGF, FGF7, HGF and to a lower extent also VEGF stimulated MEK/ERK, though only EGF was able to induce JUN activation (pJUN). Analysis of HH-EGFR cooperation response gene expression in GLI1 expressing keratinocytes simultaneously treated either with EGF, HGF, FGF7, or VEGF revealed that only the combination of GLI1 and EGF led to synergistic induction of JUN, SOX9, FGFR1, SPP1, TGFA and SOX2. Only SOX2 expression was also enhanced by GLI1 and FGFR7 treatment (Fig 4B). The canonical GLI targets PTCH and BCL2 (Kasper et al., 2006b) were not hyper-activated by any of the combinations, rather we observed an unexplained reduction of PTCH mRNA expression by combined GLI1 and VEGF, HGF or FGF7 treatment (Fig 4B). As expression of oncogenic RAS has been shown to promote the transcriptional and oncogenic activity of GLI (Pasca di Magliano et al., 2006; Stecca et al., 2007), we studied the effect of combined GLI1/RAS activation on the expression of HH-EGFR response genes. As shown in Fig 4C, co-expression of GLI1 and oncogenic KRAS<sup>G12V</sup> (KRAS<sup>+</sup>) did not lead to increased expression of HH-EGFR cooperation response genes. Rather, KRAS<sup>+</sup> attenuated the expression of JUN, FGFR1, CXXCR4, TGFA and SPP1 in the presence of GLI1. By contrast and consistent with previous reports showing enhancement of GLI activity by oncogenic RAS (Stecca et al., 2007), expression of the EGFR-independent GLI targets PTCCH and HHIP (Kasper et al., 2006b) (data not shown) was significantly increased by GLI1/KRAS<sup>+</sup>. Thus, the regulation of HH-EGFR cooperation response genes requires the specific combination of HH/GLI and EGFR activation. Whether MEK/ERK-dependent activation of JUN/AP1 is the critical determinant for cooperation of HH/GLI and RTK pathways such as EGFR signalling remains to be addressed.

**HH-EGFR cooperation response genes mediate synergistic HH/GLI-EGFR signal integration in cancer**

Having demonstrated a critical function of EGFR in HH/GLI-driven BCC, we next focused on the possible role of selected HH-EGFR cooperation response genes in mediating the oncogenic effect of HH-EGFR cooperation. Therefore, we first analysed the expression of cooperation response genes (i.e. Sox2, Sox9, Spp1, Jun, Tgfα and Cxxcr4; note that closely related Fgf19 homologues do not exist in mouse) in BCC-like tumours of mice with epidermis-specific expression of a dominant active form of GLI2 (K5cre<sup>ES</sup>;Cleg2, Grachtchouk et al., 2011; Pasca di Magliano et al., 2006) as well as in allograft tumours established from Ptch<sup>+/-</sup> mouse BCC (ASZ001). We found elevated mRNA levels of the HH-EGFR targets Sox2, Sox9, Spp1, Jun, Tgfα and Cxxcr4 in GLI2-induced BCC-like tumours compared to normal skin of control mice (Fig 5A). Likewise, allograft tumours established from grafted Ptch<sup>+/-</sup> BCC cells expressed elevated mRNA levels of Spp1, Tgfα, Sox9, Jun, Sox2, Cxxcr4 and the known HH-EGFR target gene Il1r2 (Kasper et al., 2006b), when compared to levels in Ptch<sup>+/-</sup> BCC cells cultured in vitro before grafting (Fig 5B). By contrast, levels of Gli1 and the EGF-independent GLI target Bcl2 (Kasper et al., 2006b) did not differ between allografts and in vitro cultured BCC cells. These data suggest activation of EGFR signalling during in vivo tumour growth of ASZ001 BCC cells. Indeed, only allograft tumours from Ptch<sup>+/-</sup> BCC cells showed high levels of activated EGFR (pEGFR), while in vitro cultured BCC cells did not (Fig 5C). Allograft tumours established from Ptch<sup>+/-</sup> BCC cells also showed activation of Mek/Erk and Jun, similar to Ptch<sup>+/-</sup> BCC cells treated with EGF in vitro (Supporting Information Fig S6). To show in vivo regulation of cooperation response genes by HH-EGFR signalling, we analysed the expression of Jun, Sox2, Sox9, Tgfα, Cxxcr4 and Spp1 in epidermal cells of tamoxifen-treated K5cre<sup>ES</sup>;SmoM2;EGFR<sup>+/+</sup> and K5cre<sup>ES</sup>;SmoM2;EGFR<sup>+/+</sup> (I<sup>TAM</sup>) mice (n = 3 for each genotype). As shown in Fig 5D, SmoM2 expression led to enhanced levels of Jun, Sox9, Sox2, Tgfα, Cxxcr4 and Spp1 mRNA in K5cre<sup>ES</sup>;SmoM2;EGFR<sup>+/+</sup> (I<sup>TAM</sup>) mice. Deletion of Egfr resulted in decreased levels of HH-EGFR response genes (K5cre<sup>ES</sup>;SmoM2;EGFR<sup>+/+</sup> (I<sup>TAM</sup>)). Together with the finding that HH-EGFR response genes are expressed in mouse BCC-like tumours and human BCC (Supporting Information Fig S7), these results suggest that combined HH/GLI and EGFR signalling control the activation of cooperation response genes in BCC.

To address the role of HH-EGFR cooperation response genes in BCC, we analysed the effect of RNAi-mediated inhibition of Jun, Sox2 and Cxxcr4 on tumour growth of Ptch<sup>−/−</sup> BCC cells. Fig 5E shows that individual inhibition of Jun, Sox2 or Cxxcr4 in BCC cells significantly reduced tumour take of nude mice, suggesting that Jun, Sox2 and Cxxcr4 constitute critical downstream mediators of oncogenic HH-EGFR signalling important for in vivo tumour growth of BCC cells.

**HH/GLI-EGFR cooperation response genes define the phenotype of tumour-initiating pancreatic cancer cells**

Given the substantial overlap of HH/GLI and EGFR signalling in many human cancers we set out to address whether HH-EGFR cooperation and the respective cooperation response gene signature are also deployed in cancers other than BCC. Here, we studied the role of HH-EGFR cooperation in pancreatic adenocarcinoma cells, which represent one of the most aggressive and still incurable malignancies with a documented role of HH/GLI and EGFR signalling (Li et al., 2007; Nolan-Stevaux et al., 2009; Pasca di Magliano et al., 2006; Yauch et al., 2008). Given the critical role of HH/GLI in cancer stem cells (Stevaux et al., 2009; Pasca di Magliano et al., 2006; Yauch et al., 2009), we focused on the role of HH-EGFR cooperation in tumour-initiating pancreatic cancer cells. For this purpose we developed...
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Figure 4. Activation of cooperation response genes requires the specific combination of HH/GLI and EGFR signalling.

A. Analysis of RAS/MEK/ERK signalling and JUN activation in human HaCaT keratinocytes in response to various receptor tyrosine kinase (RTK) ligands. Note that although EGF (10 ng/ml), FGF7 (50 ng/ml), HGF (50 ng/ml) and to a lower extent also VEGF (50 ng/ml) induce ERK1/2 activation (pERK1/2), only EGF treatment is able to stimulate JUN activation (phosphorylated JUN, pJUN).

B. CRG regulation by RTK pathways. qPCR analysis of HH/GLI-EGFR cooperation response gene expression in response to either GLI1 activation, treatment with RTK ligands EGF, VEGF, HGF and FGF7, or a combination of GLI1 and the RTK ligands (see A). PTCH and BCL2 served as reference for direct GLI target genes whose expression is independent of parallel EGFR signalling (Kasper et al, 2006b). As bFGF treatment did not induce activation of MEK/ERK in HaCaT cells (see A), we did not analyse the combination of GLI1/bFGF.

C. CRG and canonical GLI target regulation by GLI1-RAS signalling. Expression of JUN, SOX9, FGF19, CXCR4, TGFA, SPP1 and SOX2 (left), and PTCH and HHIP (right) in response to combined GLI1 and oncogenic KRAS (KRAS\(^{+}\)). GLI1 transgene levels are unaffected by KRAS\(^{+}\) expression. Error bars represent SEM. \(p < 0.05\), \(**p < 0.01\), \(***p < 0.001\); ns: not significant (\(p > 0.05\)).
Figure 5. HH-EGFR cooperation response genes are expressed in mouse BCC models and required for in vivo BCC growth.

A. CRG expression in GLI-induced skin tumours. qPCR analysis of gene expression in tumours of K5cre;Cleg2 mice (BCC) compared to normal skin (NS). Tumours express high levels of the human GLI2 transgene as well as its targets Gli1 and Ptc1 (green bars). Likewise, Sox2, Sox9, Spp1, Jun, Tgfa and Cxcr4 mRNA levels are significantly elevated in tumours compared to normal skin (blue bars). EGFR expression itself is not significantly changed between tumour and normal skin samples.

B. CRG expression in BCC allograft tumours. Activation of the HH-EGFR targets Sox2, Sox9, Spp1, Jun, Tgfa, Cxcr4 and Il1r2 during in vivo tumour growth of mouse BCC cells. Ptch\(^{−/−}\) ASZ001 BCC cells were grafted onto nude mice and tumours harvested after 4 weeks (ASZ allograft). Values represent the ratio of mRNA levels in ASZ allograft samples to those in ASZ cells grown in vitro before grafting. Note that data in A. and B. are plotted on a log10 scale.

C. EGFR activation in BCC allograft tumours. Western blot analysis showing activation of EGFR (pEGFR) in ASZ allografts compared to ASZ cells grown in vitro before grafting.

D. EGFR-dependent CRG expression in mouse BCC. qPCR analysis of SmoM2-induced activation of Jun, Sox9, Sox2, Tgfa, Cxcr4 and Spp1 in primary mouse keratinocytes isolated from the skin of transgenic mice with the indicated genotype.

E. Role of CRG in BCC growth. RNAi knockdown of Jun (shJun), Sox2 (shSox2) and Cxcr4 (shCxcr4) reduces in vivo tumour growth of ASZ001 BCC cells in nude mice (n = 6). For RNAi knockdown efficiencies see Supporting Information Fig S10. Cont: grafted ASZ001 BCC cells transduced with non-target control shRNA. Error bars represent SEM. *p < 0.05, **p < 0.01; ***p < 0.001.
a modified 3D tumoursphere assay that selects for rare yet highly clonogenic, tumour-initiating pancreatic cancer cells that form large spheres under non-adherent conditions. We hitherto refer to these spheres as macrospheres (Fig 6A, B, for more details see Supporting Information, Materials and Methods and Fig S8 of Supporting Information). qPCR analysis of single, tumour-initiating macrospheres isolated from 3D cultures of human pancreatic cancer cells (L3.6sl, Panc-1 and L3.6pl) revealed high-level expression of stem cell genes such as OCT4, Nanog and Prominin-1/CD133 (Fig 6C). When compared to corresponding pancreatic cancer cells grown under standard 2D culture conditions, tumour-initiating macrospheres also

Figure 6. High-level expression of HH-EGFR CRG in tumour-initiating pancreatic cancer cells.

A. Sphere growth of rare pancreatic cancer cells. If grown in 3D culture, human pancreatic cancer cells (here: L3.6sl) form macrospheres (MS) at low frequency (0.8–1.2%). If single macrospheres are isolated from 3D cultures (arrows in left image) and grown for serial passages in 2D, the cells will again form macrospheres at a constant low frequency if re-seeded in 3D cultures (right image, also see Fig S8 and Supporting Information).

B. Tumour-initiation by sphere-forming pancreatic cancer cells. Limiting dilution xenograft experiments showing that as few as 100 pancreatic cancer cells (here L3.6sl) derived from single isolated macrospheres are sufficient to initiate tumour growth in vivo (n = 4/4). By contrast, at least 10⁴ pancreatic cancer cells grown in 2D culture need to be grafted to establish tumours in vivo (n = 4 for each dilution experiment), showing that macrospheres isolated from 3D cultures of pancreatic cancer cells are highly enriched for tumour-initiating cells.

C. CRG expression in tumour-initiating pancreatic cancer cells. qPCR analysis (n = 4) showing elevated mRNA levels of stemness genes (CD133, Nanog, OCT4, red bars), HH pathway genes (SHH, DHH, IHH, GLI1) (green bars) and HH-EGFR cooperation response genes (JUN, SOX9, FGF19, TGFA, SPP1, CXCR4, blue bars) in tumour-initiating macrosphere cells compared to the corresponding cancer cells grown in 2D cultures. Graphs show results for three human pancreatic cancer cells lines (L3.6sl, Panc-1 and L3.6pl).

D. EGFR signalling in pancreatic cancer cells. Western blot analysis of pancreatic cancer cells (L3.6sl, Panc-1 and L3.6pl) showing activation of EGFR/ERK/JUN signalling in response to EGF treatment. Pharmacological inhibition of EGFR by Erlotinib (Erlo) prevented activation of the EGFR/MEK/JUN cascade.

E. Regulation of CRG expression by GLI1-EGFR signalling. Induction of HH-EGFR cooperation response genes (JUN, SOX9, FGF19, CXCR4, TGFA, SPP1) by combined GLI1/EGFR activation in L3.6sl pancreatic cancer cells. Unlike HH-EGFR response genes, transcriptional activation of the canonical GLI target PTCH is independent of EGF treatment. Error bars represent SEM. *p < 0.05, **p < 0.01, ns: not significant (p > 0.05).
expressed elevated mRNA levels of HH/GLI signalling components (GLI1, SHH, DHH and IHH) and notably, increased levels of HH-EGFR cooperation response genes (JUN, SOX9, FGF19, TGFA, SPP1 and CXCR4; Fig 6C). Furthermore and similar to our data of human keratinocytes and murine BCC cells, activation of EGFR led to activation of MEK/ERK/JUN signalling in pancreatic cancer cells (Fig 6D). Importantly, combined activation of GLI1 and EGFR signalling resulted in enhanced activation of the HH-EGFR cooperation response genes JUN, SOX9, FGF19, CXCR4 and SPP1. TGFA was also enhanced by GLI1/EGF but its increase did not reach statistical significance (Fig 6E). In agreement with data from keratinocytes and BCC cells, PTCH expression was induced by GLI1 but unaffected by concomitant EGFR activation (Fig 6E). Taken together, these findings demonstrate increased expression of HH-EGFR cooperation response genes in tumour-initiating pancreatic cancer cells and suggest a common molecular mechanism HH-EGFR cooperation response gene regulation in BCC and pancreatic cancer cells.

To address a putative functional role of HH/GLI-EGFR cooperation in the tumour-initiating subpopulation of pancreatic cancer cells, we monitored the effect of single and combined targeted inhibition of HH/GLI and EGFR signalling on the growth of tumour-initiating macrospheres. Single perturbation of GLI1, JUN or EGFR function by RNAi or pharmacological inhibitor treatment resulted in a moderate reduction of tumour-initiating spheres (Fig 7A, B). By contrast, combined inhibition

Figure 7. Cooperative HH-EGFR signalling and cooperation response genes control the growth of tumour-initiating pancreatic cancer cells.
A. GLI1-dependent sphere growth of pancreatic cancer cells. RNAi mediated inhibition of GLI1 expression reduces macrosphere growth in 3D cultures of L3.6sl, Panc-1 and L3.6pl cells.
B. Combined inhibition of GLI and EGFR/JUN signalling. Panc-1 cells were treated with erlotinib (erlo) or GANT61 (GANT) at the concentrations indicated and/or stably transduced with lentiviral shRNA against EGFR (shEGFR), GLI1 (shGLI1) or JUN (shJUN). Note that the combination of shEGFR/GANT, shGLI1/erlo and shJUN/GANT nearly completely abolishes the formation of tumour-initiating macrospheres.
C. CRC function in tumour-initiating pancreatic cancer cells. RNAi-mediated inhibition of the GLI-EGFR targets CXCR4, FGF19, SOX9 and SOX2 in pancreatic cancer cells (data shown for L3.6sl cells) significantly reduces the growth of tumour-initiating macrosphere cells in 3D cultures.
D. Quantification of 3D cultures shown in C. For RNAi knockdown efficiencies see Supporting Information Fig S10. Data represent the mean values of 4 independent experiments. Error bars represent SEM. *p < 0.05, **p < 0.01, ***p < 0.001.
of GLI1/EGFR or GLI1/JUN strongly reduced the formation of tumour-initiating stem cells. Intriguingly, knockdown of GLI1 and EGFR/JUN sensitized the cells to lower concentrations of the EGFR inhibitor erlotinib and the GLI antagonist GANT61, respectively (Fig 7B). These data suggest that cooperation of EGFR/JUN signalling with GLI1 function is critical for the growth of tumour-initiating pancreatic cancer cells.

Next, we addressed the role of HH-EGFR cooperation response genes in tumour-initiating pancreatic cancer cells, by RNAi knockdown of CXCR4, FGF19, SOX2 and SOX9. As shown in Fig 7C and D, RNAi against each of the HH-EGFR response genes efficiently prevented macroscopically reduced tumour growth. As FGF signalling has previously been shown to activate Gli2 expression (Brewster et al, 2000), the effect of FGF19 inhibition may be due to a decrease in GLI levels in response to diminished FGF19/FGFR4 signalling (Xie et al, 1999). However, neither GLI2 nor GLI1 levels were significantly reduced by knockdown of FGF19 (Supporting Information Fig S9A). Like inhibition of FGF19, FGFR inhibitor treatment dramatically reduced the formation of tumour-initiating macroscopically reduced tumour growth of pancreatic cancer cells compared to control knockdown cells (Fig 8A-E). By contrast and in line with previous reports (Nolan-Stevaux et al, 2009; Yauch et al, 2008), RNAi against SMOH did not affect in vivo tumour growth (Fig 8F).

To analyse the in vivo relevance of these data, we performed xenograft assays using pancreatic cancer cells (L3.6sl) with RNAi knockdown of GLI1, JUN, SOX9, FGF19 or CXCR4. We found that inhibition of each target had a striking inhibitory effect on the in vivo tumour growth of pancreatic cancer cells compared to control knockdown cells (Fig 9A-E). By contrast and in line with previous reports (Nolan-Stevaux et al, 2009; Yauch et al, 2008), RNAi against SMOH did not affect in vivo tumour growth (Fig 9F).

The finding that each of the HH-EGFR cooperation response genes tested reduced in vivo growth of pancreatic cancer cells prompted us to address the possibility of positive regulatory interactions between HH-EGFR response genes. We therefore inhibited the expression of JUN, SOX9, FGF19 or CXCR4 and then measured the effect on the expression of the unperturbed HH-EGFR cooperation response genes including SPP1. Inhibition of SOX9 significantly reduced JUN, CXCR4 and SPP1 mRNA levels, while inhibition of JUN reduced CXCR4 and SPP1 levels. Intriguingly, shRNA against FGF19 strongly inhibits CXCR4 and SPP1 expression, while inhibition of CXCR4 had a dramatic reciprocal negative impact on FGF19 expression. By contrast, PTCH mRNA levels were not significantly affected by any of the perturbation experiments (Fig 9A).

DISCUSSION

Previous studies by our group and others have pointed to a role of HH-EGFR signal cross-talk in the growth of cancer cell lines, though the therapeutic relevance of these results remained unclear mainly because of the in vitro nature of the studies and the possible off-target effects of the inhibitors used (Mimeault et al, 2006; Schnidar et al, 2009). Using preclinical in vivo models of cancer development, we now provide genetic and pharmacological evidence for a critical function of EGFR signalling in HH/GLI-driven cancers such as BCC. Therefore, these results identify EGFR as a valid therapeutic target for HH-driven BCC, supporting the concept of combination treatments with SMO and EGFR inhibitors as efficient therapeutic options.

An intriguing finding of this study was that our systematic screen for downstream mediators of the synergistic transformation effect identified a set of HH-EGFR cooperation response genes (CRG) that is directly regulated by GLI, synergistically enhanced by EGFR signalling and enriched for critical determinants of the oncogenic phenotype of both BCC and tumour-initiating pancreatic cancer cells (i.e. JUN, SOX9, SOX2, FGF19 and CXCR4). The striking inhibitory effect of HH-EGFR CRG inhibition on in vivo tumour growth of BCC and tumour-initiating pancreatic cancer cells suggest that EGFR cooperates with HH/GLI to initiate and promote tumour growth by synergistic activation of HH-EGFR CRG. Intriguingly, this effect appears specific to the combination of EGFR/GLI activation, as HGF/MET, FGF7/FGFR, VEGF and oncogenic KRAS signalling failed to cooperate with GLI1 in HH-EGFR CRG regulation.

Notably, HH/GLI-EGFR cooperation synergistically induced the expression of SOX2 and SOX9, two transcription factors involved in the regulation of stem cell fate (Vidal et al, 2005; Yamanaka, 2007), as well as of CXCR4, which not only marks metastatic CD133+ pancreatic cancer stem cells (CSC) but also controls their metastatic behaviour (Hermann et al, 2007). It is therefore tempting to speculate that selected HH-EGFR response genes together with GLI1 and the GLI target and stemness gene Nanog (Po et al, 2010; Zhiden et al, 2010) play a critical role in the determination of stem-like characteristics of tumour-initiating cancer cells, consistent with the identification of stem cells as cellular origin of HH-induced cancers and the documented role of HH/GLI in cancer stem cells (Clement et al, 2007; Dierks et al, 2008; Grachtchouk et al, 2011; Kasper et al, 2011; Mueller et al, 2009; Peacock et al, 2007; Varnat et al, 2009; Wang et al, 2011; Wong & Reiter, 2011; Zhao et al, 2009).

In summary, our data support a model where cooperation of HH/GLI and EGFR signalling induces high-level expression of cooperation response genes including SOX9, JUN, FGF19, CXCR4 and SOX2, thereby promoting tumour initiation and tumour growth. Positive regulatory interactions between FGF19, CXCR4, JUN and SOX9 are likely to contribute to tumourigenesis by selectively amplifying the expression of HH-EGFR regulated genes and/or by maintaining high level expression of HH-EGFR response genes required for sustained tumour growth (Fig 9B). Finally, our study also underlines the power of analysing oncogenic pathway cooperation to identify gene sets with a critical role in tumour-initiation and cancer growth that may be exploited for novel therapeutic approaches. The identification of FGF19 and CXCR4 as druggable HH/GLI-EGFR target genes provides proof of concept for such an approach. Intriguingly, as some HH-EGFR cooperation response genes are linked within regulatory networks downstream of HH-EGFR cooperation, it will be important to evaluate the therapeutic
efficacy of selected combinations of HH/GLI, EGFR and HH-EGFR response gene inhibitors in BCC and pancreatic cancer.

**MATERIALS AND METHODS**

**Transgenic mice and xenografts**

SmoM2 (R26SmoM2) (Jeong et al, 2004; Mao et al, 2006), EGFR<sup>fl/fl</sup> (Natarajan et al, 2007), K5creER<sup>R26</sup> (K5creER<sup>R26</sup>) (Indra et al, 1999), K5cre (Ramirez et al, 2004) and Cleg2 (Pasca di Magliano et al, 2006) mice were maintained on a C57BL/6 background. Activation of SmoM2 expression and epidermal deletion of EGFR in K5cre<sup>R26</sup>SmoM2;EGFR<sup>+/+</sup> and K5cre<sup>R26</sup>SmoM2;EGFR<sup>++/++</sup> mice, respectively, was accomplished by i.p. injection of 1 mg tamoxifen (Sigma, USA) per day. Mice were sacrificed 120 days post birth and subsequently analysed for tumour development and gene expression.

For in vivo tumour growth studies, 1 × 10<sup>6</sup> murine BCC or human pancreatic cancer cells in 25% Matrigel (BD Laboratories) were injected subcutaneously into the lower flanks of Foxn1<sup>nuf/nuf</sup> nude mice (Charles River Laboratories, USA). For oral administration, afatinib (Boehringer Ingelheim) was dissolved in 0.5% natrosol (Aqualon)/

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Figure 8. Inhibition of HH/GLI-EGFR target genes in pancreatic cancer cells prevents in vivo tumourigenesis.

A-F. Effect of RNAi knockdown of GLI1, JUN, SOX9, FGF19, CXCR4 and SMOH on in vivo growth of pancreatic cancer cells. 1 × 10<sup>5</sup> pancreatic cancer cells (L3.6sl) either transduced lentivirally with non-target control shRNA (cont) or with shRNA specific for the respective target were grafted contralaterally onto the lower flank of nude mice (n = 8 for each group). Similar to RNAi-mediated GLI1 inhibition (A), shRNA against the HH/GLI-EGFR targets JUN (B), SOX9 (C), FGF19 (D) and CXCR4 (E) interfere with in vivo tumour growth. By contrast, RNAi against SMOH (F) does not significantly affect in vivo growth of pancreatic cancer cells. Error bars represent SEM. *p < 0.05, **p < 0.01, ***p < 0.001, ns: not significant (p > 0.05).
20 mg/ml 2-hydroxypropyl-beta-cyclodextrine (Sigma Aldrich, USA) at a final concentration of 2 mg/ml and administered orally at a concentration of 15 mg/kg/day.

Tumour volume was calculated according to the formula \[ \frac{4}{3} \pi \left( \frac{\text{length}}{2} \right) \times \left( \frac{\text{width}}{2} \right) \times \left( \frac{\text{height}}{2} \right) \].

All animal experiments and mouse husbandry were done in the animal facility at the University of Salzburg in accordance with institutional and federal guidelines.

RNA interference and lentiviral transduction

For lentiviral RNAi knockdown experiments, the following shRNA constructs (Sigma-Aldrich mission TRC library) were used: shEGFR (TRCN0000055220), shRNA GLI1 (TRCN0000020486), shRNA human and mouse SOX2 (TRCN0000010753), shRNA SOX9 (TRCN0000020386), shRNA FGF19 (TRCN0000040258), shRNA mouse Cxcr4 (TRCN0000028750), shRNA JUN (TRCN0000039590), shRNA mouse Jun (TRCN0000055207), control

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EMBO Mol Med 4, 218–233

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The paper explained

PROBLEM:
The Hedgehog pathway is currently very intensely studied in the field of oncology and molecular medicine. The therapeutic efficacy of several new Hedgehog antagonists developed by different biotech and pharmaceutical companies is currently evaluated in clinical trials. First results from these studies are promising, though limited response rates, insufficient efficacy and development of drug resistance underline the need for improved regimens. Combining Hedgehog antagonists with inhibitors targeting cooperative signals may prove an efficient therapeutic strategy. Detailed knowledge about such synergistic interactions driving cancer and rigorous evaluation of the therapeutic benefit in appropriate in vivo models is an important prerequisite for the development of novel rationale-based combination therapies simultaneously targeting such cooperative signals.

RESULTS:
In the present study, we show that genetic and pharmacologic inhibition of EGFR signalling—one of the most prominent targets in today’s oncology, reduces tumour development in clinically relevant mouse models of Hedgehog/GLI driven skin cancer. Furthermore, we present a gene set that is synergistically regulated by Hedgehog-EGFR signal cooperation and essential for in vivo growth of Hedgehog/GLI dependent basal cell carcinoma and tumour-initiating pancreatic cancer cells. Thus, the work identifies novel downstream mechanisms mediating the oncogenic effect of synergistic Hedgehog-EGFR signal interactions.

IMPACT:
Our results confirm EGFR signalling as valid drug target in Hedgehog dependent cancers and provide a rationale for combination therapies based on simultaneous targeting of Hedgehog, EGFR and cooperation response genes including CXCR4 or FGF19. As antagonists against most of these effectors are already available and validated in clinical settings, such a drug regimen can be rapidly transferred to clinical settings to evaluate its therapeutic benefit compared to current single treatment approaches.

scrambled shRNA (SHC002) and shRNA against human CXCR4 (clone 12272, Addgene; Orimo et al, 2005). The functionality of the shRNAs was validated by qPCR and/or Western blot analysis (Supporting Information Fig S10 and Fig 2C). Lentivirus production and transductions were done as described previously (Kasper et al, 2007). Transduced cells were selected for puromycin resistance prior to further analysis.

Cell culture and inhibitor treatments
Panc-1, L3.6sI and L3.6pl (Bruns et al, 1999) cells were grown in DMEM media (PAA) with 10% fetal bovine serum (FBS) (PAA), penicillin (62.5 μg/ml), and streptomycin (100 mg/ml), at 37 °C in 5% CO₂.

For 3-dimensional (3D) cultures, 1 × 10⁴ cells were seeded in 12-well plates in 0.4% agar on top of 0.5% bottom select agar (In vitrorgen) according to standard protocols of anchorage independent growth assays. Cultures were grown for 4 weeks at 37 °C in a humidified atmosphere containing 5% CO₂. Pancreatic cancer spheres grown in 3D cultures were isolated, purified by centrifugation and single cell suspensions generated by subsequent trypsin digest for further analysis (for details see Supporting Information). GANT61 (Merck), erlotinib (LC Laboratories) and afatinib (Boehringer-Ingelheim) were dissolved in DMSO. Spheres were documented on a stereomicroscope with Cell^D Image capture system and quantified using Colony Counter Software (Microtech Nition).

RNA Isolation, qPCR analysis and promoter studies
Total RNA was isolated using TRI-reagent (Molecular Research Center Inc.) followed by a LiCl purification step. Total RNA of sphere cultures and 2D cultured reference cells was isolated with the RNAqueous kit (Ambion Applied Biosystems) and cDNA synthesized with Superscript II reverse transcriptase (Invitrogen). qPCR was done on a Rotorgene 3000 (Qiagen) using iQ Sybr Green Supermix reagent (Bio-Rad). In silico prediction of putative GLI binding sites was done using the ScanAce algorithm (Roth et al, 1998). Fragments with high scoring binding sites were PCR amplified and cloned into the pGL4 luciferase reporter vector (Promega). Luciferase reporter assays were carried out as described previously (Kasper et al, 2006b; for details see Supporting Information). Site-directed mutagenesis of GLI binding sites was done using the QuickChange XL site-directed mutagenesis kit (Stratagene) according to manufacturer’s instructions. All constructs were confirmed by sequencing.

Chromatin immunoprecipitation was carried out with SimpleChIP Enzymatic ChiP kit (Cell Signaling Technology) according to the manufacturer’s instructions. Chromatin was isolated from HaCaT keratinocytes expressing GLI1 for 48h (Regl et al, 2002) and precipitated with anti-Gli1 antibody (sc-6152, Santa Cruz Biotechnology) as described previously (Laner-Plamberger et al, 2009). Primer sequences used for amplification of promoter fragments harbouring GLI binding sites are listed in Supporting Information Table S3.

Identification of cooperation response genes
Gene expression profiling was done on a bead array technology platform (Illumina Inc., USA). For each time point human HaCaT keratinocytes either expressing GLI1, treated with EGF, or stimulated with anti-Gli1 antibody (sc-6152, Santa Cruz Biotechnology) as described previously (Laner-Plamberger et al, 2009). Primer sequences used for amplification of promoter fragments harbouring GLI binding sites are listed in Supporting Information Table S3.
Scores < 0.9 were considered to represent targets synergistically activated in response to GLI/EGF stimulation. Synergistic regulation of HH-EGFR cooperation response genes was verified by qPCR analysis.

**Author contributions**

ME and SK analysed EGFR function and HH-EGFR response genes in basal cell carcinoma and pancreatic cancer cells. DM and AL characterised tumour-initiating cells, HD, HS, DM, KZ and H-CB identified direct GLI target genes. MS, FS, CH-K, ANE, MEV, CKB and AAD performed immunohistochemistry and provided material before publication and analysed data. HH, WN and CW contributed to HH-EGFR target gene identification. HL, CW and FA designed the experiments and analysed data. ME, SK and FA wrote the manuscript.

**Acknowledgements**

We are grateful to Dr. Alexandra Kaser-Eichberger for help with chromatin immunoprecipitations, Dr. Anna-Maria Frischauf for discussions and to Aydah Sabah and Claudia Vogelgesang for excellent technical support. Financial support for this work came from: the Austrian Science Fund FWF grant P20652 (to F.A.), the Austrian genome project Gen-AU (Medsys, project MoGlI (to F.A.), the German Ministry for Research (BMBF) (bilateral Medsys project MoGlI 0315394A), the Max Planck Society, the NGFN-Plus project project Mutanom (01GS08105 (to H.L.)), and the focus area program “Biosciences and Health” of the University of Salzburg (to F.A.). M.S. acknowledges funding by the Doctoral Program “Inflammation and Immunity” DK W1212, the EC program LSHC-CT-2006-037731 (Growth-stop) and the Austrian Federal Government’s GEN-AU program “Astromouse” (GZ 200.147/1-VI/1a/2006 and 820966). A.A.D. was supported by NIH grants CA087837 and CA118875.

Supporting Information is available at EMBO Molecular Medicine online.

The authors declare that they have no conflict of interest.

**References**


Riobo NA, Haines CM, Emerson CP Jr (2006a) Protein kinase C-delta and phosphoinositide 3-kinase and Akt are essential for Sonic Hedgehog signaling. Proc Natl Acad Sci USA 103: 4505-4510


Wong SY, Reiter JF (2011) Wounding mobilizes hair follicle stem cells to form tumors. Proc Natl Acad Sci USA 108: 4093-4098


