Application of ICH Q2/Q14 to Procedure Development and Changes for Monoclonal Antibodies and Gene Therapy Products

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- 1. Method replacement: framework
- 2. Example 1: generic method, residual Protein A ELISA
- 3. Example 2: from ELISA to mass spectrometry for host cell proteins
- 4. Example 3: gene therapy





## **Guidelines on method development, replacement and validation**

Analytical method/procedure lifecycle, from craddle to grave:

- ICH
  - Q14 Analytical Procedure Development
  - Q2(R2) Validation of Analytical Procedure

- PDA:
  - Technical report 57, to be replaced by:
  - BSR-PDA Standard 07 Analytical Method Qualification-Validation for Biologic V22 05-01-2024 | PDA

• Note:

The strategy around method replacement is sometimes called « bridging »

One of Rotterdam iconic bridges, Erasmusbrug:





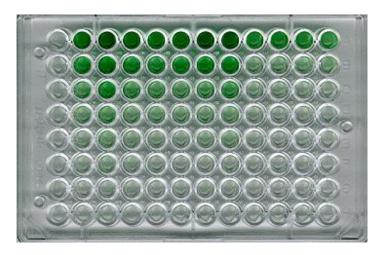
# Application of ICH Q2(R2)/Q14 to an ELISA procedure

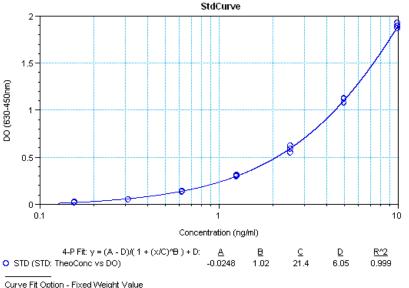


## Change to an analytical procedure or change of analytical procedure?

#### From an ELISA to an ELISA procedure

- Protein A is a ligand used in certain downstream processes to capture the active (=an antibody)
- This ligand might leach into the drug substance
- ELISA is routinely used to quantify residual protein A



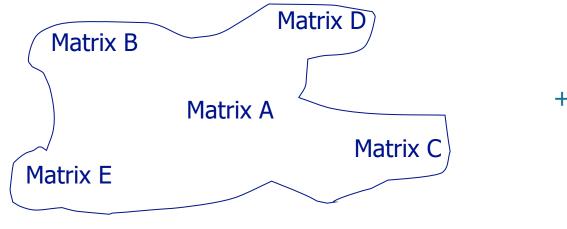


- Analytical target profile:
  - Quantification limit = 240 ng/mL drug substance
  - Maximum allowable variability = 60% total error on reportable result

## Change to an analytical procedure or change of analytical procedure?

#### From an ELISA to an ELISA procedure

- 5 validations exercises demonstrate that for a variety of antibodies and formulations (="Matrices"), the method is fit
- Applying the method for a new antibody is, analytically speaking, a change to the method, ie, a change in sample
- How should we formulate the question of the validity of the method to a new type of sample?



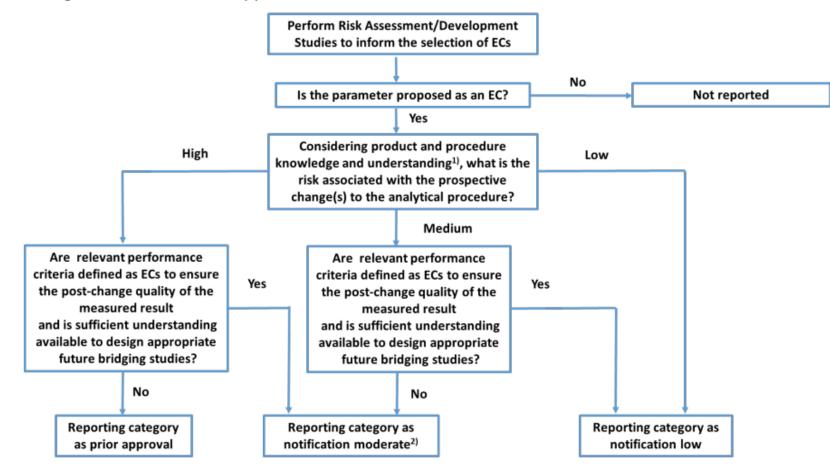
+ Matrix E = ? Valid or Not?

Validated space



## Is it a change within a method, as per ICH Q14?

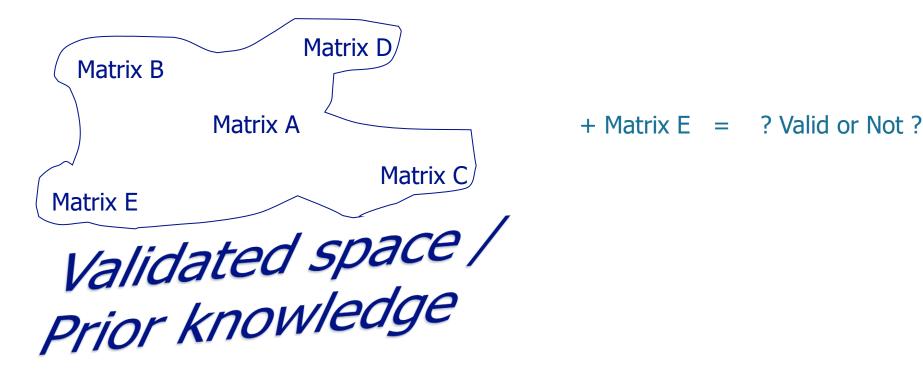
**Figure 2:** Risk-based approach for identification of ECs and reporting categories for associated changes in the enhanced approach



Inspired by patients. Driven by science.

# Is it the use of prior knowledge within ICH Q2(R2)?

- 5 validations exercises demonstrate that for a variety of antibodies and formulations (="Matrices"), the method is fit
- The validity of the method for a new antibody is, by applying ICH Q2(R2), an evaluation of prior knowledge, if justified





#### ICH Q2(R2) Guideline

#### Figure 1: Validation study design and evaluation

• Objectives/performance characteristics • Analytical procedure lifecycle • Analytical procedure management • Appropriate development data • Prior knowledge ICH Q14 ICH Q2 Validation protocol Validation report Validation strategy: Document validation results and data: • Evaluation of prior knowledge, • Evaluation against acceptance criteria including available development or or parameter ranges validation data with justification · Conclusions and acceptance of Additional experiments and evaluation analytical procedure performance ٠ according to ICH Q2 methodology or alternative approach with justification

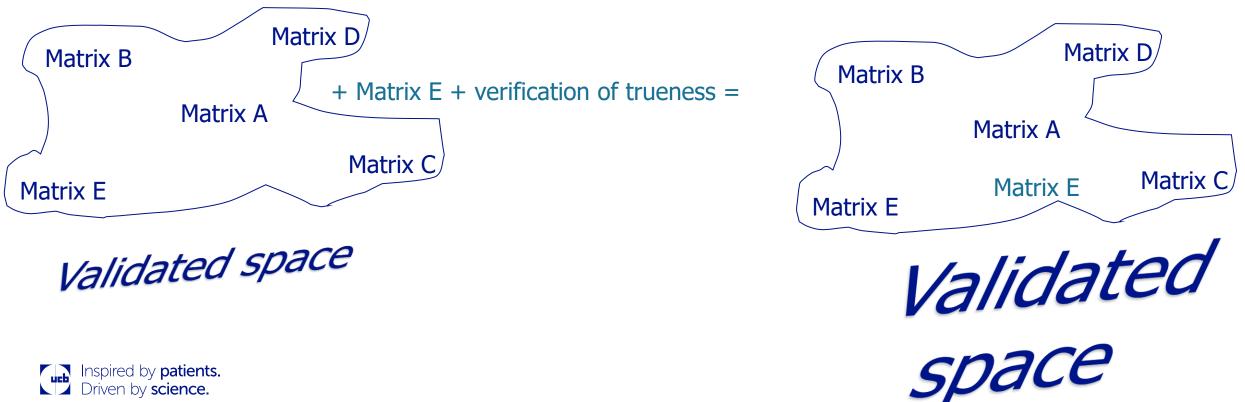


Validation tests and/or evaluation of data

# Change to an analytical procedure or change of analytical procedure

#### From ELISA to ELISA

- Considering the procedure knowledge, the risk linked to the prospective change (ie, analyzing in Matrix E) is considered low
- The only risk is an interference of the matrix, eg, aspecific interaction between the antibody and protein A
  - Trueness is therefore verified by spiking one sample of antibody and protein A



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# Change from an ELISA to a mass spectrometry procedure

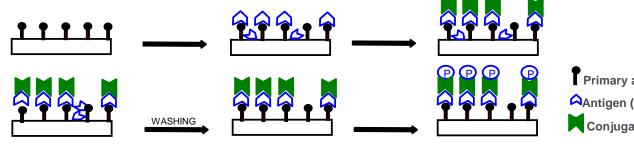


## A more drastic change: From ELISA to mass spectrometry for the quantification of HCP

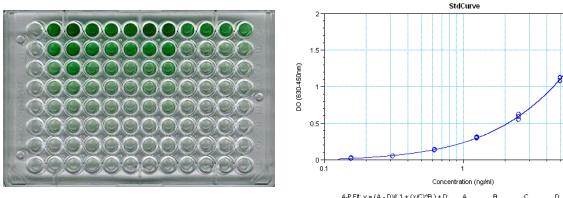
- Host cell proteins: process-related impurities, produced by the CHO or *Escherichia coli* cells
- Residual quantity of host cell proteins has to be controlled at, eg, DS level
- Current gold standard for the quantification of the host cell proteins: ELISA







Primary antibody
Antigen (eg HCP)
Conjugated secondary antibody



# Concentration (ng/ml) 4-P Fit: y = (A - D)/(1 + (x/C)^B) + D: A B C D R^2 O STD (STD: TheoConc vs DO) -0.0248 1.02 21.4 6.05 0.999 Curve Fit Option - Fixed Weight Value

# **To: Mass spectrometry**





## Change to an analytical procedure or change of analytical procedure?

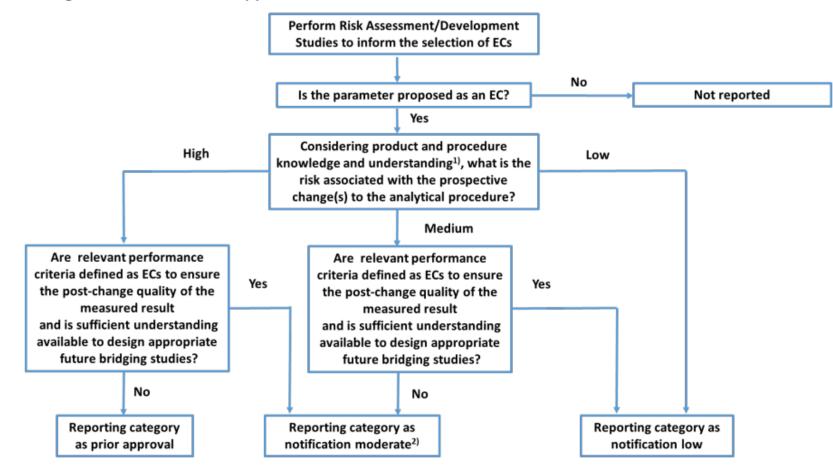
#### From ELISA to... mass spectrometry

- ELISA is routinely used to quantify host cell proteins
- Mass spectrometry is being validated for the same goal, same ATP
- Analytical target profile:
  - Quantification limit = ng/mL drug substance
  - Maximum allowable variability = 60% total error on reportable result
- How can the enhanced approach facilitate switching from ELISA to MS?
- "Changes to analytical procedures can occur throughout the product lifecycle and could involve modification of existing procedures or a complete replacement including introduction of a new technology." (ICH Q14, chapter 7)



## Is it a change between methods, as per ICH Q14?

**Figure 2:** Risk-based approach for identification of ECs and reporting categories for associated changes in the enhanced approach

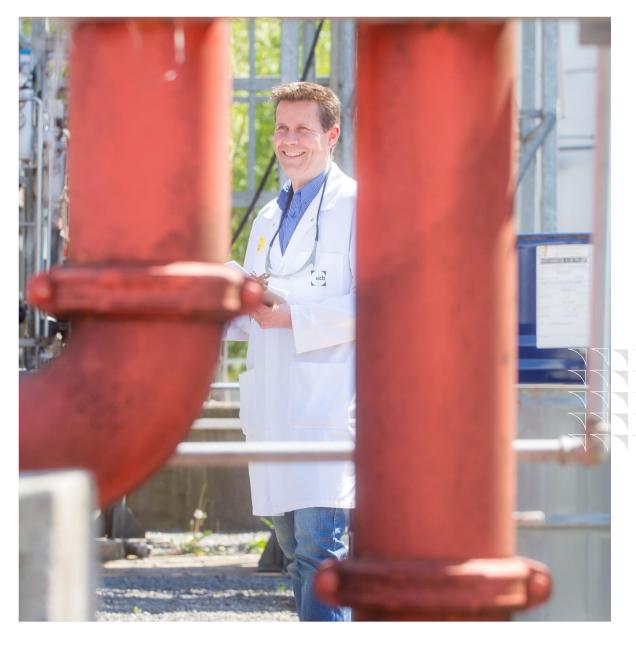


## Change to an analytical procedure or change of analytical procedure

#### From ELISA to... mass spectrometry

- Mass spectrometry has several advantages to control the quality of the product
  - It does not rely on recognition of HCP by antibodies
  - It is a physicochemical method rather than immunochemical method
  - It allows the identification of individual HCPs
- But the change is very drastic:
  - Established Conditions helps changes within one technology (from ELISA to ELISA, eg, dilutions of samples)
  - Could the thinking of EC help if we change from ELISA to MS? The set conditions themselves drastically change
- Are we doomed to bridge the two methods although the scientific expectation is that it will be a comparison between apples and pears?



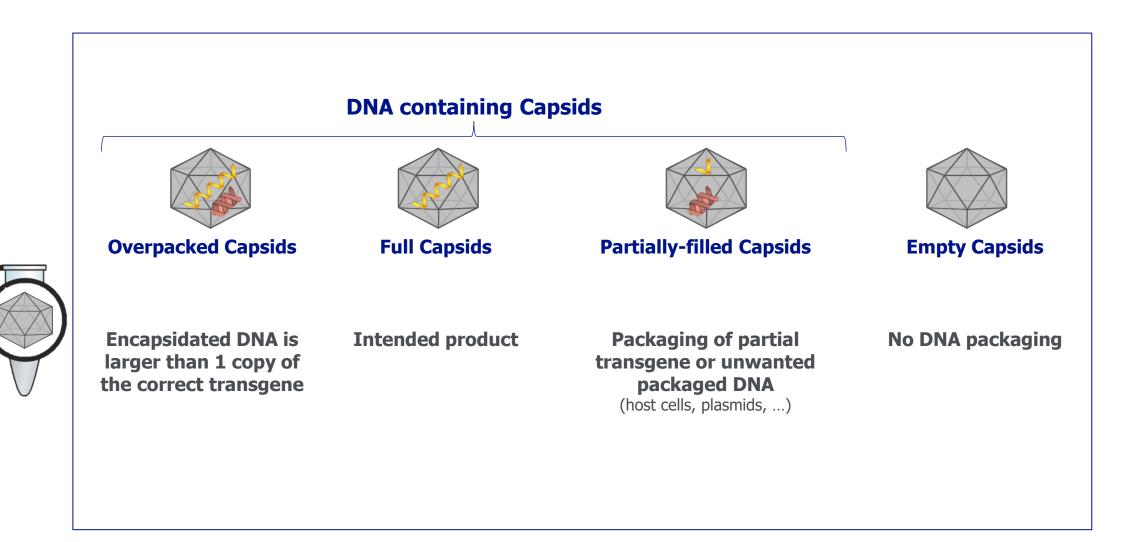


## Enhanced approach for rAAV capsid content variants by SEC-MALS

## Michel Degueldre



## rAAV capsid content variants in CMC

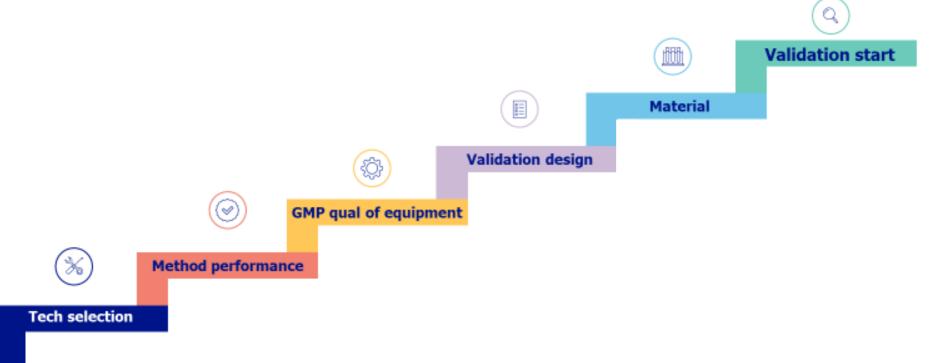


AAV Empty Capsids: For Better or for Worse?, Molecular Therapy, 2014 Inspired by patients. Gimpel et al. Molecular Therapy, Methods and Clinical Development, Vol 20, March 2021 Drivers by science. DHC White Paper i(Jan 2023) n public consultation untill April 2023

British Pharmacopoeia: Advanced Therapy Medicinal Products Guidance Characterisation of the Capsid Particle Population in rAAV Products. https://www.pharmacopoeia.com/download/document/atmpguidance. Optimizing AAV analytics to improve the safety, efficacy, and yield of AAV-based gene therapies. In: Alliance for Regenerative Medicine. https://alliancerm.org/indication-data/optimizing-aav-analytics/.

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# **Analytical tools in the GT landscape**

DS/DP release and stab testing – Top most used techniques

Vg/capsid titer ratio (PCR/ELISA)



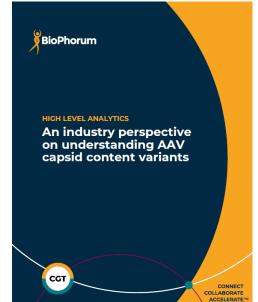








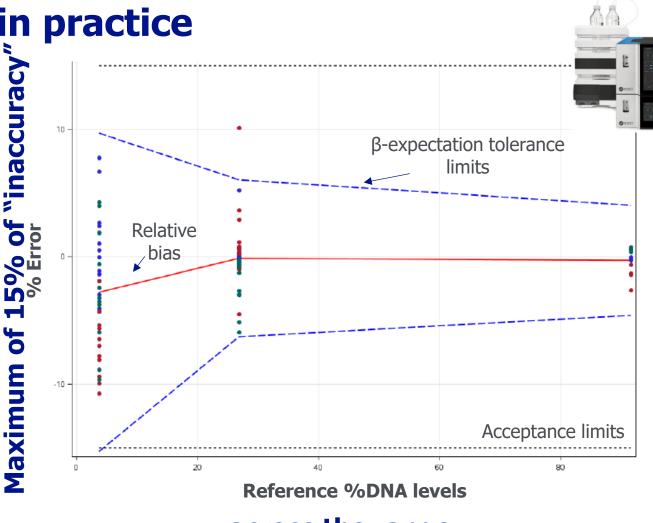
- AUC has software that is a P1CFR Part 11 compliant "Workarounds" are required to meet heli authorities' expectations.
- PCR/ELISA approach relies on two different methods to get a ratio eventually
  - Inherent variability of each ethod
  - It might not suit it founded use; lack of precision.
- AEX separation is sensitive to the change of negative charge state of the sample - it is velopment might be necessary for any transgeree and/or serotype changes.
- → SEC-MALS was selected
- ✓ E2E vision pre-tox up to clinic
- ✓ CMC Acceleration



# **Method prevalidation – TAE in practice**

#### SEC-MALS

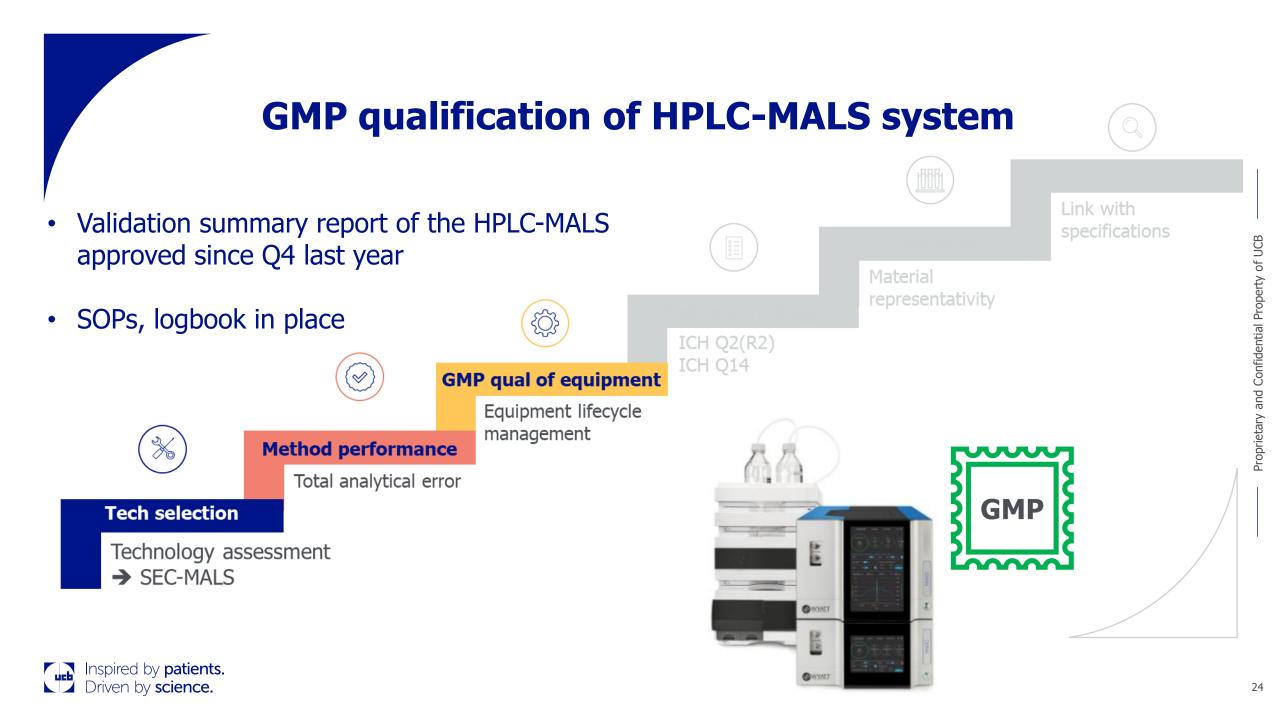
- 3 levels of %DNA containing capsid
- Linearity / precision / trueness assessment assessed based on TAE profile

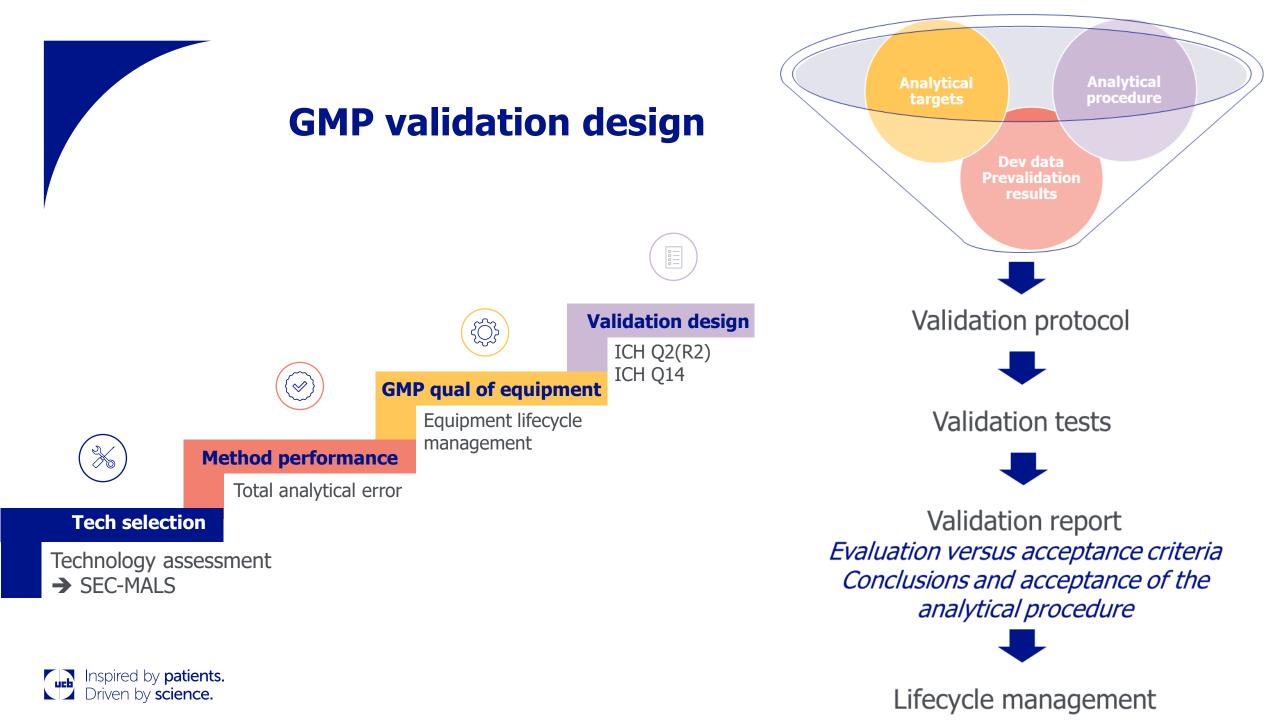


across the range [4;92]% of DNA containing capsid



Proprietary and Confidential Property of UCB





# The specification range

#### A question of quality (and variability) – DS/DP – Product variant species

Release limits are expected to be tighter than the shelf-life limits as the proportion of full capsid species might decrease in stability study

The method still needs to be proved to be stability-indicating %DNA containing capsid is considered as a purity parameter, therefore:

TAE	Range of method validation
Error on the measurement	Variability of the process manufacturing Minimal range of release limits
<b>4</b>	Stability
	Range extension for (lower) shelf-life lim

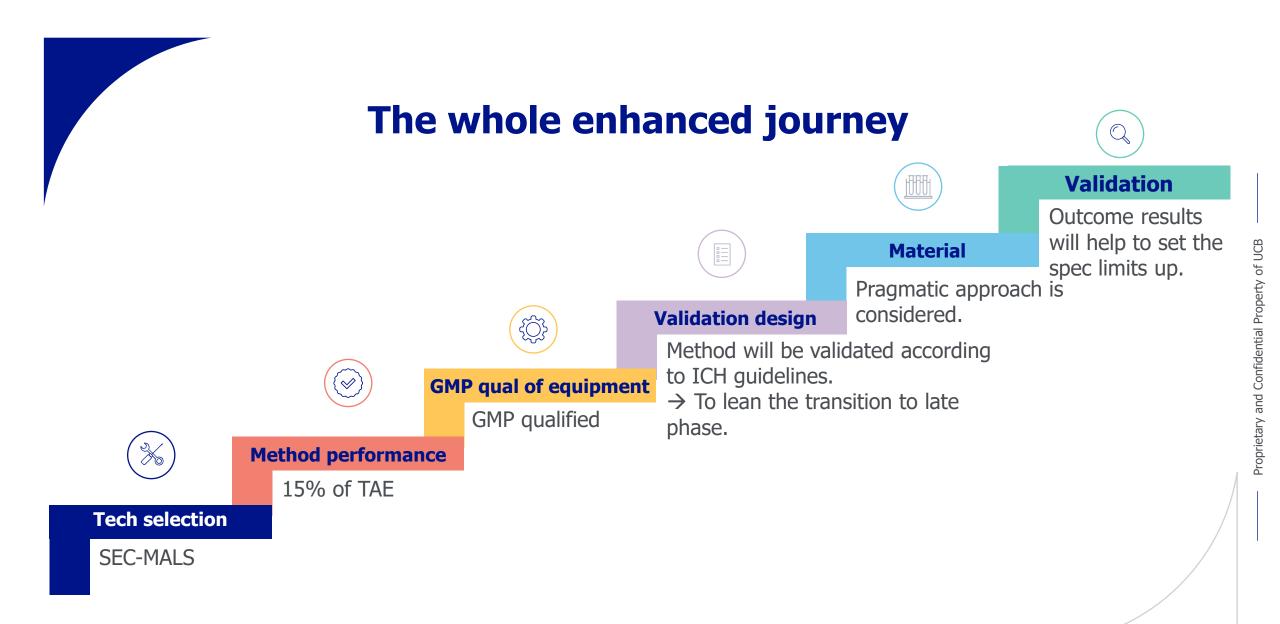
Limits setting of the attribute "%DNA containing capsid by SEC-MALS" is challenging in early phase because of limited knowledge of the product/platform

Specifications and limits are chosen to confirm product quality, here drug efficacy

 $\rightarrow$  Notion of stability-indicating profile to be built through product lifecycle/development

Inspired by **patients.** Driven by **science**. <u>Q1A(R2) Guideline.pdf (ich.org)</u>





## Conclusions

- ICH Q2(R2) and Q14 give a reasonable frame to method development and validation
- Use of prior knowledge for development and validation is a huge advantage to get more robust methods
- Method replacement, ie, replacing one technology by another for a certain quality attribute, is still seeking its way...

## **Acknowledgments**

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- Gene Therapy Process and Analytical Sciences
- Biological Method Development
- Physico-Chemical Analytics







