that the radiocomplex remained intact for up to 24 hours without metal dissociation, indicating its suitability for future in vivo assessments. These promising results pave the way for structural optimization through spacer units and subsequent bioconjugation studies for the development of new radiopharmaceuticals.

Keywords: Gallium, Radioisotopes, Theranostics, Hexadentate Chelators, Imine group.

Conflicts of interest: Not declared.

Acknowledgments/Funding: CNPQ, FAPESP-CEPID #2021-10265-8.

https://doi.org/10.1016/j.htct.2026.106295

24

ROBUST AND RIGOROUS IC50 DETERMINATION FOR PRECLINICAL DRUG DISCOVERY

Letícia Fernanda Alves,
Gilberto Carlos Franchi Júnior,
Alessandra Rodrigues Cardoso Padovam,
Leticia Pires de Oliveira, Pedro Paulo Corbi,
Carmen Silvia Passos Lima,
Diego Samuel Rodrigues

Universidade Estadual de Campinas, Campinas, SP, Brazil

Determining dose-response curves is a critical first step in preclinical drug discovery. Typically, experimental dose-response data are fitted using nonlinear sigmoidal models. This process requires careful attention to fitting criteria and model comparison. Not infrequently, drug candidate compounds may lack sufficient potency at the tested concentrations or produce data that lead to unavoidable poor fitting. A key parameter to estimate in such cases is the half-maximal inhibitory concentration (IC50). This study illustrates the use of the R package drda as the state-of-the-art statistical tool to address these fitting challenges, with a reputation for having been extensively tested in fitting applications with synthetic data and under random sampling from a real dataset of 379,533 cell line and drug pairs. For model evaluation, drda provides the Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and Likelihood Ratio Test (LRT) to assess goodness of fit for logistic regressions with varying parameter complexities. Combined with graphical diagnostics, results from our benchmark real dataset show that AIC, BIC, and LRT are essential for the rigorous estimation of IC50. In fact, the systematic use of metrics increases reliability in dose-response studies by minimizing the risk of pursuing ineffective compounds and reducing the chance of discarding potentially active molecules, thereby supporting more efficient and innovative preclinical drug discovery.

Keywords: Dose-response data analysis, Model calibration and selection, Preclinical drug discovery.

Conflicts of interest: Not declared.

Acknowledgments/Funding: The authors thank grants from São Paulo Research Foundation (FAPESP): 2024/21475-1, and 2021/10265-8 (“CancerThera”). This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brazil (CAPES) – Finance Code 001.

https://doi.org/10.1016/j.htct.2026.106296

25

EGFR-TARGETING GE11-DERIVED PEPTIDE DIFFERENTIALLY MODULATES TRIPLE-NEGATIVE BREAST CANCER AND GLIOBLASTOMA CELL PROLIFERATION IN VITRO

Julia Naomi Ono, Danielle Vieira Sobral,
Fernanda Ferreira Mendonça,
Luciana Malavolta, Leonardo Lima Fuscaldi

Faculdade de Ciências Médicas da Santa Casa de São Paulo, São Paulo, SP, Brazil

Introduction: Triple-negative breast cancer (TNBC) represents one of the most aggressive subtypes of breast cancer. Glioblastoma (GBM) is the most lethal primary brain tumor, characterized by poor prognosis. Both malignancies frequently overexpress the epidermal growth factor receptor (EGFR), which contributes to tumor progression by promoting proliferation, angiogenesis, and resistance to apoptosis. The GE11 peptide, YHWYGYTPQNVI, exhibits high affinity for EGFR and has been explored as a targeting ligand in molecular imaging strategies. Here, a modified GE11-derived peptide, YHAYGYTPQNVI, was employed, in which tryptophan was substituted by alanine to reduce photosensitivity. **Objectives:** To evaluate the in vitro effects of the YHAYGYTPQNVI peptide on cell proliferation and viability in TNBC (MDA-MB-231) and GBM (U-87 MG) cells. **Materials and Methods:** MDA-MB-231 and U-87 MG cells were cultured in RPMI-1640 or DMEM, respectively, supplemented with 10% fetal bovine serum (37° C; 5% CO2). Cell proliferation was assessed by growth curve analysis. Cells were seeded in 6-well plates (5×104 cells/well) and treated with YHAYGYTPQNVI (56.1 μM). Viable cell counts were performed on days 1, 3, 5, and 7, comparing with untreated control (CT). Cell viability was evaluated by the MTT assay in MDA-MB-231 cells seeded in 96-well plates (5×10^3 cells/well) and treated with YHAYGYTPQNVI (5.61 μM). MTT measurements were obtained on days 1, 5, and 7, and viability was expressed as a percentage relative to CT. Data are presented as mean $\pm$ SD. Statistical analyses were performed using Student’s *t*-test or ANOVA followed by Tukey’s test, with significance set at $p<0.05$. **Results:** Growth curve analysis of MDA-MB-231 cells revealed no statistically significant differences between the GE11-derived peptide-treated and CT groups, as illustrated on day 7: YHAYGYTPQNVI = $(3.18 \pm 0.40) \times 105$ versus CT = $(3.43 \pm 0.58) \times 105$ [$p = 0.4501$; $n = 6$]. Consistently, MTT assays indicated a moderate reduction in cell viability (~15–25%); however, this reduction was not statistically significant over time, with viabilities of 83.66 $\pm$ 6.24% (day 1), 74.11 $\pm$ 12.24% (day 5), and 79.76 $\pm$ 8.02% (day 7) [$p = 0.1885$; $n = 7$]. In contrast, growth