



# EBF consideration for NAb assay development and design with emphasis on matrix, sensitivity and sample pre-treatment

Anna Laurén – on behalf of the EBF NAb project team



### Objective

- ➤ In the recent year, the EBF team for neutralising antibody assays (NAb) has focused on discussing assay constraints for a successful NAb assay
- ➤ Aim has been to create a reality check across industry based on team experiences what makes a sufficiently good NAb assay:
  - Assay formats
  - NAb negative control pool matrix and individual samples
  - Reflection on theoretical assay sensitivity
  - Ways to solve serum interference and drug interference by sample pre-treatment
- ➤ Experience built on ~25 cases from the NAb expert team

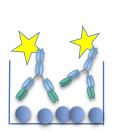


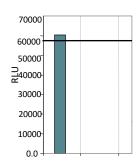
# NAb assay competitive ligand binding assay (CLBA)

Example: CLBA for Mab-Drug with soluble target\*

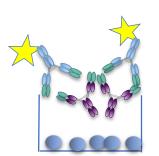
Target coated on plate

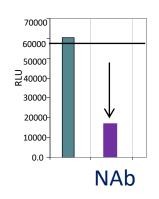
Binding of labeled drug yields high assay signal:

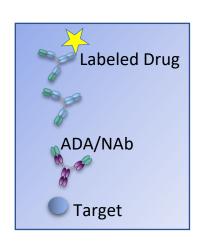




#### Signal decrease by NAb:







+ sequential protocol might be beneficial

<sup>\*</sup>opposite set up (drug coated + read out via labeled target)

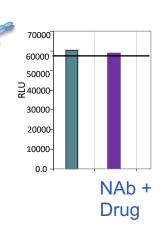


# **CLBA Drug and Target Interference**

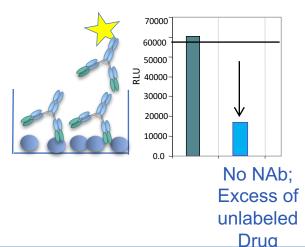
Example: CLB for Mab-Drug with soluble target

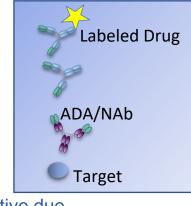
- Target coated on plate
- Consider optimal protocol and coating for each project

Case a):
False negative due
to "Drug on Board":

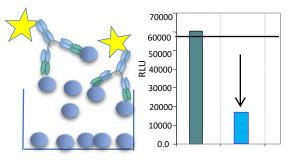


Case b):
False positive due
to "Drug on Board":





Case c): False positive due to Target Interference

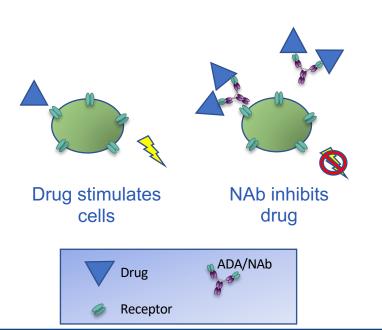


No NAb; interference of soluble target



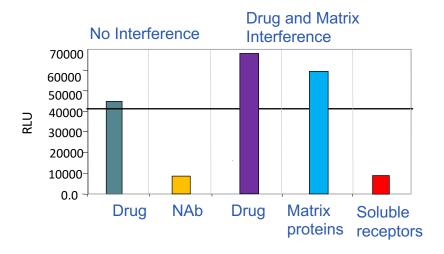
# Direct Cell based assay (CBA) for agonistic Drug

- Stimulation by drug yields high signal
- Nab againts drug yields low signal



Drug and matrix interference and increase assay signal:

- false negativeSoluble receptors may decrease assay signal
- false positive





# Indirect CBA for antagonistic Drugs

- Stimulation by target yields high assay signal
- Nab againts drug yields high assay signal

Target stimulates cells

Drug inhibits target

NAb inhibits drug

ADA/NAb

Ligand

Drug

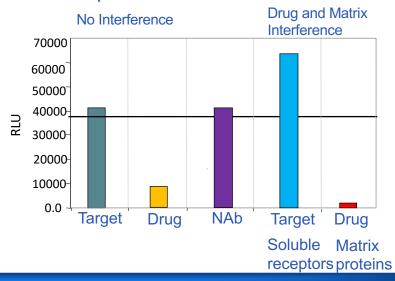
Receptor

Drug/matrix interference may decrease assay signal:

false negative

Target interference/soluble receptors increase assay signal:

false positive





# How can the matrix influence your NAb assay?

- ➤ Cell based assays (CBA)
  - Endogenous toxicity can kill cells: example Complement system can kill cells – reduced signal
- ➤ Cell based assays (CBA) and Competitive ligand binding assay (CLBA)
  - Higher variability of assay signals at low MRDs
  - Circulating target can interfere with drug-target-PC interaction
  - Circulating natural antagonist can inhibit target
  - Concomitant medication can interfere in the assay system



# Selection of matrix pool during assay development

#### Experiences from the NAb team

- ➤ Most frequent matrix: Serum
- NC matrix pool based on healthy individuals (majority of cases)
- ➤ If endogenous proteins influence assay signal: establish a pool from target population (when available)
- > Screen individuals in the NAb assay before pooling and remove outliers
- Include 6-50 individuals in the NC matrix pool
  - Better to use a higher number of samples to minimise variability when bridging with new pool



# Establishment of cut-point (CP)

- Validation
  - ✓ In majority of cases the individuals representative of study population were used for CP (~30 individuals)
  - ✓ Healthy matrix individuals were used when assay was included already in Phase 1 or when the target population was rare
- ➤ In Study:
  - ✓ Establish communication with clinical teams for early sample analysis for CP
  - ✓ In study CP shall be assessed with ADA negative pre-dose samples
  - ✓ For high risk project: In study CP should be determined as soon as the first 30 individuals were screened and included in the study



### Bridging of new matrix pool

- ➤ Experience with matrix pool based on at least 10-20 individuals gives less variance between pools
- > Two alternatives exists from the team experience:
- ➤ Alternative 1: Bridging is most common
  - Comparing to old acceptance criteria
  - Statistical comparison of old and new pool, adjustment of CP in case of difference
  - Performed by 7 out of 9 companies
- ➤ Alternative 2: No Bridging in rare cases
  - Re-validate the CP was done by 2 out of 9 companies
- Scientific justification should be done by company



# Theoretical sensitivity in cell based assays

- > A theoretical sensitivity can be calculated based on below information
- ➤ When selecting the cell line during assay development the following is important to consider:
  - Concentration of drug and ligand in the linear assay range
  - Molecular weight of the drug
  - MRD of the sample
- Another important factor: Selection of PC and how it would compete with drug to drug target
  - Consider epitope binding and affinity for PC to drug and receptor
- > Already available potency assays may be un-relevant
  - Concentration of drug used in potency assays may be to high
  - Matrix interference unknown Potency assays are developed with drug in buffer



### How to calculate theoretical sensitivity

- Concentration of drug used for stimulating the cells is converted to a molar concentration
- > Concentration of antibody is converted to a molar concentration
- > Assumption, 1 antibody can bind 2 drugs and will give 100% Neutralisation
- > Example:
  - 1) Drug X: 20 kDA
  - 2) MRD 20
  - 3) Control Ab: 150kDa
  - 4) 25 ng/ml drug @ 20kDa = 1.25nM drug in well with cells
  - 5) 1.25nM/2 = **0.625nM** Ab can neutralise drug fully in well with cells
  - 6) 0.625nM Ab x MRD = **1875ng/ml Ab in sample** = Theoretical sensitivity



# Theoretical sensitivity gives an estimate on how good the assay can be

Examples from cell based assays with no sample pre-treatment

Drug	Drug concentration for stimulation (ng/mL)	Molecular weight (kD)	MRD	Theoretical sensitivity (ng/mL)	Actual sensitivity (ng/mL)	Type of PC
Α	25	20	20	1875	330	mAb
В	840	20	4	12600	- unknown	affinity pAb
С	0.25	20	100	94	277	affinity pAb
D	0.04	15	20	4	28	mAb
E	0.035	20	10	0.0013	130	mAb
F	0.9	30	20	45	70	mAb
G	1.5	30	20	75	122	mAb
Н	3.5	30	14	126	150	mAb
	2.5	30	17	115	85	mAb
J	0.4	4	4	30	500	mAb
K	0.13	4	4	5	15	mAb
L	6	4	2	225	3000	affinity pAb



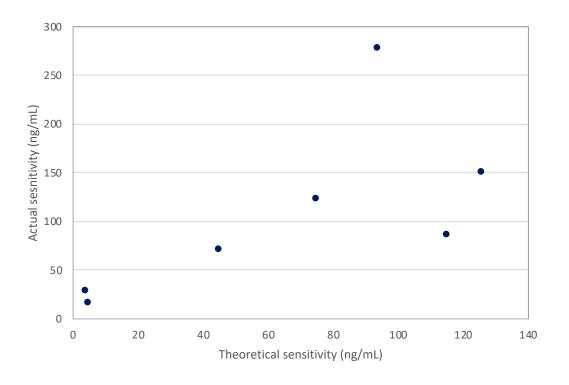
# Reasonable correlation between Theoretical and Actual sensitivity in 7 out of 12 assays

Theoretical sensitivity (ng/mL)	Actual sensitivity (ng/mL)	Type of PC	
94	277	affinity pAb	
4	28	mAb	
45	70	mAb	
75	122	mAb	
126	150	mAb	
115	85	mAb	
5	15	mAb	
*12600*	- unknown	affinity pAb	
*1875*	330	mAb	
*0.0013*	130	mAb	
225	*3000*	affinity pAb	

<sup>\*</sup> outlier

Reasonable indication

No indication





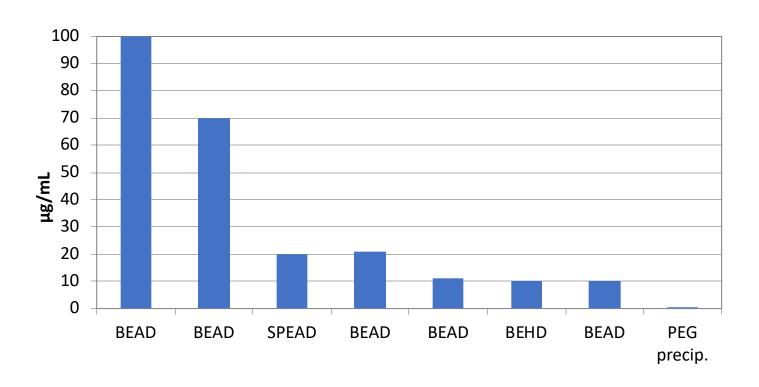
# Sample Pre-treatment, Matrix and Drug Tolerance

- > Residual drug tolerance issues in NAbs is a common problem
- > Can lead to false negatives as well as false positives
- > Investigate both NC and PC (at least LPC) spiked with drug at Cmin
  - Add additional drug and PC concentrations if relevant
- ➤ If sufficient DT cannot be achieved, then a number of pre-treatments can be tested to address this including;
  - SPEAD, BEAD, acid dissociation, PEG precipitation, ACE etc
  - References given in back-up slides



# Typical Drug Tolerance levels achieved using Sample Pre-Treatment in CBA Nabs

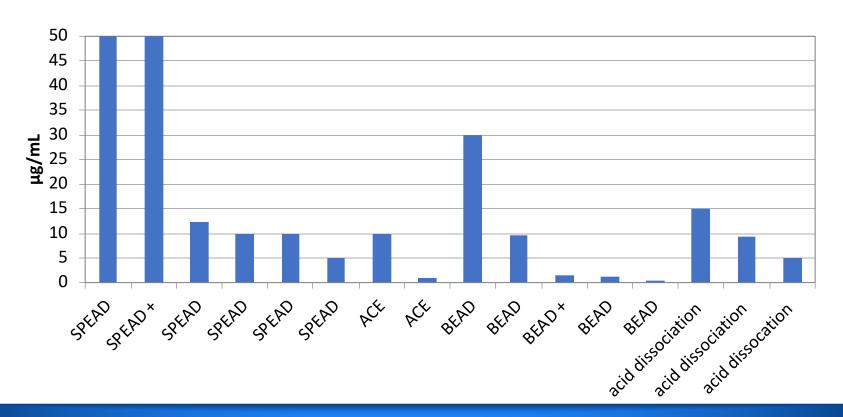
- 1 outlier removed





# Typical Drug Tolerance levels achieved using Sample Pre-Treatment in CLBA Nabs

- 1 outlier removed





# Typical Data observed after Sample Pre-Treatment

#### Cell based NAbs;

- $\triangleright$  6 out the 9 examples (67%) have DT of  $\sim$  0.5 20  $\mu$ g / mL
- > DT > 30 μg/mL can be reached in a rare cases (3 out of 9)

#### CLBA based NAbs;

- > 13 out the 17 examples (76%) have DT of ~ 0.5 20 μg / mL
- > DT > 30 μg/mL can be reached in a rare cases (4 out of 17)



### Summary

- Matrix can impact outcome of NAb assay performance
  - Screen to select a suitable serum pool
  - New matrix should be bridged (when possible) with no need to re-establish
     CP
- ➤ Estimates of theoretical sensitivity can be used to understand if available cells are feasible to use for a NAb assay
- NAb assays can have problems with interference from matrix and drug in samples
  - Interference can give both false positive and false negative NAb results
  - Assay design and sample pre-treatment can be used to minimise interference
  - Sample pre-treatment have worked successfully in both CBA and CLBA



### Acknowledgment

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- Lead: Anna Laurén Svar Life Science
- > Team members:
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     Novo Nordisk
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  - Per Holse Mygind Ascendis Pharma
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  - Marcel van der Linden Genmab
- > Team Sponsor: Tobias Haslberger Abbvie



# Thank you and time for questions





# **Contact Information**

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**EBF** European Bioanalysis Forum vzw

www.e-b-f.eu



# Back-up References pre-treatment in ADA/NAb assays

- Acid dissociation: Patton A et al. An acid dissociation bridging ELISA for detection of antibodies directed against therapeutic proteins in the presence of antigen. Journal of immunological methods. 2005;304(1-2):189-95.
- > SPEAD: Smith HW et al. Detection of antibodies against therapeutic proteins in the presence of residual therapeutic protein using a solid-phase extraction with acid dissociation (SPEAD) sample treatment prior to ELISA. Regulatory Toxicology and Pharmacology. 2007;49(3):230-7.
- ➤ ACE: Bourdage JS et al. An affinity capture elution (ACE) assay for detection of anti-drug antibody to monoclonal antibody therapeutics in the presence of high levels of drug. Journal of immunological methods. 2007;327(1-2):10-7.
- Acid dissociation and affinity adsorption by agarose beads: Lofgren JA, Wala I, Koren E, Swanson SJ, Jing S. Detection of neutralizing anti-therapeutic protein antibodies in serum or plasma samples containing high levels of the therapeutic protein. Journal of immunological methods. 2006;308(1-2):101-8
- ➢ BEAD: Niu H et al. A biotin-drug extraction and acid dissociation (BEAD) procedure to eliminate matrix and drug interference in a protein complex anti-drug antibody (ADA) isotype specific assay. J Immunol Methods. 2017 Jul;446:30-36
- ➤ BEHD: Xu W et al. Bead-extraction and heat-dissociation (BEHD): A novel way to overcome drug and matrix interference in immunogenicity testing. J Immunol Methods. 2018 Nov; 462, 34-41
- PandA: Zoghbi J, et al, A breakthrough novel method to resolve the drug and target interference problem in immunogenicity assays. J Immunol Methods. 2015 Nov;426:62-9.
- > Target competition: Sloan JH, et al. An innovative and highly drug-tolerant approach for detecting neutralizing antibodies directed to therapeutic antibodies. 2016, Bioanalysis Vol. 8
- PEG precipition: Unpublished data using PEG without acid