

Tyrosine Kinase Inhibitors and Everolimus Reduce IGF1R Expression in HPV16-positive and -negative Squamous Cell Carcinoma

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Abstract. *Background/Aim:* The effects of tyrosine kinase inhibitors (TKI) in head and neck squamous cell cancer (HNSCC) are not fully understood. We investigated the effects of selective TKIs erlotinib, gefitinib, nilotinib, and dasatinib and the mTOR-inhibitor everolimus on the expression of insulin-like growth factor 1 receptor (IGF1R) in HPV-positive and HPV-negative squamous cancer cell lines. *Materials and Methods:* HPV-negative UM50C-11A and UM50C-14C cells and HPV-positive CERV196 cells were treated with TKIs or everolimus. Protein concentration of IGF1R was measured using ELISA. *Results:* IGF1R expression was significantly reduced by all tested TKIs and everolimus in both HPV-negative cancer cell lines. In HPV-positive squamous cancer cells we observed significant protein inhibition. *Conclusion:* The crosstalk between epidermal growth factor receptors and IGF1R could be of central interest for the development of novel medical approaches for individualized therapy.

Head and neck squamous cell cancer (HNSCC), most frequently occurring in the oral cavity and the oropharynx, comprises malignant tumors that can affect the entire upper aerodigestive tract. Main risk factors for HNSCC include tobacco and alcohol consumption (1). The prevalence of HNSCC is increasing worldwide (2, 3), due to an infection with

high-risk subtypes of the human papilloma virus (HPV) (4, 5). The tumor-node-metastasis (TNM) staging for HNSCC published in 2017 has been updated due to related findings. Currently, p16^{INK4A} immunostaining is included as a surrogate parameter for an HPV infection of HNSCC (6). The types of HPV are classified into low-risk and high-risk, according to the probability of inducing cancer. Approximately 20% of HNSCC cases present with HPV infection (7). The high-risk type of infections requires more time to overcome, and the risk of the integration of viral DNA into the host genome is higher. The integration results in an overexpression of the viral oncogenes E6 and E7 with subsequent stimulation of cell proliferation resulting in genomic instability (8). High-risk type (16 and 18) of infections are found in nearly 90% of HPV-associated oropharyngeal tumors (9). Patients with HPV-positive oropharyngeal cancer are younger (aged 30-50 years) and are often diagnosed with early occurrence of lymphogenic neck metastases (10-12). However, HPV-positive HNSCC carries a more favorable prognosis than HPV-negative cancers – although recent studies have not shown promising results regarding the de-escalation of treatment (13-15). Current treatment options for patients with HSNCC include a combination of chemotherapy, radiation, and surgery. Moreover, new target therapy approaches with the application of monoclonal antibodies (e.g. cetuximab), checkpoint-inhibitors, or tyrosine kinase inhibitors (TKIs, e.g. imatinib, nilotinib, dasatinib, erlotinib, and gefitinib) are intensively investigated and are already integrated in experimental therapy options.

The modulation of key signaling pathways for the development of HNSCC is intensively investigated (16). Deregulated tyrosine kinases play an important role in tumor progression by modifying cell signaling cascades. Selective TKIs inhibit key signaling tyrosine kinases by competing for the adenosine triphosphate binding site (17). Up to date, TKIs are established in the therapy of various tumors (18). Nilotinib and dasatinib inhibit BCR-ABL and are used for the treatment

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of chronic myelogenous leukemia (CML) (19, 20). Other TKIs, such as gefitinib and erlotinib, inhibit the epidermal growth factor receptor (EGFR) and are used in the treatment of non-small cell lung cancer (21-23). The mammalian target of rapamycin (mTOR) inhibitor everolimus (24) is also used in the treatment of malignant tumors (25). Recent studies conducted by our group revealed positive effects of everolimus on HPV-positive squamous carcinoma cells (26). However, tumor-specific reactions induced by the modulation of several TKIs and mTOR are not yet fully understood.

The insulin-like growth factor-1 receptor (IGF1R) is a receptor tyrosine kinase that is expressed in several human tissues. After IGF1R activation by IGF1, the tyrosine kinase domains of IGF1R become active *via* transphosphorylation, initiating downstream signaling through the phosphoinositide-3-kinase/Akt/mTOR and Ras/mitogen-activated protein kinase/ERK kinase/extracellular-signal-regulated kinase pathways. The activation of the IGF1R pathway can stimulate differentiation, migration, proliferation, survival, and angiogenesis in a context-specific way. IGF1R is overexpressed and investigated as a therapeutic target in several human cancers (27-31). Increased levels of circulating insulin-like growth factor-1 (IGF-1) are associated with an increased risk of colorectal, breast, prostate, and lung cancer (32-35). Increased level of circulating IGF1 is associated with increased risk of second primary malignancy in HNSCC (36). High levels of IGF1R are associated with high tumor (T)-stage, shorter disease-specific survival, and decreased overall survival (30). Inhibition of IGF1R can slow tumor growth in several human xenograft models (28, 37, 38). Furthermore, IGF1R signaling is associated with increased resistance to various antitumor therapies (39). This includes targeted EGFR inhibition, and it has been suggested that IGF1R contributes to EGFR-TKI (gefitinib) resistance *via* a pro-survival mechanism in HNSCC cells (40).

Up to date, eight HNSCC tumor sample studies are available, and all samples exhibited significant expression of IGF1R and IGF1R phosphorylation. The findings suggest that IGF1R may be relevant *in vivo*, and, thus, combined EGFR/IGF1R inhibition could be beneficial for some patients as a targeted molecular therapy (40).

However, there is lack of evidence regarding the influence of TKIs and everolimus on the expression of IGF1R. Therefore, we investigated the effect of the TKIs erlotinib, gefitinib, dasatinib, and nilotinib and the mTOR-inhibitor everolimus on IGF1R in an *in vitro* study with one HPV-positive and two HPV-negative squamous cancer cell lines.

Materials and Methods

Experiment design. Two human HPV16-negative squamous cancer cell lines [University of Michigan Squamous Cell Carcinoma (UMSCC)] provided by T.E. Carey, Ph.D. (University of Michigan,

Ann Arbor, MI, USA) and one human HPV16-positive squamous cancer cell line (CERV196; Cell Lines Service GmbH, Eppelheim, Germany) were examined. The HPV16-negative cell lines were harvested from a skin metastasis of an oral cavity SCC of the floor of the mouth after surgery and radio-chemotherapy (UMSCC-14C) and from an untreated laryngeal SCC of the epiglottis (UMSCC-11A). The HPV16-positive cell line descended from a cervix SCC. The HPV-negative cells were cultured in Eagle's minimum essential medium (Gibco, Life Technologies, Carlsbad, CA, USA), containing 2 mM of L-glutamine and 10% fetal calf serum and antibiotics/antimycotics, according to the supplier's instructions. CERV196 cells were cultured in Eagle's minimum essential medium (Gibco, Life Technologies), supplemented with 2 mM of L-glutamine, 1.0 g/l sodium bicarbonate, 0.1 mM of non-essential amino acids, 1.0 g/l sodium pyruvate, and 10% fetal bovine serum (Gibco, Life Technologies). Incubation was performed under standardized conditions at 37°C, 5% CO₂, and 95% humidity. Cells were subcultured by adding a PBS solution supplemented with 0.05% trypsin and 0.02% ethylenediaminetetraacetic acid (EDTA, Sigma Aldrich; Merck KGaA, Darmstadt, Germany) at 37°C for 5 min.

Erlotinib, gefitinib, nilotinib, dasatinib, and everolimus were sponsored by Professor R.D. Hofheinz (Oncological Department, University Hospital Mannheim, Medical Faculty Mannheim, University of Heidelberg, Germany). All drugs were stored at room temperature and dissolved in dimethyl sulfoxide when needed. We added 20 µmol/l of each drug to the cultures, and the cells were incubated at 37°C for 24, 48, 72, and 96 h. Untreated cells served as negative controls under identical conditions.

Enzyme-linked immunosorbent assay for IGF1R and proliferation assay. Experiments were repeated at least three times (n=3). The alamarBlue (AbD Serotec, Raleigh, NC, USA) cell proliferation assay was used to assess the proliferation of HNSCC cells, following the manufacturer's protocol. Protein concentrations were measured using the sandwich enzyme-linked immunosorbent assay (ELISA) technique according to the manufacturer's instructions. DuoSet ELISA (DYC391, R&D Systems, Minneapolis, MN, USA) was used for IGF1R. MRX Microplate Reader (DYNEX Technologies, Chantilly, VA, USA) was used to measure optical density at a wavelength of 450 nm and wavelength correction of 540 nm. The detection range was 250-16000 pg/ml for IGF1R. The interassay coefficient of variation provided by the manufacturer was below 10%.

Statistical analysis. For statistical analysis, mean values were used. Mean values are presented ± standard deviation. SAS 9.3 software (SAS Institute, Inc., Cary, NC, USA) was used for the two coefficient variance test and Dunnett's test. A *p*-value of ≤0.05 was considered statistically significant. Professor C. Weiss (Head of the Department of Medical Statistics, Biomathematics and Information Processing, Medical Faculty Mannheim, University of Heidelberg, Germany) supported us in the statistical evaluation.

Results

IGF1R was detected in the three tested cell lines, with expression levels increasing over the culture time of untreated cells and after incubation with nilotinib. The

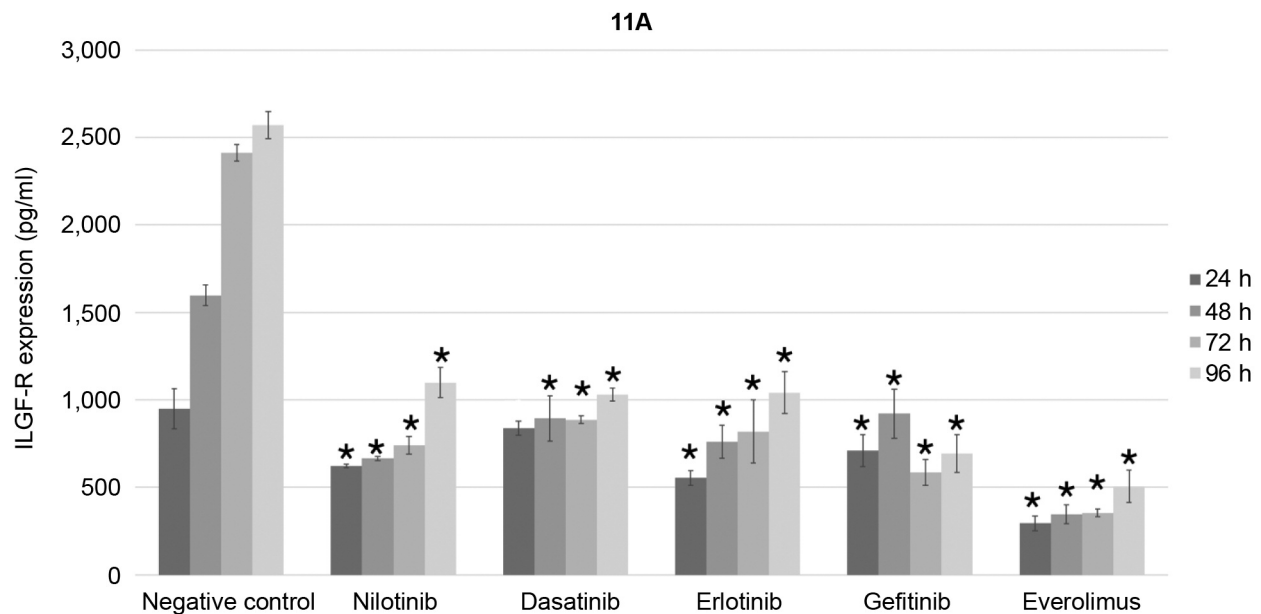


Figure 1. IGF1R expression in UMSSC-11A cells after incubation with nilotinib, dasatinib, erlotinib, gefitinib, or everolimus relative to the negative control. Data are mean values with standard deviations. Significance (p -value of ≤ 0.001) is marked with *.

highest IGF1R expression (3892 pg/ml) was measured in the untreated UMSSC-14C culture after 96 h of incubation. The addition of nilotinib, dasatinib, erlotinib, gefitinib, or everolimus led to a significant (all $p < 0.001$) decrease in IGF1R levels in both HPV-negative cell lines, except for dasatinib treatment after 24 h ($p = 0.2180$). The strongest effect was observed after incubation with everolimus in both HPV-negative cell lines. The expression patterns in the treated cells were similar in UMSSC-11A cells except for gefitinib treatment. The expression levels in treated cells were similar after incubation with any of the tested drugs in UMSSC-11A cells. The expression levels of IGF1R in the negative control were higher in UMSSC-14C cells relative to UMSSC-11A cells. The expression levels in treated UMSSC-14C cells were similar to those of treated UMSSC-11A cells. The strongest effect on IGF1R inhibition in UMSSC-14C was observed after incubation with everolimus. For the HPV-positive cell line, the data were not as uniform. Irrespective of drug treatment, expression levels of IGF1R were significantly lower in HPV-positive cancer cells compared with HPV-negative cancer cells. Interestingly, nilotinib-treated cells showed an almost identical expression compared with the negative control. Moreover, treatment effects could be seen only after 24 h. Nilotinib only led to a significant reduction ($p < 0.001$) of IGF1R after 72 h, whereas no significant alteration was seen at the other measurement points. The expression patterns and the grade of expression of IGF1R were similar after incubation with dasatinib, erlotinib, gefitinib, or everolimus. The addition of dasatinib,

erlotinib, gefitinib, or everolimus led to a significant reduction ($p < 0.001$) of IGF1R expression after 48, 72, and 96 h, but no significant effect was seen after 24 h. Details are provided in Figures 1-3.

Discussion

Intensive research has been accomplished to improve therapy approaches that add to classic therapies (combinations of surgery, radiation, and chemotherapy). The monoclonal antibody cetuximab targeting EGFR has been established for HNSCC treatment (41), but other drugs also targeting EGFR such as the humanized antibody panitumumab and small molecule TKIs erlotinib and gefitinib have not yet reached significant effects compared with classic platinum-based therapy (42-52). Activation of EGFR, which is overexpressed in 90% of HNSCC, leads to receptor kinase activation followed by activation of signal transducer and activator of transcription 3 (STAT3) pathways, resulting in the promotion of cell proliferation, angiogenesis and invasion, and apoptosis inhibition (53, 54). EGFR-overexpression in HNSCC correlates with poor prognosis and radiation resistance (53, 55). Other TKIs inhibiting BCR-ABL such as nilotinib have not yet included in *in vivo* approaches but have been studied *in vitro* (56, 57). Further, mTOR inhibition with everolimus (mostly used in combination therapies) has not shown promising results in HNSCC treatment, and response rates remain moderate (58-60). Because numerous clinical studies could not

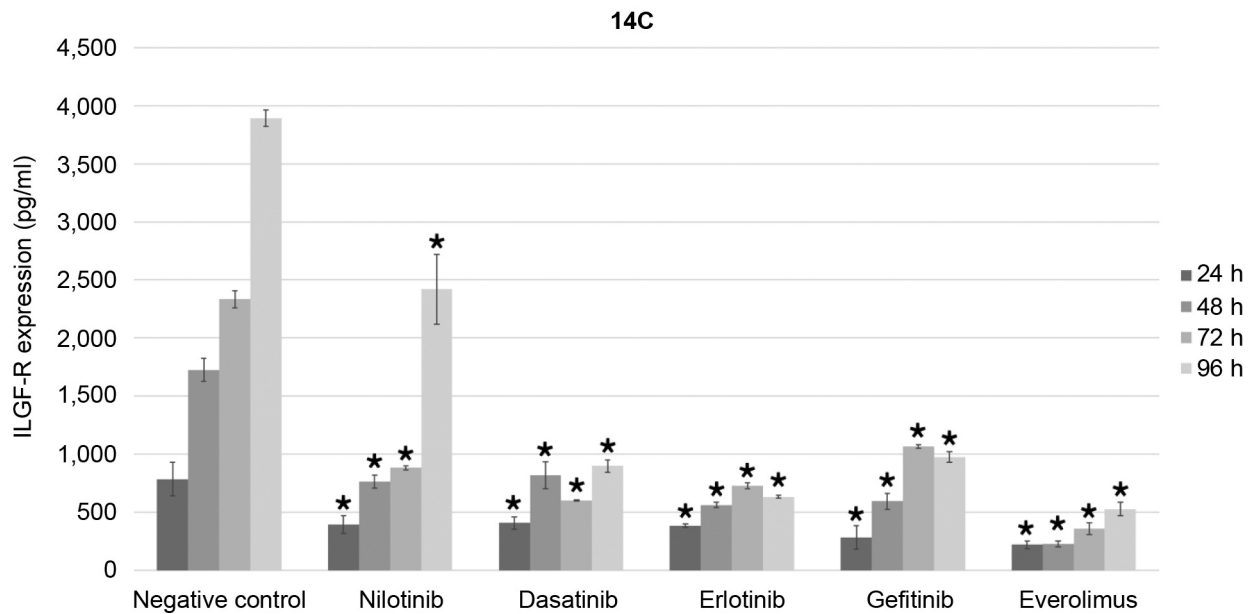


Figure 2. IGF1R expression in UMSCC-14C cells after incubation with nilotinib, dasatinib, erlotinib, gefitinib, or everolimus compared with the negative control. Data are mean values with standard deviations. Significance ($p \leq 0.001$) is marked with *.

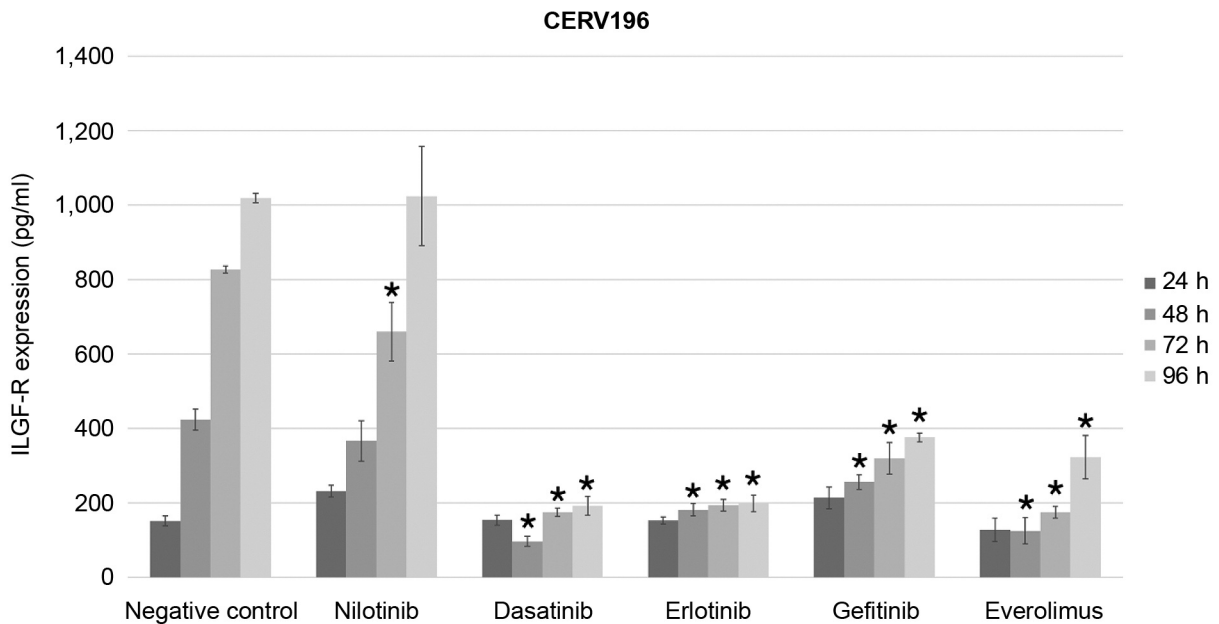


Figure 3. IGF1R expression in CERV196 cells after incubation with nilotinib, dasatinib, erlotinib, gefitinib, or everolimus relative to the negative control. Data are mean values with standard deviations. Significance ($p \leq 0.001$) is marked with *.

demonstrate beneficial effects in HNSCC treatment with TKI or mTOR inhibition, we designed this study to better understand the molecular mechanism of this failure because these drugs have been successfully established in the

treatment of other tumor entities (e.g. CML and non-small cell lung cancer (20, 23). IGF1R is overexpressed in human cancers such as ovarian cancer, glioblastoma, and sarcoma and may therefore be suitable as a potential target protein

(27, 29, 31). In patients with HNSCC, it has been demonstrated that high expression levels of IGF1R are associated with high tumor (T)-stage, decreased overall survival, and shorter disease-specific survival (30). Because IGF1R can play a critical role in cancer development including proliferation and metastasis, TKIs directly targeting the IGF1R catalytic domain have been developed, and inhibitions of a broad range of human tumor types *in vitro* have been reported (61-68). Several current studies concentrate on the direct inhibition of IGF1R with TKIs and TKI combinations, but there is a lack of data regarding the direct effect of the tested TKIs on IGF1R in HNSCC. Therefore, this study was designed to close this gap by investigating effects of the small molecule TKIs erlotinib, gefitinib, dasatinib, and nilotinib and the mTOR-inhibitor everolimus on HPV-negative and HPV-positive SCC. Our results revealed a significant reduction of IGF1R expression in both TKI- and mTOR-inhibitor-treated HPV-negative and HPV-positive cultures relative to untreated cells. Gefitinib has been reported to induce nuclear accumulation of IGF1R in mucinous lung adenocarcinoma, and nuclear IGF1R induces G₁ arrest and promotes resistance (69). This mechanism might also play a role in HNSCC resistance to gefitinib. Yet, only few resistance mechanisms to EGFR-TKI have been identified. The ability to bypass EGFR-dependent signaling pathways (including the IGF1R pathway) as well as the presence of resistance mutations have been proven (70). In our results, IGF1R expression was significantly decreased by all the tested TKIs and by everolimus. The reduced expression may be due to survivin, which is a recently identified protein expressed in HNSCC and a possible molecular target correlating with clinical parameters and treatment outcome (71, 72). It has already been demonstrated that activation of IGF1R reduces sensitivity to EGFR-TKIs in HNSCC cell lines *via* a reduction of apoptosis, and it was demonstrated that resistance to lapatinib, an EGFR- and Her2/Neu-TKI (like gefitinib), correlates with enhanced survivin expression in HNSCC cells. This suggests that the regulation of survivin expression may be a key element in IGF1R-dependent therapeutic resistance (40, 73, 74). Additional experiments are necessary to investigate the expression of survivin in cell lines under the influence of TKIs and everolimus, as current data suggest a higher expression in cells resistant to the EGFR-TKI lapatinib (74). Nevertheless, the expression of IGF1R was suppressed by the tested small molecule TKIs in HPV-negative and HPV-positive SCC cells within 96 h. These results suggest a beneficial therapeutic effect in the tested cell lines, but a limitation of our study is that acquired resistance and IGF1R upregulation might appear later. Other groups have examined the effect of the exposure to gefitinib over several months and showed that acquired resistance to EGFR-TKIs in A431 SCC cells is mediated by

a loss of IGF-binding proteins, and it was demonstrated that elimination of persistent IGF1R-induced Akt activity was required to reestablish gefitinib sensitivity (75). It has also been suggested that persistent IGF1R activity may predict resistance to anti-EGFR therapy in HNSCC (40). Also, cholangiocarcinoma cells escaped EGFR-TKI treatment with erlotinib by developing an adaptive mechanism undergoing an IGF1R-involving phenotypic switch (76). In our cultures, erlotinib reduced the levels of IGF1R within 96 h. The multi-TKI dasatinib (BCR-ABL, SRC, EGFR) has been demonstrated to suppress invasion and induce cell cycle arrest and apoptosis of HNSCC and non-small cell lung cancer cells *in vitro* and to increase radiation sensitivity by interfering with nuclear localization of EGFR and by blocking DNA repair pathways (77, 78). However, these effects could not be demonstrated in *in vivo* experiments (44). Promising results have been shown when combining the IGF1R inhibitor BMS754807 with either the human epidermal growth factor receptor family inhibitor BMS59962 or dasatinib, resulting in substantial synergy and growth inhibition *in vitro* (79). Everolimus treatment led to reduced IGF1R expression at all measurement points in the tested HPV-positive and HPV-negative cultures. The dual targeting of insulin and insulin-like growth factor 1 receptor enhances mTOR-inhibitor-mediated antitumor efficacy in hepatocellular carcinoma *in vitro*, but no comparable data are yet available in the literature regarding HNSCC (80). Up to date, everolimus has failed in HNSCC treatment (42). IGF1R could be influenced by everolimus treatment, as the IGF1 pathway might play a similar role in the EGFR bypass mechanism as mentioned above. For a subset of medullary thyroid carcinoma, it has been demonstrated that IGF1 influences the antiproliferative activity of everolimus (81).

In conclusion, these novel insights might contribute to a better understanding of the poor therapeutic effects of TKIs and everolimus in HNSCC. Future research investigating survivin in UMSCC-11A and -14C and in CERV196 and other TKIs would be of central interest. This is the first study analyzing the influence of TKIs and everolimus on IGF1R in HPV-negative UMSCC-11A and -14C and HPV-positive CERV196 cultures.

Conflicts of Interest

The Authors declare no conflicts of interest in relation to this study.

Authors' Contributions

Benedikt Kramer: conception of the study, writing of the manuscript, generation of figures, data analysis; Angela Schell: data analysis, writing of the manuscript; Christoph Aderhold: performance of experiments, conception of the study, data analysis; Lena Huber: performance of the experiments, data analysis; Cornelia Emika Mueller: performance of the experiments, data

analysis; Nicole Rotter: providing conceptional design of the study, data analysis; Richard Birk: writing of the manuscript, conception of the study, generation of figures, data analysis. The manuscript was critically reviewed by all Authors.

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