

Outcomes from large molecule MS Task force team



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Outlines



- Background
- Scope of application
- Outcomes as Q&A format
- Future perspective

Background

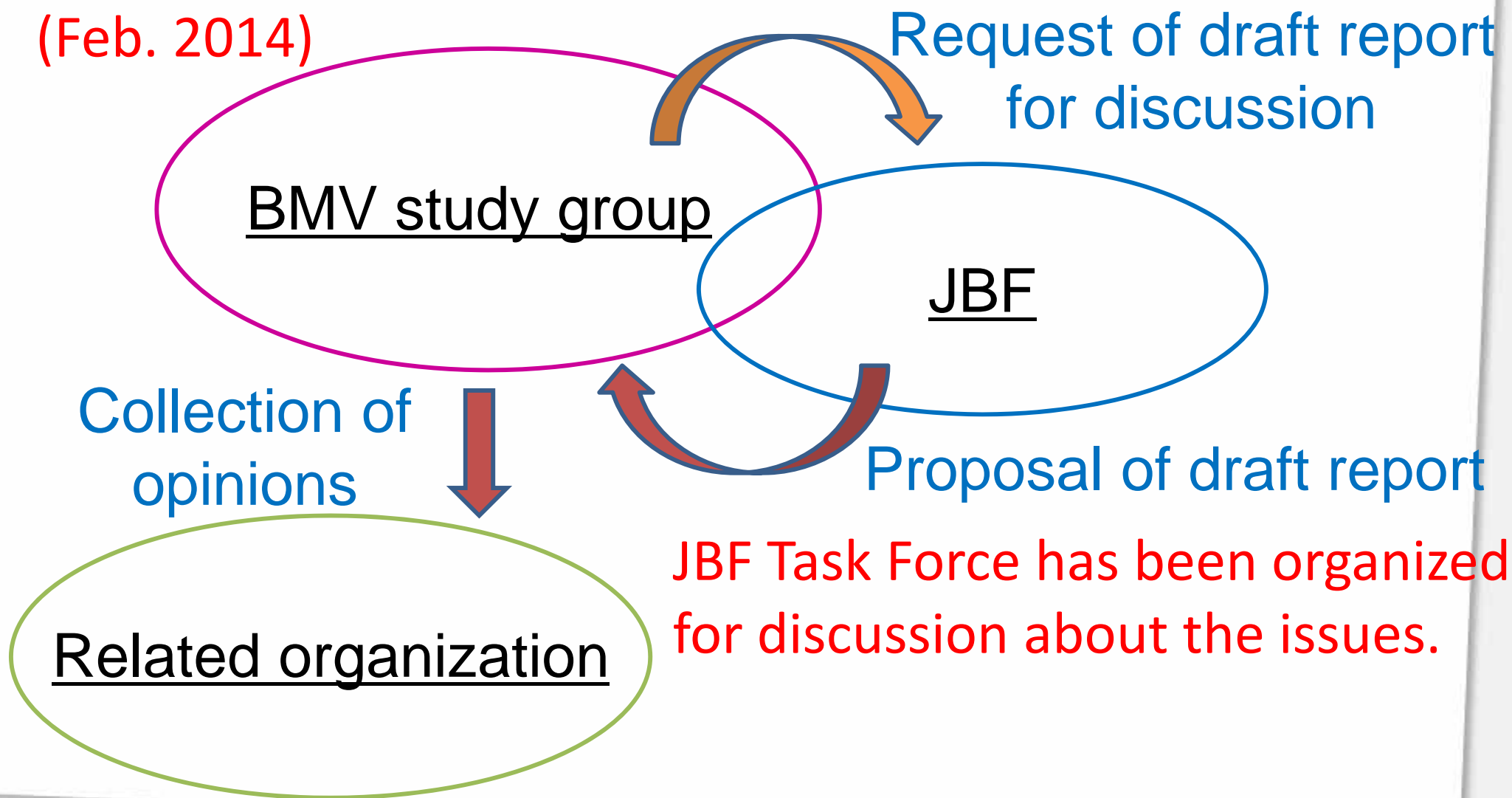


- Recently, large molecules sometimes should be analyzed by LC/MS instead of LBA.
- “Guideline on Bioanalytical Method Validation in Pharmaceutical Development” ([LC guideline](#)) notified in July 2013 by the Ministry of Health, Labour and Welfare
- There are some difficulties to apply the LC guideline directly to the bioanalysis of large molecules using LC methods with **pretreatment of enzymatic digestions or ligand bindings**.

BMV study group and JBF



Kick off Large molecule LC WG
(Feb. 2014)



Activity of JBF Task Force



- Discussion about...
 - ✓ a basic point of view
 - ✓ scope of application
 - ✓ extraction of the point for discussion
 - ✓ format of work product
- Preparation of the work product

Scope of application



- JBF Task Force focused on “Drug”, not endogenous large molecules.

#	Intact	Digested	
	Oligonucleotide, peptide and protein	Peptide	Protein
SIL-IS	Available	Available	Whole protein Digested fragment Flanking peptide
Timing of IS addition	No need for discussion	No need for discussion	Case by case
Pretreatment	· Physical-chemical approach · Use of ligand binding technique	· Physical-chemical approach · Enzymatic digestion · Use of ligand binding technique	
Others	Adsorption, aggregation, use of ion-pair reagents, peak through a column, etc.		

The issues about the pretreatment with enzymatic digestion (including IS matter) or ligand binding technique were extracted for discussion

Work product



- JBF Task Force has aimed to compile a Q&A document on LC guideline for some considerations or recommendations regarding the bioanalysis of large molecules by LC/MS.

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Reference standard



- Biotechnology-derived pharmaceuticals are generally heterogenous.
- Careful attention to the quality of reference standard is required for the change of its lot.
- It is recommended to follow “Guideline on Bioanalytical Method Validation in Pharmaceutical Development” ([LBA guideline](#)).

Critical reagents



In cases where the ligand binding (immunoaffinity capturing) is used for sample pretreatment,

- Expiration or retest date would not be required for critical reagents.
- The evaluation of data from calibration standards and QC samples would be sufficient to confirm the quality of critical reagents throughout the period of use.
- It is recommended to use a single lot of reagent for a batch analysis to avoid the effects of lot-to-lot variation .

Number of measurement for sample analysis



- One measurement ($n=1$) for each sample analysis is usually acceptable.
- The number of measurement should be defined based on the evaluation of precision during assay development and confirmed in validation study.

Internal standard (IS)

- **Stable isotope-labeled (SIL) protein** is ideal to compensate for variations in sample preparation with enzymatic digestion or/and ligand binding technique. However, its synthesis is generally difficult and expensive at this time.
- **SIL-peptide** (digested fragment) and **non-labeled analog proteins** can be used for IS. The difficulty of the correction of digestion efficiency variations by these IS requires the optimization of enzymatic digestion.
- **SIL-flanking peptide IS** could resolve this correction issue.
- It is recommended to add **SIL-peptide IS** after the pretreatment by ligand binding technique. Because the binding activity for ligand would be different between protein and peptide.

Considerations: Enzymatic digestion



- Other (non-target) protein concentrations and types are different between individuals, and change under pathological condition.
 - ✓ Sufficient amount of digestive enzymes should be used in the pretreatment theoretically.
 - ✓ However, that leads to the production of a large amount of impurity peptides from non-target proteins and the further digestion of the target peptide by a small amount of impurity enzymes.

Considerations: Enzymatic digestion



➤ Method development

- ✓ Selection of target peptide(s)
- ✓ Selection of IS type
- ✓ Optimization of digestion conditions
 - Effects of non-target proteins/peptides on digestion efficiency
 - Stabilization of the target peptide(s)

➤ Method validation

- ✓ Use of QC samples with individual matrices
- ✓ Increase of number of individual matrix to confirm the selectivity

Discussion on the criterion for accuracy and precision



- Consensus was reached that there are several cases where the acceptance criteria of LC guideline are difficult to apply for the bioanalysis of large molecule by LC/MS due to the complexity of the assay (enzymatic digestion or affinity capturing etc.).
- There are many discussion about the acceptance criteria for bioanalysis of large molecule by LC/MS. One recommendation was to apply the acceptance criteria of LBA guideline. However, the way to express the criteria is very important not to confuse readers.

Accuracy and precision



- The acceptance criteria should be established in advance based on scientific justification.
- Basic acceptance criteria proposed:
 - ✓ Accuracy: $\leq \pm 20\%$ (at LLOQ; $\leq \pm 25\%$)
 - ✓ Precision: $\leq 20\%$ (at LLOQ; $\leq 25\%$)
- A wider range is thought to be acceptable when an alternative method is not available.

Selectivity



- Selectivity should be evaluated in accordance with [LC guidelines](#).
 - ✓ At least 6 individual sources

- Specificity stated in [LBA guidelines](#) is unnecessary in principle.
 - ✓ LC/MS possess considerably higher selectivity based on the mass-to-charge (m/z) ratios in addition to LC separation.
 - ✓ Complete separation of the target from analogues in pretreatment is not necessarily required.

ISR and Cross validation



- In principle, ISR and cross validation should be conducted in accordance with [LC guidelines](#).
- However, the appropriate criteria (assay variability) should be defined based on the criteria in **the validation study**.

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Future Perspective



- JBF TF has prepared the draft Q&A format regarding the bioanalysis of large molecule by LC/MS.
- However, further discussion with the related organizations is needed to finalize the work product.