Arlene Siefker-Radtke,^{1*} Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

¹Department of Genitourinary Medical Oncology, The University of Texas MD Anderson Cancer Center, Houston, TX, USA; ²Department of Cancer Medicine, INSERM U981, Gustave Roussy, Université Paris-Saclay, Villejuif, France; ³Department of Oncology and Hematology, National Cancer Center Hospital East, Chiba, Japan; ⁴Division of Hematology-Oncology, Department of Medicine, Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, South Korea; ⁵Section of Radiotherapy and Imaging, Institute of Cancer Research and Royal Marsden NHS Foundation Trust, Sutton, UK; ⁶Medical Oncology Department, Levine Cancer Institute, Charlotte, NC, USA; ⁷Janssen Research & Development, Spring House, PA, USA; ⁸Janssen Research & Development, Beerse, Belgium; ⁹Greenberg Bladder Cancer Institute, Johns Hopkins Medical Institutions, Baltimore, MD, USA.

*presenting author

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KEY TAKEAWAY

- Presence of FGFRalt highly enriches for mUC tumors exhibiting a LumP subtype
- Treatment with erdafitinib trended towards improved clinical outcomes in a biomarker-defined LumP patient population compared with overall cohort

 $\mathsf{FGFRalt}, fibroblast\,growth\,factor\,receptor\,alteration;\,\mathsf{LumP},\,\mathsf{luminal}\,papillary;\,\mathsf{mUC},\,\mathsf{metastatic}\,urothelial\,cancer.$



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Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

CONCLUSIONS



Molecular subtypes were evenly distributed in *FGFR WT* tumors with a large proportion constituting the LumP subtype

LumP subtype was enriched in *FGFR*-altered tumors

Both *FGFR* mutations and fusions enrich for LumP tumor subtype

FGFRalt, fibroblast growth factor receptor alteration; LumP, luminal papillary; WT, wild type.

Urothelial Cancer



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INTRODUCTION

- Erdafitinib is an oral pan-FGFR TKI approved to treat adult patients with locally advanced or mUC with susceptible *FGFR*alt, and whose disease progressed on ≥1 line of prior systemic therapy
- In non-muscle invasive and resectable muscle-invasive UC, FGFRalt is highly associated with luminal subtype characterized by expression of luminal markers, low expression of basal markers, and with immune cold/poor immune infiltration
- In a randomized open-label phase 3 THOR study (Cohort 2), erdafitinib showed improvement in objective response and PFS compared with pembrolizumab, with no significant improvement in OS in patients with mUC and selected FGFR gene aberrations¹
- In this study, a molecular analysis was performed exploring subtypes of tumor samples submitted for the THOR study (cohort 2) to further understand clinical findings

erda, erdafitinib; FGFR, fibroblast growth factor receptor; FGFRalt, fibroblast growth factor receptor alteration; mUC, metastatic urothelial cancer; OS, overall survival; PFS, progression-free survival; TKI, tyrosine kinase inhibitor; UC, urothelial cancer.

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METHODS

- All available tumors from patients enrolled in THOR Cohort 2 (NCT03390504; FGFRalt positive, N=201) and a subset of FGFR WT (N=116), who were anti-PDL1/PD1 naïve, were used to perform whole transcriptome RNA sequencing, of which 152 and 84, respectively, passed quality control (Figure 1)
- FGFR status was determined using Qiagen therascreen FGFR RT-PCR test
- Consensus single-sample classifier was applied to the RNAseq data to determine molecular subtypes
- Tumor subtypes were correlated with treatment response to erdafitinib or pembrolizumab, ORR, PFS, and OS

Figure 1. Study design

RNA sequencing of THOR (NCT03390504) cohort 2 patients screened for susceptible *FGFR* alts with no prior ICI-based treatment (n=317) • 201 *FGFRalt*+

• 116 *FGFR* WT

QC passed (prelim) 236 screened samples (ITT n=152 *FGFRalt*+ treated by erda/pembro); n=84 WT



Molecular subtype association vs. ORR/PFS/OS

erda, erdafitinib; FGFRalt, fibroblast growth factor receptor alteration; ICI, immune checkpoint inhibitor; ITT, intent-to-treat; MIBC, muscle invasive bladder cancer; ORR, overall response rate; OS, overall survival; pembro, pembrolizumab; PFS, progression-free survival; QC, quality control; WT, wildtype.

NAVIGATION **KEY TAKEAWAY** CONCLUSIONS INTRODUCTION **METHODS:** FIGURE 1 RESULTS Baseline characteristics Molecular subtype FGFR-altered tumors FGFR alterations and subtypes ORR by tumor subtype PFS by tumor subtype OS by tumor subtype APPENDIX



MIBC-consensus subtype algorithm

Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

RESULTS

 In erdafitinib- and pembrolizumab-treated groups, majority of patients harbored a *FGFR* mutation (76.9% and 80.5%) vs. translocation (23.1% and 17.2%), respectively (Table 1)

Table 1. Baseline characteristics				
	Erdafitinib	Pembrolizumab		
	(N=65)	(N=87)		
Age, years	· O-			
< 65	26 (40,0)	29 (33.3)		
≥ 65	39 (60.0)	58 (66.7)		
Sex				
Female	15 (23.1)	26 (29.9)		
Male	50 (76.9)	61 (70.1)		
Race	S			
Not reported	23 (35.4)	16 (18.4)		
Asian	11 (16.9)	8 (9.2)		
White	31 (47.7)	63 (72.4)		
Geographic regions O				
Europe	48 (73.8)	67 (77.0)		
North America	1 (1.5)	3 (3.4)		
Rest of the World	16 (24.6)	17 (19.5)		
Visceral metastasisª				
Absent	20 (30.8)	19 (21.8)		
Present	45 (69.2)	68 (78.2)		
ECOG PS				
0	34 (52.3)	39 (44.8)		
1 5	25 (38.5)	41 (47.1)		
2 0	6 (9.2)	7 (8.0)		
FGFR alterations				
Multiple	0	2 (2.3)		
Mutation	50 (76.9)	70 (80.5)		
Translocation	15 (23.1)	15 (17.2)		
Number of prior lines of systemic therapy		· · · · ·		
9	62 (95.4)	87 (100)		
2	2 (3.1)	0		
Missing	1 (1.5)	0		

×



Urothelial Cancer



Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

RESULTS

 Molecular classification of tumors (Figure 2) identified a significant proportion of LumP subtype in tumors harboring FGFRalt compared with FGFR WT (78.3% vs. 36.9%, *p*<0.001) and versus other subtypes: basal/squamous (Ba/Sq; 11.2% vs. 31.0%), stroma-rich (6.6% vs. 10.7%), NE-like (0% vs. 2.4%), LumU (3.3% vs. 17.9%), and LumNS (0.7% vs. 1.2%), respectively (Figure 3)



ALT, alteration; Ba/Sq, basal/squamous; FGFR, fibroblast growth factor receptor; LumNS, luminal non-specified; LumP, luminal papillary; LumU, luminal unstable; NE-like, neuroendocrine-like; QC, guality control; WT, wildtype.



NE-like



Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

n Janssen Science, and is not NAVIGATION RESULTS Figure 3. FGFR-altered tumors enrich for luminal-P **KEY TAKEAWAY** FGFR WT (N=84) FGFRalt (N=152) CONCLUSIONS Stroma-rich Stroma-rich (n=10) INTRODUCTION LumU (n=10) 6.6% NE-like (n=5) 6.6% (n=2) 3.3% **METHODS:** 2.4% LumNS Ba/Sq (n=1) 0.7% 00.0 (n=17) RESULTS Ba/Sq FGFR WT FGFR Alt^a 11.2% (n=26) Baseline characteristics LumP, % 36.9 78.3 31.0% LumU (n=15) 21.7 Non-LumP, % 63.1 Molecular subtype 17.9% ^ap<<4.991e-10 (LumP vs. Non-LumP). FIGURE 3: FGFR-altered tumors LumP LumP umNS (n=119) FGFR alterations and subtypes (n=1) (n=31) 1.2% 78.3% 36.9% ORR by tumor subtype PFS by tumor subtype OS by tumor subtype Ba/Sq, basal/squamous; FGFR, fibroblast growth factor receptor; FGFRalt, fibroblast growth factor receptor alteration; lumNS, luminal non-specified; lumP, luminal papillary; lumU, luminal unstable;

NE, neuroendocrine; non-LumP, all other subtypes excluding LumP; QC, quality control; WT, wildtype.

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APPENDIX

Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

RESULTS

 FGFRalt type showed differential association with subtypes; 3.2% of fusions and 14.1% of mutations were detected in Ba/Sq subtype while 74.2% and 79.3%, respectively, were detected in LumP (Figure 4)



p values indicate comparisons within each tumor subtype.

Ba/Sq, basal/squamous; FGFR, fibroblast growth factor receptor; lumNS, luminal non-specified; lumP, luminal papillary; lumU, luminal unstable; NE, non-existent; NS, not significant.



Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

RESULTS

 Clinical outcomes evaluated within LumP subset showed a significant improvement in ORR of erdafitinib-treated versus pembrolizumab-treated patients (41.7 vs. 19.7%; p=0.01), which was consistent with ITT population (40.0% vs. 21.6%) (Table 2)

Table 2. ORR by tumor subtype

Subtype	e Erdafitinib		Pembrolizumab		<i>P</i> value
	N	ORR (95% CI)	N	ORR (95% CI)	
Non-LumP	17	41.2% [18.4%, 67.1%]	16	25.0% [10.3%, 56.0%]	
LumP	48	41.7% [27.6%, 56.8%]	71	19.7% [11.2%, 30.9%]	0.0129
ITT ¹	175	40.0%	176	21.6%	

ITT, intent-to-treat; lumP, luminal papillary; non-LumP, all other subtypes excluding LumP; ORR, overall response rate.



Arlene Siefker-Radtke,¹ Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

RESULTS

 Numerical improvement were observed in PFS in LumP subtype between erdafitinib vs. pembrolizumab (5.5 vs 2.7 months) compared with the ITT population (4.4 vs 2.7) (Table 3)

Table 3. PFS by tumor subtype

	Erdafitinib		Pembrolizumab		
Subtype	Events/N	mPFS (95% CI), mo	Events/N	mPFS (95% CI), mo	<i>P</i> value
Non-LumP	17/17	4.83 [1.97, 8.25]	16/16	2.74 [1.28, 9.23]	NS
LumP	41/48	5.52 [4.40, 6.34]	62/71	2.73 [1.68, 4.17]	NS
ITT ¹	175	4.4 [4.1, 5.5]	176	2.7 [1.6, 3.0]	NS

erda, erdafitinib; ITT, intent-to-treat; lumP, luminal papillary; mPFS, median progression-free survival; non-LumP, all other subtypes excluding LumP; NS, not significant; pembro, pembrolizumab; PFS, progression-free survival.



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RESULTS

 Improvement in ORR and PFS of erdafitinib over pembrolizumab in LumP subtype did not translate to OS (10.9 vs. 12.9 months), which was similar to ITT population (10.9 vs. 11.1 months) (Table 4)

Table 4. OS by tumor subtype

	Erdafitinib		Pembrolizumab		
Subtype	Events/N	mOS (95% CI), mo	Events/N	mOS (95% CI), mo	<i>P</i> value
Non-LumP	16/17	12.35 [7.92, 23.3]	12/16	8.08 [3.78, NA]	NS
LumP	37/48	10.94 [8.31, 18.8]	51/71	12.94 [9.95, 20.9]	NS
ITT ¹	175	10.9 [9.2, 12.6]	176	11.1 [9.7, 13.6]	NS

erda, erdafitinib; ITT, intent-to-treat; lumP, luminal papillary; mOS, median overall survival; non-LumP, all other subtypes excluding LumP; NS, not significant; pembro, pembrolizumab.





Arlene Siefker-Radtke," Yohann Loriot,² Nobuaki Matsubara,³ Se Hoon Park,⁴ Robert A. Huddart,⁵ Earle F. Burgess,⁶ Jiarui Zhang,⁷ Neil Beeharry,⁷ Shibu Thomas,⁷ Nicole Stone,⁷ Kris Deprince,⁸ Spyros Triantos,⁷ Woonyoung Choi⁹

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DISCLOSURES:

ASR served on scientific advisory boards for Astellas Pharma, AstraZeneca, Basilea, Bavarian Nordic, G1 Therapeutics, Genentech, Gilead Sciences, Immunomedics, Janssen, Loxo, Merck, Mirati, Nektar Therapeutics, Seattle Genetics, and Taiho Oncology. A complete list of author disclosures are available on the ASCO website.

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