

MAM in streamlined biosimilar development

GRx+Biosims meeting, Oct 21 to 23, 2024 Washington DC

Anita Krishnan PhD Associate Vice President Head of Analytical Sciences



Enabling Affordable Access to Lifesaving Biosimilars, Worldwide

Transforming Healthcare. Transforming Lives.

Development considerations of MAM



Conventional methods vis-à-vis MAM

- Enriched variants (stressed/process intermediates) aid in cross-mapping attributes between both formats
- ✓ Two case studies to discuss key development considerations:
 - ✓ CS 1 product with cysteine related modifications (NR-MAM)
 - ✓ CS 2 product with high sialylation (R-MAM)

	Case study 1	Case study 2
cysteinylation	\checkmark	
glutathionylation	\checkmark	
sulfonylation	\checkmark	
DSB scramble	\checkmark	
deamidation	\checkmark	\checkmark
glycation	\checkmark	\checkmark
sialylation	\checkmark	\checkmark
subunit fragments	\checkmark	



	Case study 1	Case study 2
Pyroglutamate	\checkmark	\checkmark
C-term lysine	\checkmark	\checkmark
Met oxidation	\checkmark	\checkmark
Proline amidation	\checkmark	

✓ Key advantages of MAM

- o differentiates overlapping chromatographic species; enables accurate detection/estimation of PTMs
- better relationship mapping of product quality attributes with clinical performance
- **o** better process control of critical quality attributes

Development considerations of MAM – charge variants



Attribute-wise comparison of CEX Vs MAM with US and EU sourced products (n= 3 to 9)



- ✓ Specific acidic and basic species are overlapping in CEX, but more accurately quantifiable in MAM
- ✓ Charge variants elute as per net charge in CEX method and hence PTM estimation is complex
- ✓ Products containing a combination of acidic and basic variants need additional treatments like CpB digestion/desialation in CEX
- $\checkmark~$ US and EU origin products are comparable in both CEX and MAM

Development considerations of MAM – subunit fragments





Fragments (%) 3.0 2.5 CS 1 CM NR MAM 1.5 1.0 0.5 0.0		1H SOFF CPP PAPE	1H1L PPD PAPE	2H	
Diagnostic poptidos					2011
SFNRGEC* and/or GEC*	L	<u> </u>	n L		2011
SC*DK		\checkmark		\checkmark	\checkmark
C*PPC*PAPE		\checkmark	\checkmark		

✓ Non reduced format of MAM is capable of estimating subunit-based fragments through diagnostic peptides

✓ US and EU origin products are comparable in both NR-CE-SDS and MAM

Development considerations of MAM – glycan variants

Attribute-wise comparison of HILIC Vs MAM with US and EU sourced products (n= 3 to 9)





- ✓ MAM is capable of estimating N-glycans in mAbs through the consensus glycopeptide EEQYNSTYR
- ✓ Glycan variants are largely comparable across HILIC and MAM
- ✓ US and EU origin products are comparable in both HILIC and MAM





Confidential and privileged

Transforming Healthcare. Transforming Lives.

Scalability considerations of MAM



Portability of MAM - MS platforms



- ✓ Comparable estimations across instruments and processing software
 - ✓ Orbitrap and TOF
 - ✓ "HRMS" and "MS only" models
 - ✓ Processing software (vendor dependent/independent)

Conclusion



- ✓ New generation instrumentation supports the implementation of MAM throughout the life-cycle of the product, spanning research and quality control labs
- ✓ Conventional methods provide information about combination of modifications; usefulness of this info needs careful evaluation
- ✓ MAM can potentially replace multiple conventional methods such as CEX/cIEF, HILIC, CE-SDS, Identity methods during DS/DP batch release
- ✓ MAM as a technology is aligned to research priorities of FDA's BsUFA III enabling streamlined biosimilar development

Thank you

Anita.krishnan@biocon.com

Confidential and privileged

Transforming Healthcare. Transforming Lives.