

Novel Promising IAP Antagonist on the Horizon for Clinical Translation

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Evasion of apoptosis represents a hallmark of human cancers and is frequently caused by aberrant expression of antiapoptotic proteins.¹ Since inhibitor of apoptosis (IAP) proteins are present at high levels in many tumors and potentially block apoptosis, they are considered as promising targets for therapeutic intervention.² IAP proteins comprise eight human analogues, among them XIAP, cIAP1, cIAP2, and ML-IAP.² XIAP has been shown to inhibit caspases via binding of the BIR3 domain of XIAP to the small subunit of processed caspase-9, while the linker region preceding the BIR2 domain as well as the BIR2 domain of XIAP is critical for inhibition of caspase-3 and -7.

In an attempt to design pan-selective IAP antagonists that neutralize XIAP, cIAP proteins, and ML-IAP, Flygare et al. used a combined approach of structure-based design and solid-phase library synthesis.³ This resulted in the production of a series of compounds that mimic the four amino acid N-terminus of the endogenous IAP antagonist Smac (Figure 1). Of particular

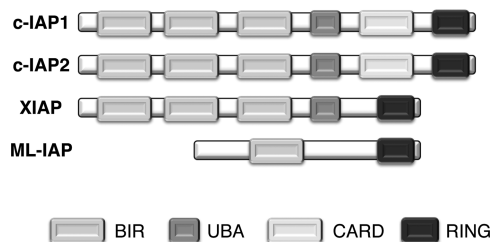


Figure 1. Structures of selected IAP proteins. The pan-selective IAP antagonists that were developed in the study by Flygare et al.³ target four of the eight human inhibitor of apoptosis (IAP) proteins, namely, XIAP, cIAP1, cIAP2, and ML-IAP. The unifying feature of these IAP proteins is the baculoviral IAP repeat (BIR) domain, while other functional motifs such as the RING, UBA, and CARD domains are expressed in a more selective manner.

interest among these compounds was the thiadiazole compound **1** (GDC-0152), which was subsequently characterized in more detail for its binding properties, antitumor activity, and pharmacokinetic profile. Binding studies using X-ray crystallography showed that GDC-0152 interacts with the Smac-binding sites of the BIR3 domain of cIAP1 and the BIR domain of ML-IAP. A fluorescence polarization-based competition assay confirmed that GDC-0152 binds in the low nanomolar range to the BIR3 domains of XIAP, cIAP1, and cIAP2; the BIR2 domain of XIAP; and the single BIR domain of ML-IAP, whereas binding to the BIR2 domains of cIAP1 and cIAP2 was found at the low micromolar range. Subsequent functional activity studies using cell-free systems, *in vitro* cellular assays, and *in vivo* xenograft studies in mice demonstrated that GDC-0152 potently disrupts protein–

protein interaction of IAP proteins and key proapoptotic molecules such as activated caspase-9 and Smac. Consistently, GDC-0152 as single agent increased enzymatic activity of caspase-3 and -7 and reduced cell viability. It is interesting to note that cytotoxic activity of GDC-0152 was found in the breast carcinoma cell line MDA-MB-231 but not in non-malignant human mammary epithelial cells. Furthermore, GDC-0152 rapidly and potently stimulated proteasomal degradation of cIAP1, whereas its inactive enantiomere was devoid of this activity. This is consistent with recent data showing that IAP antagonists can stimulate a conformational change in cIAP1 that promotes its RING dimerization and E3 ligase activity, resulting in autoubiquitination of cIAP1.⁴ In a subcutaneous xenograft model using MDA-MB-231 breast carcinoma cells in nude mice, oral administration of GDC-0152 caused marked tumor regression as a single agent, even at the lowest dose of 10 mg/kg daily. *In vivo* preclinical pharmacokinetic studies showed favorable solubility properties, moderate hepatic clearance, and moderate plasma–protein binding. Of note, GDC-0152 was well tolerated in all preclinical *in vivo* studies. In the first *in men* study, GDC-0152 displayed linear pharmacokinetics, moderate clearance, and a moderate volume of distribution, consistent with preclinical predictions.

Together, these findings indicate that GDC-0152 represents an interesting candidate for further evaluation in clinical trials. However, a couple of questions remain. First, the issue of whether or not GDC-0152 selectively exerts antitumor activity against malignant tumor cells versus nonmalignant normal human cells remains to be addressed in additional studies. While the results of this study point to a selective cytotoxicity of GDC-0152 against tumor cells, the study is so far restricted to one malignant and one nonmalignant cell line. Therefore, additional studies are required to confirm the tumor-selective cytotoxic activity of GDC-0152. Also, the mechanistic basis for this tumor selectivity has not yet been unraveled. Second, additional data on the antitumoral activity of GDC-0152 in a broader panel of cancer cell lines will help to estimate its antitumor activity, as the current study focuses on the breast carcinoma cell line MDA-MB-231, which has been reported to be particularly sensitive to IAP antagonists.^{5,6} For example, it will be interesting to explore whether GDC-0152 is active against cancer cells that exhibit high expression levels of ML-IAP, as this compound binds at low nanomolar concentrations to ML-IAP. Third, the fact that tumor regrowth is observed upon termination of treatment with GDC-0152 in the *in vivo* model raises questions concerning possible underlying mechanisms. Is there insufficient target inhibition by GDC-

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0152 in the tumor tissue? Is tumor heterogeneity responsible for a mixed response to GDC-0152 resulting in the outgrowth of resistant tumor cells once treatment with GDC-0152 has been terminated? These questions also underscore that accompanying biomarker studies to investigate target inhibition in the tumor tissue upon treatment with GDC-0152 would be very instructive to better understand the molecular basis of its *in vivo* activity. Another important question is how the antitumor activity of GDC-0152 can be best exploited in combination treatments. There is ample evidence that the combination of IAP antagonists together with additional cytotoxic principles including anticancer drugs, radiotherapy, or molecular-targeted therapeutics represents a promising strategy to yield synergistic drug interactions. Therefore, further evaluation of GDC-0152 in combination protocols is considered to be a promising future avenue of research.

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