

Analytical Characterization of Dolaflexin-ADCs

David Lee WCBP, Washington DC January 30 2018

Unleashing the Targeted Power of Antibody Drug Conjugates



Schematic Structure of a Dolaflexin-Based ADC



- High DAR, DAR=10-15
- Hydrophobicity of payload offset by polar polyacetal backbone enabling higher DAR
- Novel proprietary auristatin payload

XMT-1522 Achieves Durable Complete Regressions Across Models with Range of HER2 Expression Levels



Dolaflexin Intracellular Processing



sub-nanomolar potency; freely cell permeable

Non cell-permeable; not a Pgp substrate

Selected Analytical Considerations for Dolaflexin-ADCs



Selected Attributes	Direct Stochastic Conjugation	Dolaflexin ADC
Linker-drug	Small simple structure	 Large complex structure Comparability of Dolaflexin batches important for ADC comparability
Average DAR	Typically by HIC	HIC currently not useful for DAR
Positional Isomers / structure	 Limited number of positional isomers, can be identified and quantitated, conjugation sites identified % DAR=0, 2, 4, 6, 8 	 Heterogeneity and reactivity of Dolaflexin complicates structural analysis ADC structure defined in part by number of Dolaflexins attached, conjugation sites occupied by Dolaflexin

Dolaflexin Process





XMT-1505

Sources of Heterogeneity in Dolaflexin ADCs

Heterogeneity due to regiochemistry and loading factors:



Unit 1: 2 – 4 mole% (~ 2 units/polymer)

Unit 4: 8 – 9 mole% (3 – 4 warheads/polymer)

Unit 3: 20 mole% (10 – 12 units/polymer)

Unit 2: ≤ 70 mole% (~ 35 – 40 units/polymer)

Note: Substitution can occur on either hydroxyl group of monomer, not just as indicated

MW Determined by SEC



9

Mersana

THERAPEUTICS

NMR Spectrum of Dolaflexin





10

Selected Batch Data



		Batch #						
Attribute	Assay	1	2	3	4	5	6	7
MW (kDa)	SEC	8.3	12.5	10.8	11.2	11.4	9.3	11.3
PDI	SEC	1.3	1.6	1.5	1.4	1.4	1.3	1.4
Drug Load %	NMR	9.4	9.5	9.0	9.1	9.0	9.1	9.0
Free Drug %	LC-MS	0.4	0.7	0.1	0.2	0.2	0.4	0.1
Linker Load %	NMR	2.4	3.5	3.6	3.5	3.8	3.5	3.5

Controlling Dolaflexin Heterogeneity Conclusions

- Heterogeneity in Dolaflexin can be minimized and controlled by:
 - Control of raw material properties (e.g. Dextran MW)
 - Precise control and monitoring of reaction conditions
 - Chromatographic fractionations with established pooling criteria
- Dolaflexin Critical Quality Attributes have shown good batchto-batch reproducibility

Characterization of Dolaflexin ADCs



Dolaflexin-ADC Process



Selected Characterization Test Results

	Attribute	Assay	Result
1	DAR	RP-HPLC	DAR=11-13
2	ADC covalent structure	MALDI-TOF of cross-linked ADC	Verified intact MW of ADC and conjugated polypeptides
3	ADC covalent structure	MSSV (AUC)	Dolaflexin:mAb ~ 3:1
4	ADC covalent structure	Western blot	Verified cross-linking of LC and HC by Dolaflexin
5	ADC covalent structure	Peptide map / MS / MS	Verified correct conjugation sites
6	Secondary structure	Circular dichroism spectroscopy	Verified antibody-like structure, comparable to unconjugated mAb
7	Higher order structure	Disulfide bond mapping	Verified antibody-like SS bond pattern
8	Higher order structure	DSC	Verified ADC has similar thermal stability as mAb
9	Higher order structure	Analytical ultracentrifugation	Confirmed monomeric nature of ADC
10	Biological activity	Biolayer interferometry	Confirmed comparable binding kinetics as mAb
11	Impurities	Free Dolaflexin by HPLC	Dolaflexin not detected

DAR Determination for Dolaflexin ADCs



50 mAb 40 ADC mAu 30 20 10 0 18 22 6 10 14 26 30 Minutes

HIC of a Dolaflexin ADC

 Current HIC method is uninformative with respect to average DAR

RP-HPLC of a Dolaflexin ADC



- AF-HPA cleaved from ADC by base hydrolysis
- Protein and polymer is precipitated
- · AF-HPA concentration is quantitated by RP-HPLC
- DAR is calculated using known molar protein concentration

MALDI-TOF of Chemically Cross-linked ADC Suggests 1-3 Dolaflexins per Antibody



Multisignal Sedimentation Velocity Analysis for Average Dolaflexin:mAb





In collaboration with Peter Schuck, NIH

Dolaflexin-ADCs are Likely Intramolecularly Crosslinked by Dolaflexin



In-Source MS Fragmentation of Dolaflexin



Theoretical Mass (M+H)+	Observed Mass (M+H)+	Mass Accuracy (ppm)
602.2668	602.2660	1.33
803.5641	803.5627	1.74
1105.6755	1105.6757	0.18
728.4957	728.4943	3.28

553.3407





20

Verification of Interchain Cysteine Conjugation Through In-Source Fragmentation of Df Peptides



100

Relative Abundance

0

1130

m/z



- Conjugated peptides containing intrachain cysteines not detected
 - ID and conjugation site verified by MS/MS sequencing (data not shown)

m/z

528.5

527.5

70921

1130.9053 11<u>30.</u>57**27**3 527.2239 707.3004 984.4891 984.240**⊋**=4 100 100 100 z=4 984.7426 1131.2388 z=3 z=4 707.8020 z=2 1130.2362 z=3 527.7253 7=2 1131.5724 z=3 983.9885 984.9905 708.3032 7=2 7=4 z=4 985.4914 1131,9073528.2262 z=4 708.8033 7=2 528.7252 7=2 0 0

985.5

m/z

707

m/z

984.0

1132

Characterization of Dolaflexin ADC Conclusions

- Dolaflexin ADC has high DAR compared to typical DAR=4 ADCs
- ~ 3 Dolaflexins per ADC
- mAb likely intramolecularly cross-linked by Dolaflexin
- Conjugation occurs only at interchain cysteines

Acknowledgements

Analytical

- Dmitry Gumerov
- Susan Clardy
- Kenneth Avocetien
- Mark Nazzaro
- Alex Johnson
- Yuanyuan Li

<u>ADC</u>

- Tim Lowinger
- Mao Yin
- Lei Zhu
- Dorin Toader
- Dan Custer

Dolaflexin

- Michael Kauffman
- Venu Reddy
- Reddy Bollu
- Jacques LeBlanc
- Tom Wagler

Collaborators

• Peter Schuck, NIH

Special thanks to our patients in clinical trials and their families



Thank you!



