Antitumor activity of Tipifarnib and PI3K Pathway inhibitors in **HRAS-associated HNSCC** Abstract Number: P123

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BACKGROUND AND RATIONALE

HRAS-MAPK and PI3K-AKT-mTOR are important oncogenic pathways in head and neck squamous cell carcinoma (HNSCC) and other squamous cell carcinomas (SCCs). HRAS is mutated in ~5% and overexpressed in approximately 30% of HNSCC patients, raising the possibility that some HRAS wild-type (WT) HNSCCs may also display a degree of dependence on HRAS. PIK3CA (the catalytic subunit of PI3K), another prominent driver in HNSCC, is commonly activated either by gain of function mutations or gene amplification with some overlap between the two subsets. Multiple reports indicate that HRAS and PIK3CA pathways cooperate and crosstalk in driving tumor progression in SCCs and resistance to inhibitors of respective pathways. In this study, we explored whether combined inhibition of HRAS farnesylation (by tipifarnib) and inhibition of PI3K pathway signaling (with inhibitors of PI3Kα, AKT or mTORC1/2) would be more effective in CDX and PDX models of HRAS-associated SCCs relative to the monotherapy approaches.

In a panel of HNSCC cell lines harboring HRAS mutations or overexpression and/or PIK3CA mutations or amplification, tipifarnib reduced cell growth and, in combination with PI3Kα inhibitor alpelisib, induced cytotoxicity. Consistent with in vitro findings, robust inhibition of tumor growth was observed in majority of animals treated with the combination of tipifarnib and alpelisib. In dose-scheduling experiments in PDX models, simultaneous blockade of both targets was superior to split intermittent dosing of the two drugs, underlining the cooperativity of the two pathways in these models. Mechanistically, tipifarnib and alpelisib work through combined inhibitory effects on MAPK and PI3K pathways.

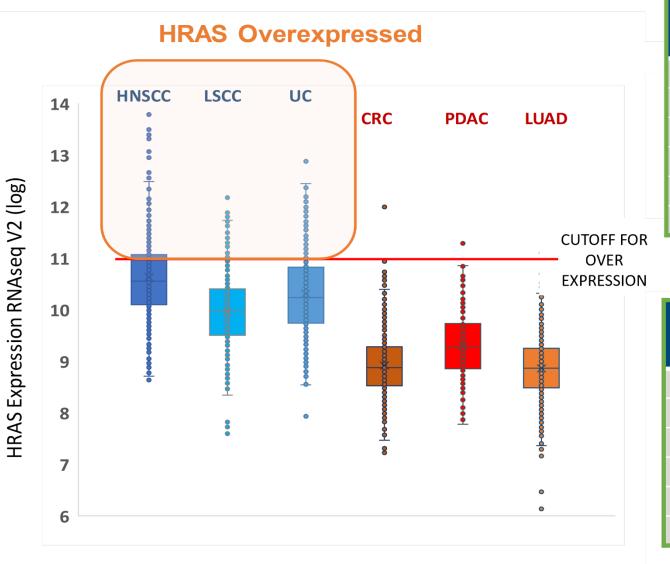
HRAS AND PIK3CA DYSREGULATIONS ARE COMMON IN HNSCC

HR	AS 6%					
PIK	(3CA 29%					
Genetic Alteration		Inframe Mutation (putative driver) Missense Mutation (putative driver) Missense Mutation (unknown significance)				
		 Truncating Mutation (putative driver) 	Structural Variant (unknown s	significance) Amplification	Deep Deletion No al	terations
PDX Model	Genotype		Cell line	Genotype		
	HRAS Mut/CNV/mRNA	PIK3CA Mut/CNV/mRNA		HRAS Mutation/expression	PIK3CA Mutation	
HN2581	G13C/2/high	WT/2/medium	CAL-33	WT/high	H1047R	
HN3504	K117L/2/high	H1047R/2/low	FaDu	WT/low	Amplified*	HF
HN2593	WT/2/high	G118D/3/high	SCC-25	WT/medium	Copy gain	
HN3690	WT/2/high	E545K/4*/high	HSC-2	WT/high	H1047R	PIK3
1113030			HSC-3	WT/medium	WT	
	WT/2/high	WT/6*/high WT/3/high	HSC-4	WT/medium	E545K	GAF
HN3067 HN2594	WT/2/high					

HRAS and PIK3CA are commonly dysregulated in HNSCC patients

Such dysregulation in HRAS occurs at level of mutations or over expression; in PIK3CA at the level of mutations or amplification

HRAS OVEREXPRESSING HNSCC MAY REPRESENT A SUBSET OF HRAS **DEPENDENT TUMORS**



	Mean	SEM	z-score*
HNSCC	10.63	0.04	24.96
LSCC	9.96	0.03	19.75
UC	10.31	0.04	21.56
CRC	8.92	0.03	NA
PDAC	9.30	0.05	6.37
LUAD	8.86	0.03	1.13
*vs. CRC			

#>CUTOFF	TOTAL	% HIGH
146	482	30.3
39	461	8.5
78	306	25.5
1	520	0.2
2	163	1.2
1	498	0.2
	78 1 2	78 306 1 520 2 163

Average HRAS expression in HNSCC is 5-10x higher than other (colorectal, pancreatic, lung adenocarcinoma) tumor types Together with HRAS mutant tumors, HRAS-overexpressing HNSCC may represent a significant subset of **HRAS dependent** tumors with distinct biology that may be targeted by tipifarnib

