

An international multi-center serum protein electrophoresis accuracy and M-protein isotyping study.

Part I: Factors impacting LoQ

Part II: LoD and follow-up of small M-proteins

**SKML nabesprekking sectie Humorale Immunologie
13 Februari 2020**

Joannes (Hans) F.M. Jacobs, M.D. Ph.D.
Radboud University Medical Center
Department of Laboratory Medicine
Nijmegen, The Netherlands



Radboudumc

IFCC* Harmonization of Reporting Strategies Working Group





- Shared serum sample set
- Run along-side patient samples
- According to their institution's SOP (standard operating procedure) for SPEP and IFE
- Total protein was measured and provided by Mayo (Reverse Biuret, Advia 1200)

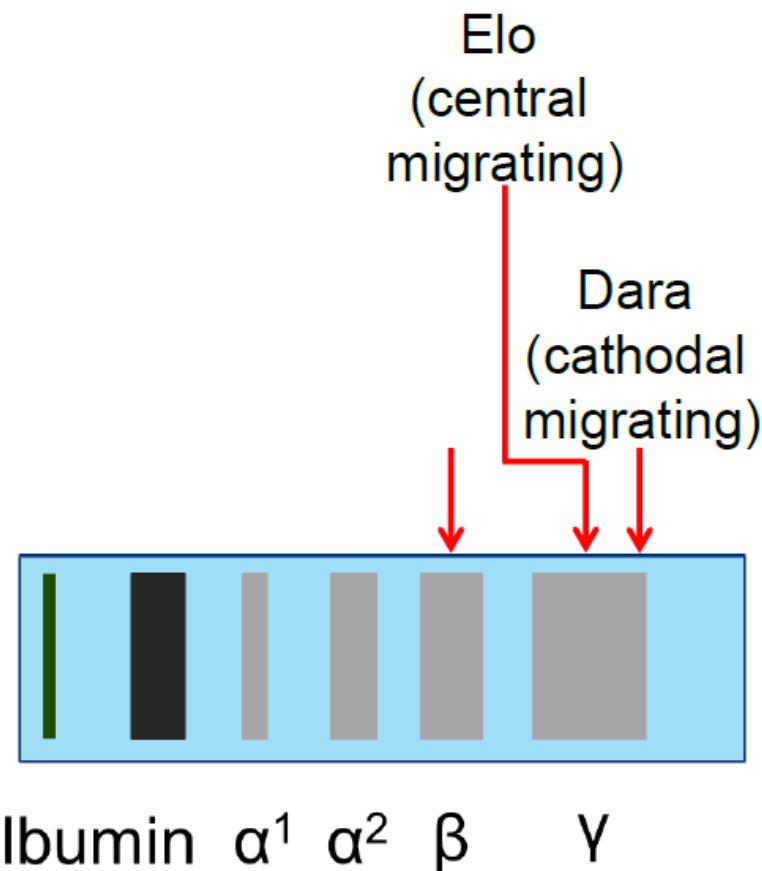
**>3,000
Blinded
Aliquots**



Blinded Shared Sample Set

Artificial “patient” samples containing a M-protein

- Pooled patient samples (~120 mL each)
- Gamma Fraction Background
 - Hypogamma background
 - < 0.5 g/dL
 - Normal gamma background
 - 0.6-1.5 g/dL
 - Hypergamma background
 - > 1.7 g/dL
- Monoclonal antibody (mAb)-spiked samples
 - 1.0-0.0125 g/dL
 - Elotuzumab (Elo)
 - Daratumumab (Dara)
 - IgG1 κ isotype
- Beta-migrating-pooled patient samples





LOQ Studies Home

Pathology Queensland, QLD

Hunter Area Pathology Service

Royal Prince Alfred Hospital

Royal Melbourne Hospital

University Hospital of Padova

Recycle Bin

EDIT LINKS

Group Announcements

[+ new announcement or edit this list](#)

Title Body

Open in Internet Explorer

... Just a reminder that SharePoint will work best if opened in Internet Explorer. We've encountered problems when trying to open SharePoint and submit forms using Chrome.

Milestones

November 2017 December 2017 January 2018 February 2018 March 2018 April 2018

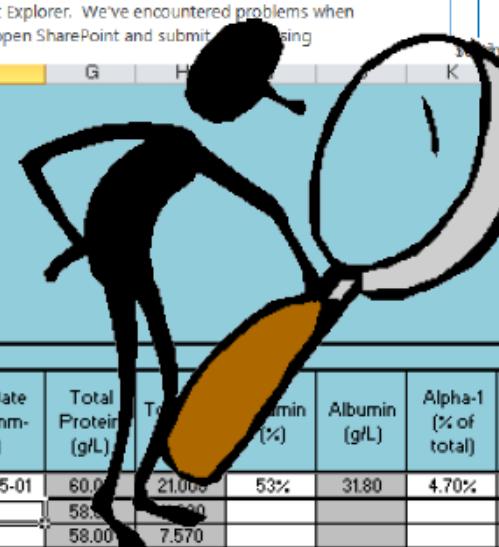


Testing Site Information

Institution Name	RBWH Chem Path
Contact Person Name	Anfernee Tseng
Contact Person E-mail	anfernee.tseng@health.qld.gov.au
Analysis Method	Capillary Electrophoresis
Product Manufacturer & Commercial Name	Sebia CAPI3
Unit of Measure	g/L

Result Entry

	Run ID	Sample ID	Expected Isotype	Run Date (yyyy-mm-dd)	Total Protein (g/L)	Total albumin (%)	Albumin (g/L)	Alpha-1 (% of total)	Alpha-1 (g/L)	Alpha-2 (% of total)	Alpha-2 (g/L)	Beta1 (% of total)	Beta1 (g/L)	Abnormality in beta fraction?	Beta M-spike (% of total)	Beta M-spike (g/L)	
11	EXAMPLE	IFCC-0	IgG kappa	2017-05-01	60.00	21.000	53%	31.80	4.70%	2.82	11.20%	6.72	7.20%	4.32	None	0.00%	0.00
12	Run 1	IFCC-1	IgG kappa		58.00	20.00											
13	Run 1	IFCC-2	IgG kappa		58.00	7.570											
14	Run 1	IFCC-3	IgG kappa		82.00	24.700											
15	Run 1	IFCC-4	IgG kappa		49.00	10.400											
16	Run 1	IFCC-5	IgG kappa		79.00	22.900											
17	Run 1	IFCC-6	IgG kappa		39.00	12.200											
18	Run 1	IFCC-7	IgG kappa		75.00	13.100											
19	Run 1	IFCC-8	IgG kappa		47.00	12.100											
20	Run 1	IFCC-9	IgG kappa		47.00	8.020											
21	Run 1	IFCC-10	IgG kappa		55.00	5.340											
22	Run 1	IFCC-11	IgG kappa		57.00	10.500											
23	Run 1	IFCC-12	IgG kappa		51.00	5.160											
24	Run 1	IFCC-13	IgG kappa		80.00	22.600											
25	Run 1	IFCC-14	IgG kappa		53.00	8.610											
26	Run 1	IFCC-15	IgG kappa		79.00	21.700											
27	Run 1	IFCC-16	IgG kappa		70.00	20.300											
28	Run 1	IFCC-17	IgG kappa		57.00	8.570											
29	Run 1	IFCC-18	IgG kappa		43.00	11.400											
30	Run 1	IFCC-19	IgG kappa		81.00	25.500											



Methodology Distribution

SPEP Method	Number of Institutions
Helena AGE	4
Sebia AGE	5
Sebia CZE	10

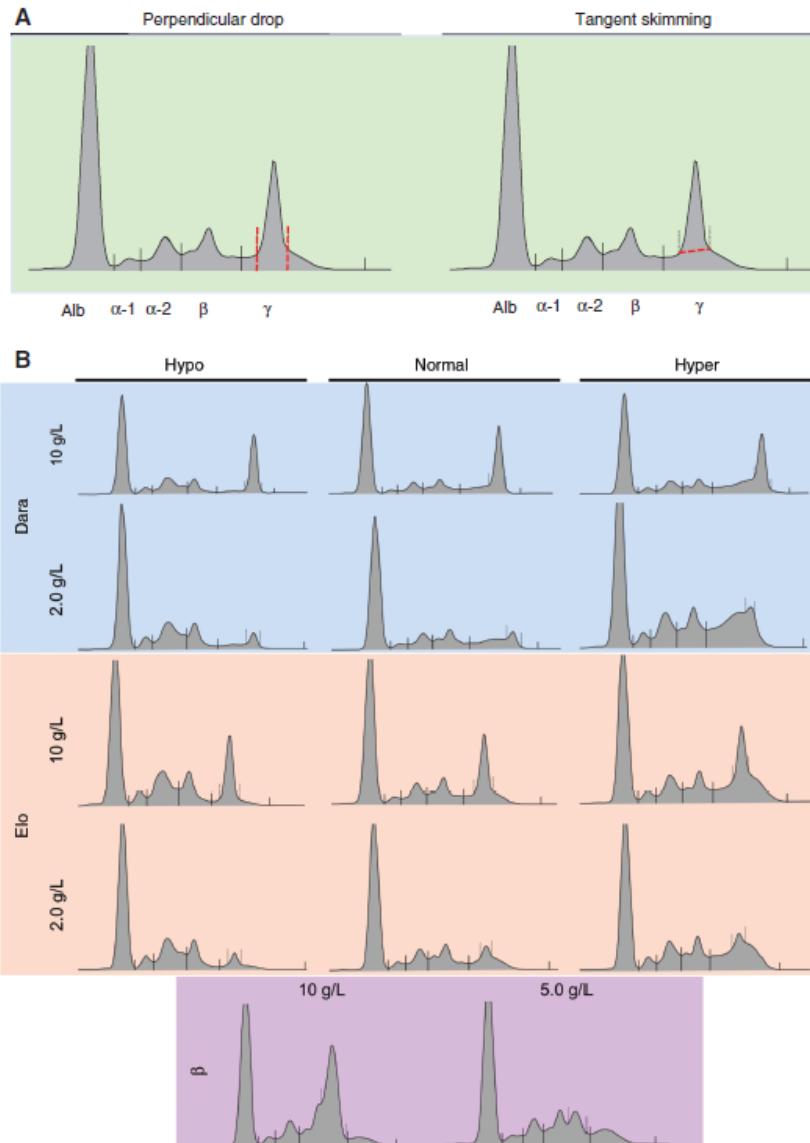
IFE Method	Number of Institutions
Monovalent Antisera	11
Pentavalent Antisera	2
Immunosubtraction	3

*Note: Some institutions provided ≥ 1 method

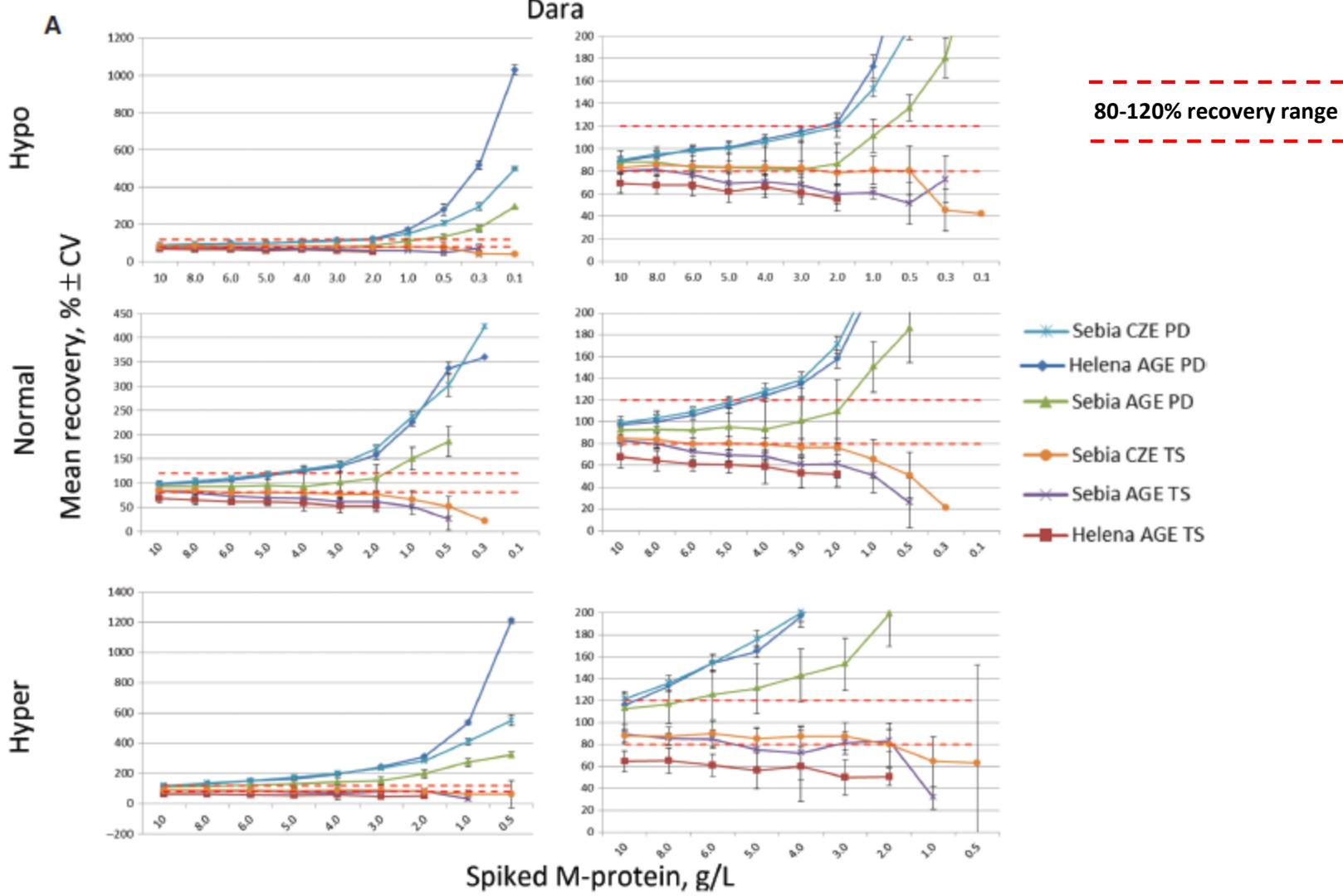
Table 1: Institutions' methodology distribution for serum protein electrophoresis and immunofixation/immunosubtraction.

	North America	Europe	Australia
SPEP			
Helena AGE			
PD			
Primary	1	1	1
Supplemental	-	-	1
TS			
Primary	-	-	-
Supplemental	-	-	1
Sebia AGE			
PD			
Primary	1	1	1
Supplemental	-	-	1
TS			
Primary	-	-	1
Supplemental	-	1	-
Sebia CZE			
PD			
Primary	1	5	2
Supplemental	-	-	-
TS			
Primary	1	1	-
Supplemental	-	4	1
IFE/ISUB			
Helena			
Mono	-	1	1
Penta	-	-	1
Sebia			
Mono	2	5	2
Penta	-	1	-
ISUB	1	2	-

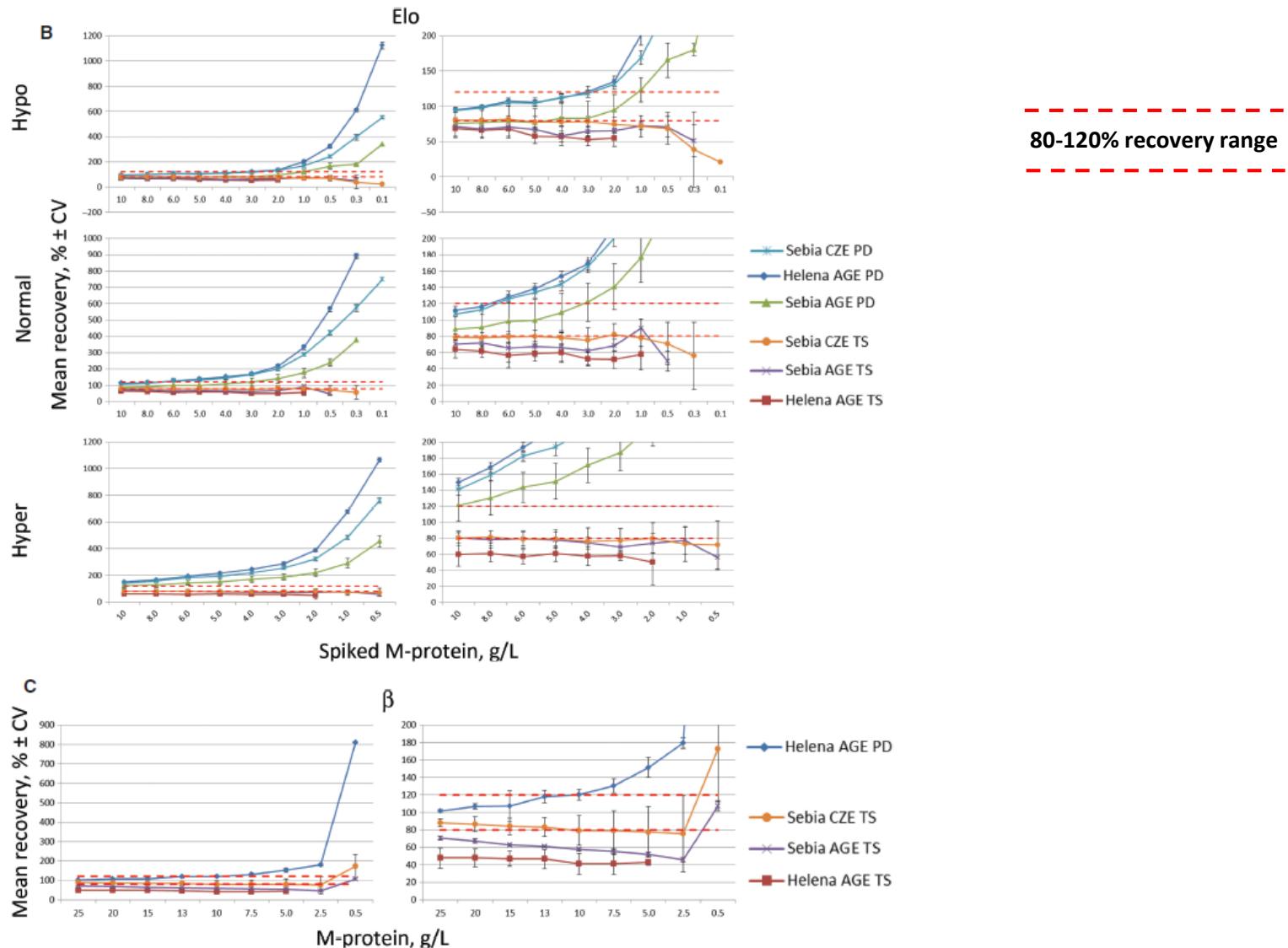
Serum protein electrophoresis



SPE: Accuracy of M-protein quantification (Dara)



SPE: Accuracy of M-protein quantification (Elo and B-migrating)



SPE: LoD



Conclusions Part I

Accuracy of M-protein quantitation is dependent on:

M-protein concentration

- Highest inaccuracy in small M-proteins

Gamma fraction background

- Highest inaccuracy with hyper-gamma

Migration pattern of M-protein

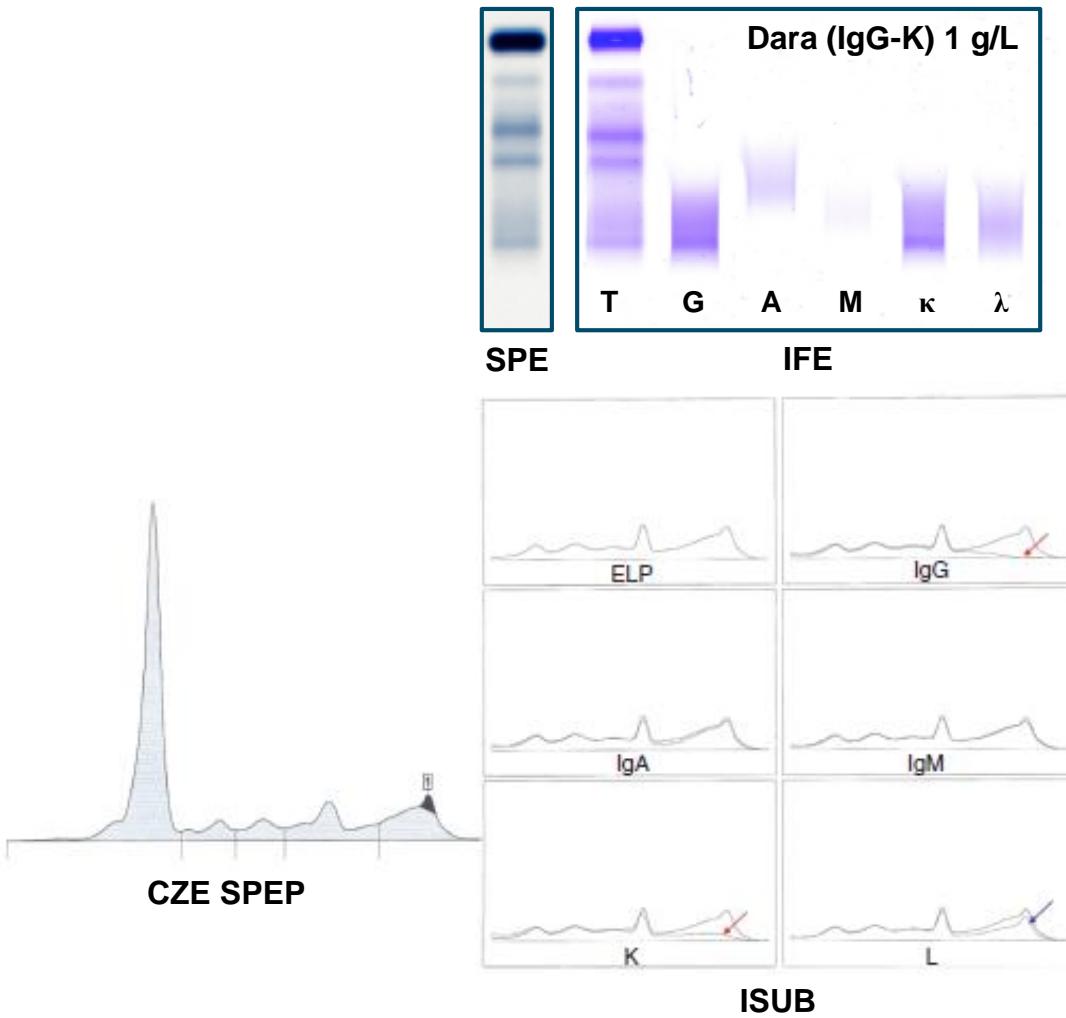
- Highest inaccuracy in central gamma migration

Gating strategy

- TS leads to underestimation
- PD leads to overestimation

'The quantitation of small M-proteins especially in high polyclonal background is associated with analytical inaccuracy'

IFE and ISUB (Dara in normal gamma region)



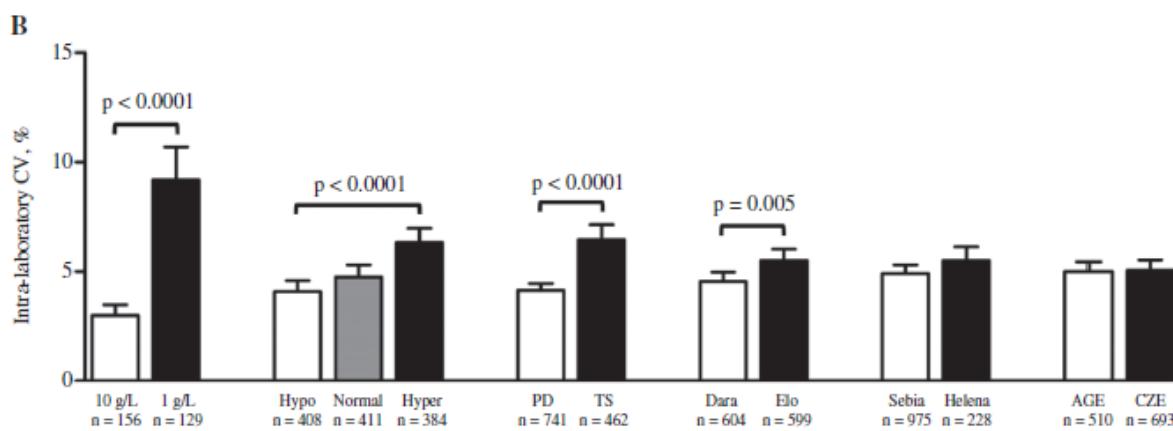
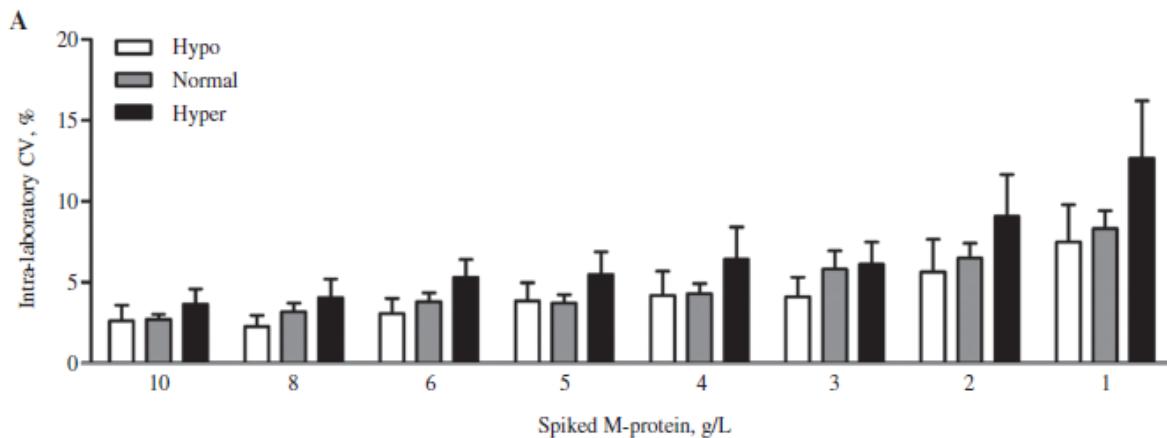
SPE, IFE and ISUB: LoD

Table 1: Limit of detection for SPEP and Immunofixation/Immunosubtraction.

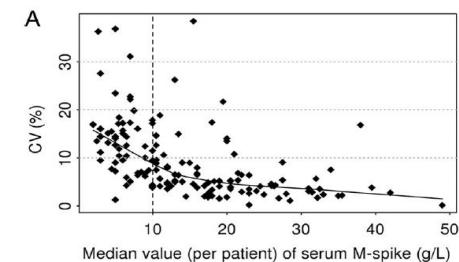
	Dara			Elo			Beta
	Hypo	Normal	Hyper	Hypo	Normal	Hyper	
SPEP LOD							
Helena AGE	0.5	0.5	1.0	0.5	0.5	1.0	<0.5
Sebla AGE	0.5	0.5	1.0	0.5	0.5	1.0	<0.5
Sebla CZE	0.5	0.5	0.5	0.5	0.3	0.5	<0.5
IFE/ISUB LOD							
Helena							
Mono	<0.1	0.5	<0.5	<0.1	0.3	<0.5	<0.5
Penta	<0.1	<0.1	<0.5	<0.1	<0.1	<0.5	-
Sebla							
Mono	<0.1	0.5	1	<0.1	0.5	2	<0.5
Penta	<0.1	0.3	<0.5	<0.1	<0.1	<0.5	-
Sebla							
ISUB	0.3	0.5	<0.5	0.3	0.3	0.5	<0.5

SPEP LOD and IFE/ISUB LOD (g/L) were defined as the lowest M-protein concentration in which an M-protein was detected and qualitatively reported in all samples analyzed. Samples marked with (<) are cases where the LOD was below the tested concentrations.

Consistency within single institute: intra-laboratory CV%

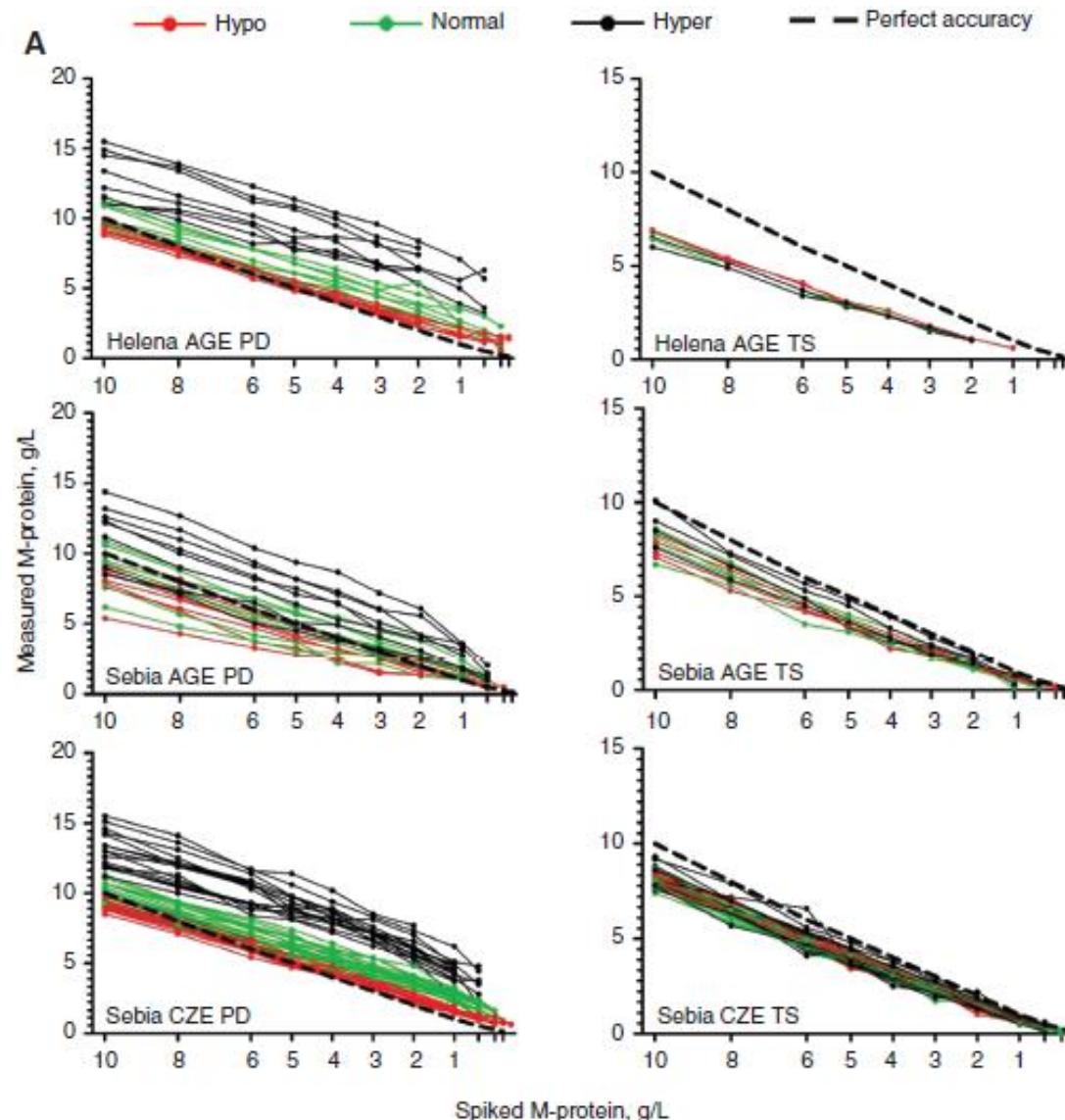


Average CV (all samples)
= 5.0%



Katzmann et al. Clin Chem 2011

Follow-up within single institute



Conclusions Part II

Satisfactory intra-laboratory precision was observed (average CV=5%)

Dependent on:

- M-protein concentration (best precision large M-proteins)
- Gamma fraction background (best precision hypo-gamma)
- Gating strategy (best precision PD gating)

*'Quantification of small M-proteins to monitor patients over time
is appropriate, when subsequent testing is performed within the
same laboratory'*

Contributions

DE GRUYTER

Clin Chem Lab Med 2020; aop

Katherine A. Turner, Jody L. Frinack, Michael W. Ettore, Jillian R. Tate, Maria Stella Graziani, Joannes F.M. Jacobs, Ronald A. Booth, Christopher R. McCudden, David F. Keren, Julio C. Delgado, Galina Zemtsovskaja, Robert O. Fullinfaw, Anna Caldini, Theo de Malmanche, Katina Katakouzinos, Matthew Burke, Giovanni Palladini, Sara Altinier, Martina Zaninotto, Gabriella Righetti, Marie Therese Melki, Stephen Bell
and Maria Alice Vieira Willrich*

An international multi-center serum protein electrophoresis accuracy and M-protein isotyping study. Part I: factors impacting limit of quantitation of serum protein electrophoresis

DE GRUYTER

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Editorial

Mario Plebani

New insights on the analytical performances for detecting and quantifying monoclonal proteins

Mayo Clinic Team – SPEP LOQ Study



Jody Frinack, MT (ASCP)
Development Technologist

- IRB protocol
- Drug purchasing
- Pools preparation
- Sharepoint set-up
- Communications
- Material Transfer Agreements
- Shipping
- Data generation



Michael Ettore
LIS Technical Specialist

- Excel set-up
- Excel macros
- Excel data organization



Katie Turner, Ph.D.
Clinical Chemistry Fellow

- Data analysis
- Data compilation
- Data presentation
- Communications



Maria Willrich, Ph.D.
Protein Immunology
Lab Director

- Principal Investigator