

The MAT2A inhibitor AG-270 combines with both taxanes and gemcitabine to yield enhanced antitumor activity in patient-derived xenograft models

Marc L Hyer, Peter Kalev, Mark Fletcher, Chi-Chao Chen, Elia Aguado-Fraile, Everton Mandley, Sheila Newhouse, Max Lein, Raj Nagaraja, Yesim Tuncay, Josh Murtie, Scott A Biller, Kevin M Marks, Katya Marjon

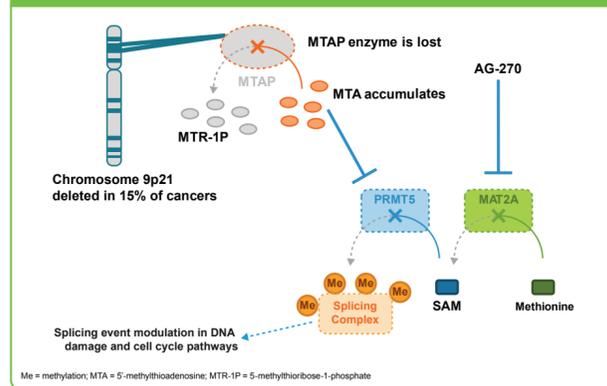
Agios Pharmaceuticals, Inc., Cambridge, MA, USA

Marc.Hyer@agios.com

BACKGROUND

- AG-270 is a first-in-class, oral, potent, reversible inhibitor of methionine adenosyltransferase 2A (MAT2A), currently being evaluated in a phase 1 trial in patients with advanced solid tumors and lymphomas with *MTAP* (S-methyl-5'-thioadenosine phosphorylase) deletion (ClinicalTrials.gov NCT03435250)
- MAT2A is a key enzyme in the methionine salvage pathway, responsible for generating the universal methyl donor, S-adenosylmethionine (SAM)^{1,2}
- MTAP* is deleted in ~15–25% of non-small cell lung cancers (NSCLC), ~25% of pancreatic, and ~30% of esophageal cancers³
- Biallelic loss of the *MTAP* gene sensitizes cancer cells to genetic depletion of protein arginine methyltransferase 5 (PRMT5) and the upstream metabolic enzyme, MAT2A (Figure 1)⁴
- To prioritize candidate combination partners for AG-270, a cell-based *in vitro* screening approach was employed using *MTAP*-null cell lines, in which AG-270 was combined with standard-of-care (SOC) agents as well as agents targeting pathways with hypothesized mechanistic links to MAT2A⁴

Figure 1. Targeting MAT2A in cancers with *MTAP* deletion



OBJECTIVES

- To identify combination partners that potentiate the cell growth inhibition effects of MAT2A blockade
- To assess the tolerability and antitumor activity of AG-270 combined with SOC agents in clinically relevant *in vivo* patient-derived xenograft (PDX) and cell-derived xenograft (CDX) models
- To investigate the mechanism of action associated with AG-270 combined with taxane therapy

METHODS

- An *in vitro* synergy screen tested 20 candidate combination partners in 37 *MTAP*-null cell lines, with full-dose curve matrices performed at Horizon using a 96-hr CellTiter-Glo readout
 - Cell lines included kidney (n = 1), colorectal (n = 4), esophageal and gastric (n = 7), pancreatic (n = 8), and lung (n = 17)
 - The strength of potential synergistic interactions between AG-270 and enhancer compounds *in vitro* in excess of Loewe additivity was measured using the Horizon-developed Synergy Score
- Splicing changes were determined from RNA sequencing data using rMATS 3.2.5; changes in usage of detained introns⁵ were determined using DEXSeq
 - The splicing changes were selected using the criterion false discovery rate-adjusted p-value < 0.05
- In vivo* xenograft studies were performed using institutional animal care and use committee guidelines; the combination analysis used belongs to the 'response additivity' class of synergy analysis,⁶ with area under the tumor growth curves (AUC) compared between single-agent and combination treatments
- Hematoxylin and eosin (H&E) staining on formalin-fixed paraffin-embedded tumor tissues was performed by Mosaic Laboratories in accordance with validated procedures, with the percentage of multinucleated tumor cells and cytomegaly assessed by a pathologist
 - Six mice were evaluated per treatment arm; all tissues were collected 12–24 hr after the last dose of AG-270

RESULTS

- A large-scale synergy screen revealed potential synergistic combinations (Figure 2)
- MAT2A inhibition led to substantial dysregulation of splicing in *MTAP*-null cells, including an increased number of transcripts containing detained introns (Figure 3A)
- Detained intron-containing transcripts fail to export into the cytosol and thus are not translated⁵
- MAT2A inhibitor-induced detained introns included genes involved in the DNA damage response and cell-cycle regulation, such as Aurora kinase B (Figure 3B)
- Quantitative reverse transcriptase (RT)-PCR analysis demonstrated that treatment with a MAT2A inhibitor led to increased expression of detained intron-containing transcripts and decreased levels of total (exon-exon) Aurora B expression (Figure 3C)

Figure 2. AG-270 synergized with antimetabolic taxanes and gemcitabine in a cell-based assay

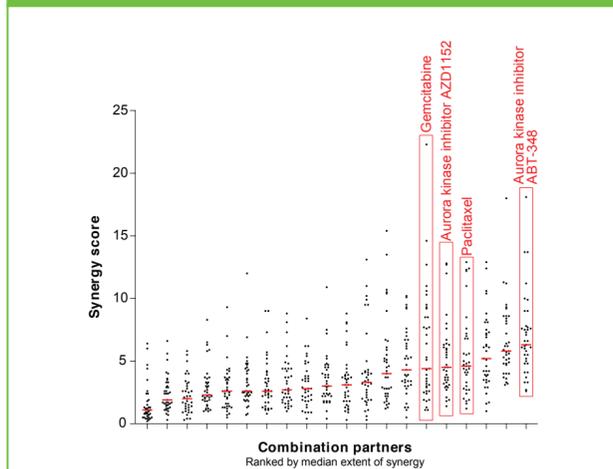
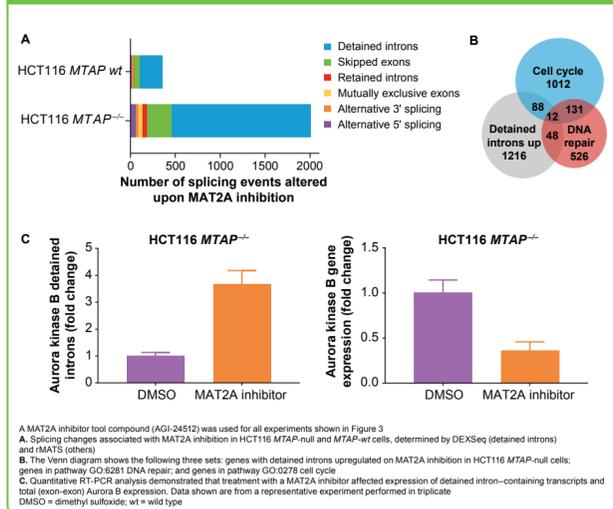


Figure 3. MAT2A inhibition disrupted splicing and altered gene expression in *MTAP*-null cells



- A summary of the efficacy of AG-270 and taxanes as single agents and in combination in xenograft models is shown in Table 1
- AG-270 demonstrated increased antitumor activity when combined with docetaxel in a lung PDX mouse model (Figure 4)
- AG-270 demonstrated increased antitumor activity when combined with docetaxel in an esophageal PDX mouse model (Figure 5)

Table 1. Efficacy data summary of AG-270 and taxanes, alone and combined

Tumor model (indication, subtype)	Taxane partner	AG-270 tumor growth inhibition, %	Taxane tumor growth inhibition, %	Combination tumor growth inhibition, %	Tolerability: Maximum mean BWL, %	Combination analysis ^{7,8}
KP4 (pancreatic)	Docetaxel	66	70	94	< 5	Synergy
ESX030 (esophageal, SCC)	Docetaxel	68	44	90	< 2.5	Synergy
LUX001 (NSCLC, SCC)	Docetaxel	70	45	91	6	Synergy
PA0372 (pancreatic)	Paclitaxel	59	29	84	< 2.5	Additive
ESX2263 ⁹ (esophageal, SCC)	Docetaxel	27	12	57	< 5.0	Additive
LUX034 (NSCLC, SCC)	Docetaxel	41	27	60	< 6	Additive
LU6412 ¹⁰ (NSCLC, Ad)	Docetaxel	52	57	92	13.3	Additive
PAX001 (pancreatic)	Paclitaxel	94	22	94	7	Weakly additive
CTG-1194 (NSCLC, Ad)	Docetaxel	15	42	52	0	Additive
PAX041 (pancreatic)	Paclitaxel	55	12	50	< 2.5	Weakly additive

Tumor growth inhibition % = $1 - \frac{(TV_0 - TV_1) / (TV_0 - TV_{veh})}{TV_0 - TV_{veh}} \times 100\%$; where TV_0 is the average tumor volume of the test group on a specific day and TV_1 is the average tumor volume of the same group on day 0, and TV_{veh} is the average tumor volume of the vehicle group on a specific day and $TV_{veh,0}$ is the average tumor volume of the vehicle group on day 0
 Paclitaxel doses used in PAX001 and PAX041 were 7.5 mg/kg; in PA0372, 15 mg/kg. Docetaxel doses used in KP4, ESX030, ESX2263, CTG-1194, LU6412, LUX034 were 5 mg/kg; in LUX001, 2.5 mg/kg. Number of animals used per arm per model was 8–12
 Dosing holidays were provided
 *1 of 12 animals was found dead in the combination group
 Ad = adenocarcinoma; BWL = body weight loss; SCC = squamous cell carcinoma

Figure 4. AG-270 enhanced docetaxel therapy in an NSCLC (SCC) *MTAP*-null PDX mouse model

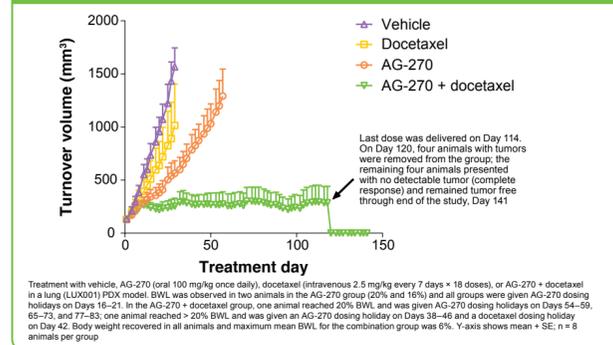
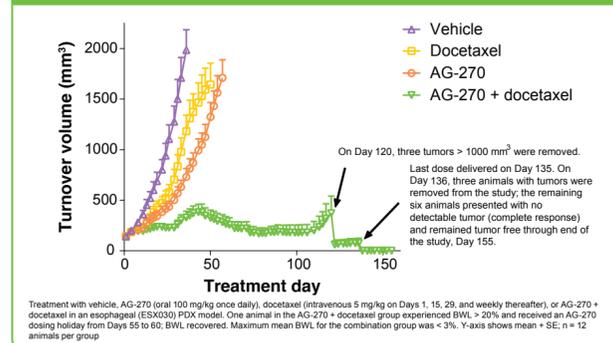


Figure 5. AG-270 enhanced docetaxel therapy in an esophageal (SCC) *MTAP*-null PDX mouse model



- The combination of AG-270 with taxanes induced cytomegaly (abnormal cell enlargement) and multinucleation in xenograft tumor cells (Figure 6)
- A summary of the efficacy of AG-270 and gemcitabine as single agents and in combination in xenograft models is shown in Table 2
- AG-270 demonstrated increased antitumor activity when combined with gemcitabine in a pancreatic CDX mouse model (Figure 7)

Tumor model (indication, subtype)	Taxane partner	AG-270 tumor growth inhibition, %	Taxane tumor growth inhibition, %	Combination tumor growth inhibition, %	Tolerability: Maximum mean BWL, %	Combination analysis ^{7,8}
KP4 (pancreatic)	Docetaxel	66	70	94	< 5	Synergy
ESX030 (esophageal, SCC)	Docetaxel	68	44	90	< 2.5	Synergy
LUX001 (NSCLC, SCC)	Docetaxel	70	45	91	6	Synergy
PA0372 (pancreatic)	Paclitaxel	59	29	84	< 2.5	Additive
ESX2263 ⁹ (esophageal, SCC)	Docetaxel	27	12	57	< 5.0	Additive
LUX034 (NSCLC, SCC)	Docetaxel	41	27	60	< 6	Additive
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Tumor growth inhibition % = $1 - \frac{(TV_0 - TV_1) / (TV_0 - TV_{veh})}{TV_0 - TV_{veh}} \times 100\%$; where TV_0 is the average tumor volume of the test group on a specific day and TV_1 is the average tumor volume of the same group on day 0, and TV_{veh} is the average tumor volume of the vehicle group on a specific day and $TV_{veh,0}$ is the average tumor volume of the vehicle group on day 0
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 Dosing holidays were provided
 *1 of 12 animals was found dead in the combination group
 Ad = adenocarcinoma; BWL = body weight loss; SCC = squamous cell carcinoma

Figure 6. Treatment with AG-270 combined with taxanes enhanced mitotic defects in xenograft tumors

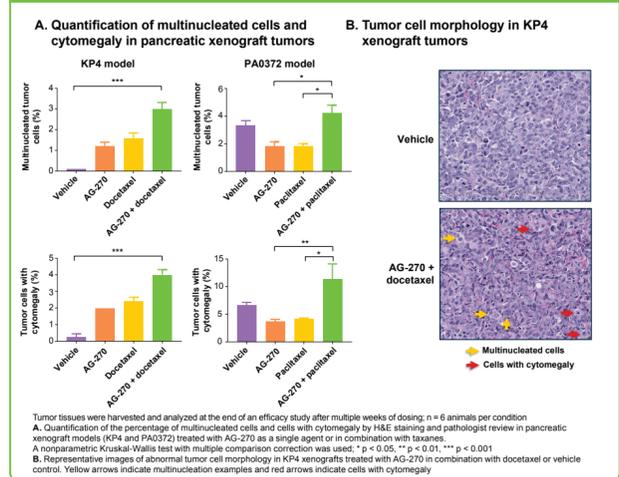
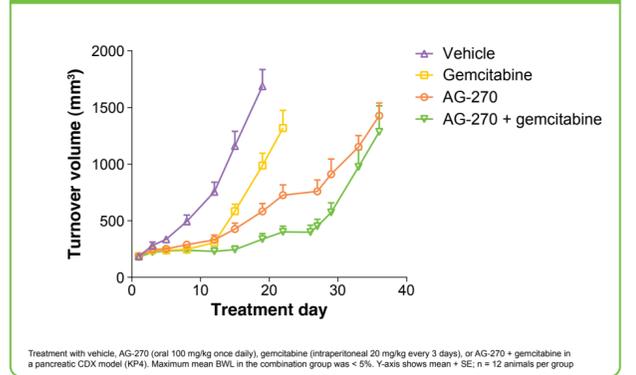


Table 2. Efficacy data summary of AG-270 and gemcitabine, alone and combined

Tumor model (indication, subtype)	AG-270 tumor growth inhibition, %	Gemcitabine tumor growth inhibition, %	Combination tumor growth inhibition, %	Tolerability: Maximum mean BWL, %	Combination analysis ^{7,8}
KP4 (pancreatic)	66	43	82	< 5	Additive
PAX041 (pancreatic)	55	16	69	< 5	Additive
LU6431 (NSCLC, SCC)	45	43	69	< 5	Additive
PAX001 (pancreatic)	83	56	89	< 5	Weakly additive
LU1513 ¹¹ (NSCLC, SCC)	74	90	101	< 11	Weakly additive

Tumor growth inhibition calculated as described for Table 1
 Number of animals used per arm per model was 8–12
 *In the LU1513 study, one of 12 animals in the combination arm lost > 20% BWL on Day 11 and was removed from the study; maximum mean BWL in this group was 10%

Figure 7. AG-270 enhanced gemcitabine therapy in an *MTAP*-null pancreatic CDX (KP4) mouse model



CONCLUSIONS

- A cell-based screen identified taxanes and gemcitabine as therapeutic agents that could yield combination benefits with AG-270
- MAT2A inhibition led to substantial dysregulation of splicing, including an increased number of transcripts containing detained introns, in *MTAP*-null cells, including in pathways that regulate the DNA damage response and cell cycle, which we suggest are mechanistically relevant to efficacy
- These data form the basis for combining AG-270 with taxanes (antimetabolic agents) and gemcitabine (DNA-damaging agent)
- Combining AG-270 with taxanes and gemcitabine yielded additive-to-synergistic antitumor activity, with the docetaxel combination yielding 50% complete tumor regressions in select models; combination benefits were observed in PDX models derived from esophageal, NSCLC, and pancreatic cancers
- The combination of AG-270 with taxanes induced mitotic defects in tumor cells, as demonstrated by increased cytomegaly and multinucleation
- These preclinical findings have inspired an ongoing phase 1 study exploring AG-270 combined with docetaxel or gemcitabine/nab-paclitaxel (ClinicalTrials.gov NCT03435250)

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Disclosures

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