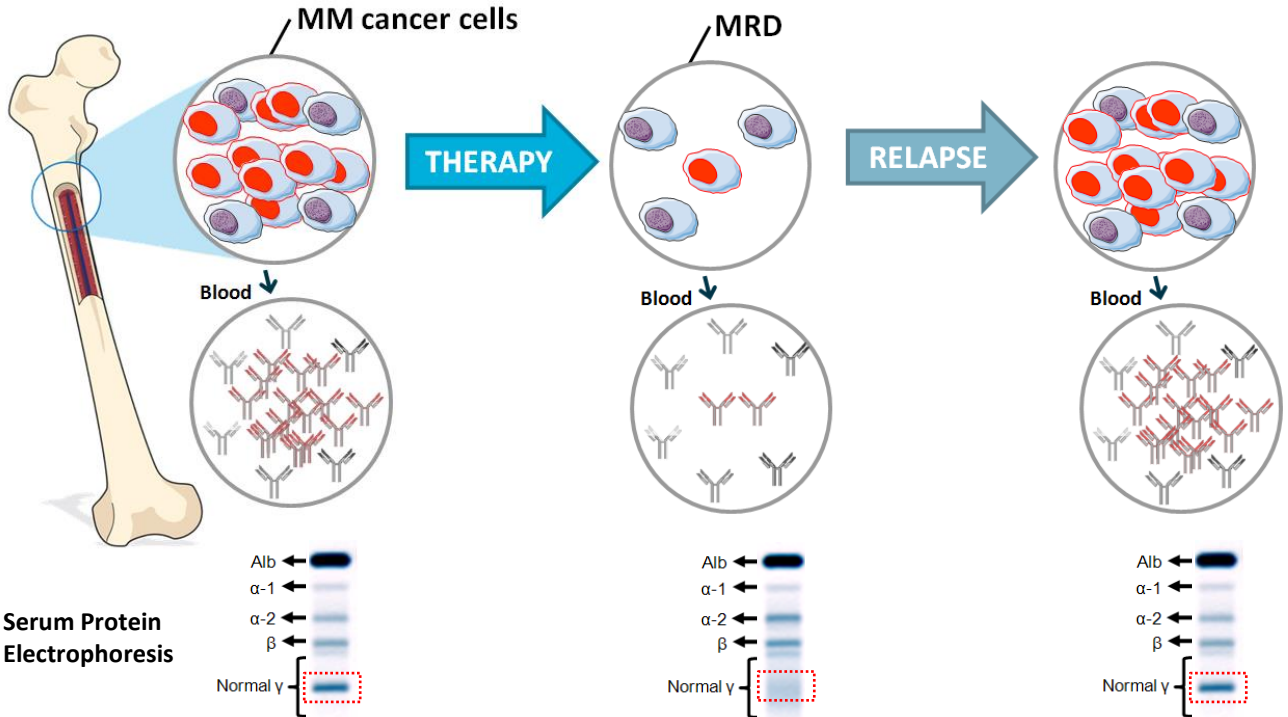


Personalized blood-based Mass Spectrometry methods introduce a new era in Multiple Myeloma diagnostics

Pieter Langerhorst
X-omics festival
11-04-2022

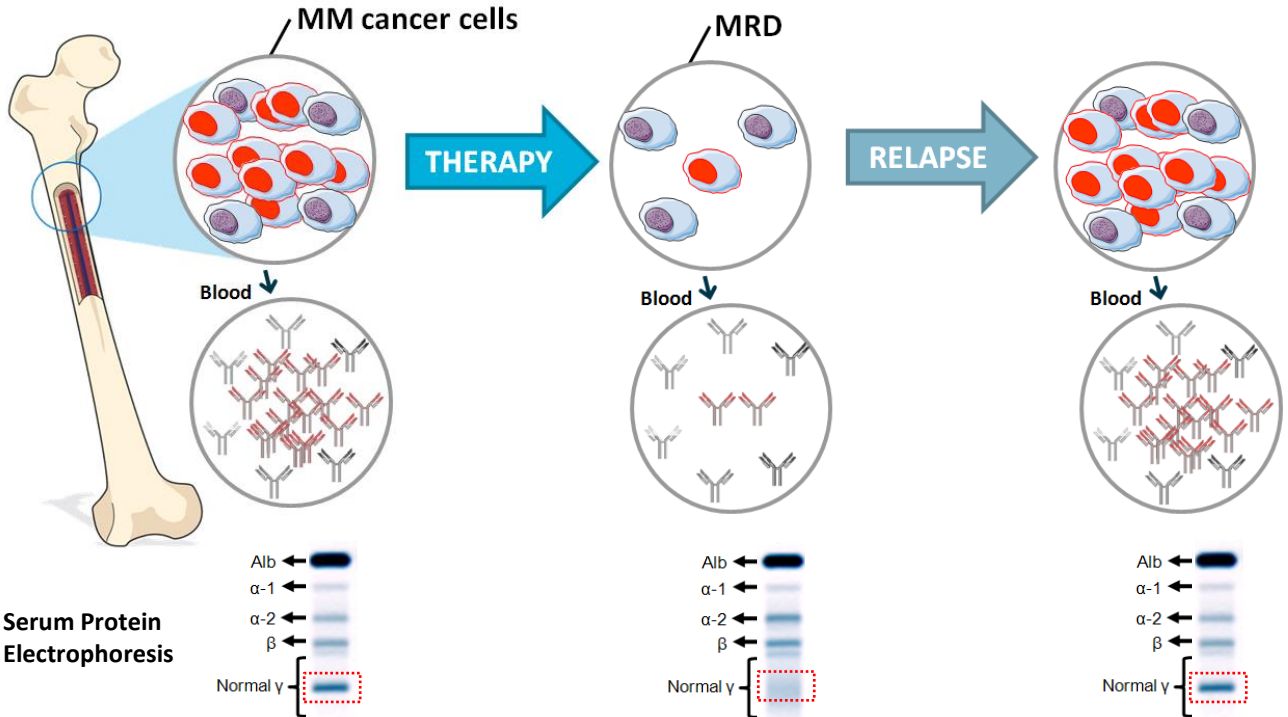
Multiple Myeloma

- 2nd most common hematological malignancy



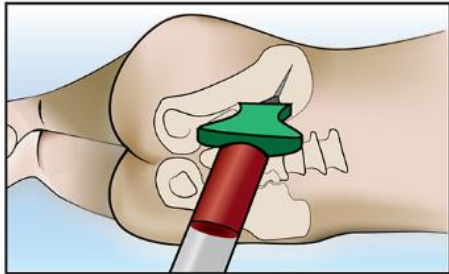
Multiple Myeloma

- 2nd most common hematological malignancy



50 % of newly diagnosed patients

Bone marrow based MRD in MM



Myeloma cell based

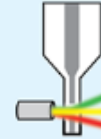
NGS/aso-qPCR



V(D)J sequences

NGS-MRD

Flowcytometry



% Myeloma cells

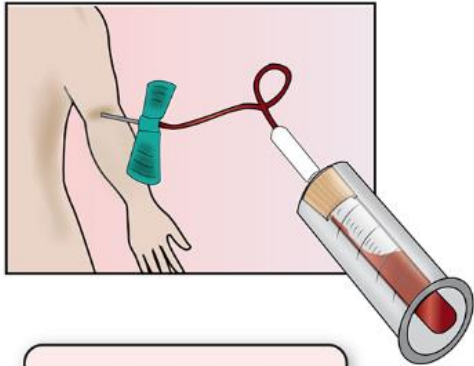
MCF-MRD

Good prognostic MRD biomarker

Challenges

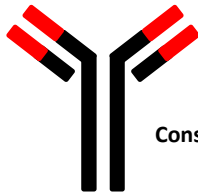
- Patchy disease
- Dry tap
- Repetitive sampling

M-protein MRD in MM

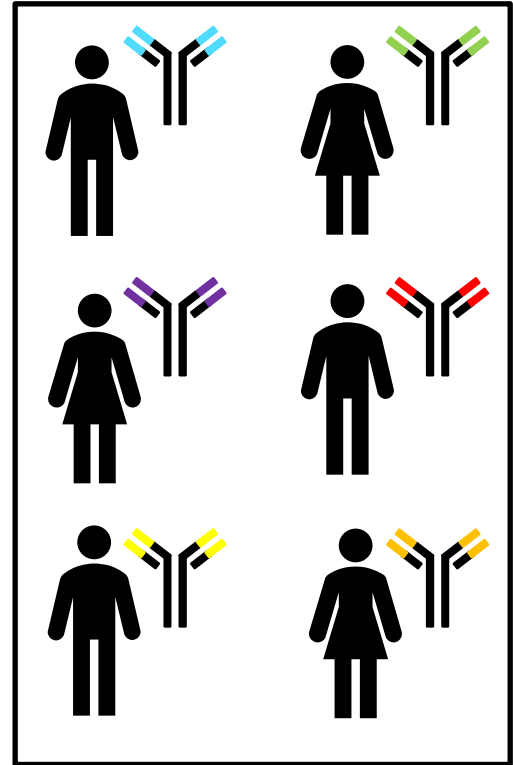


M-protein based

Variable region
Patient & tumor specific

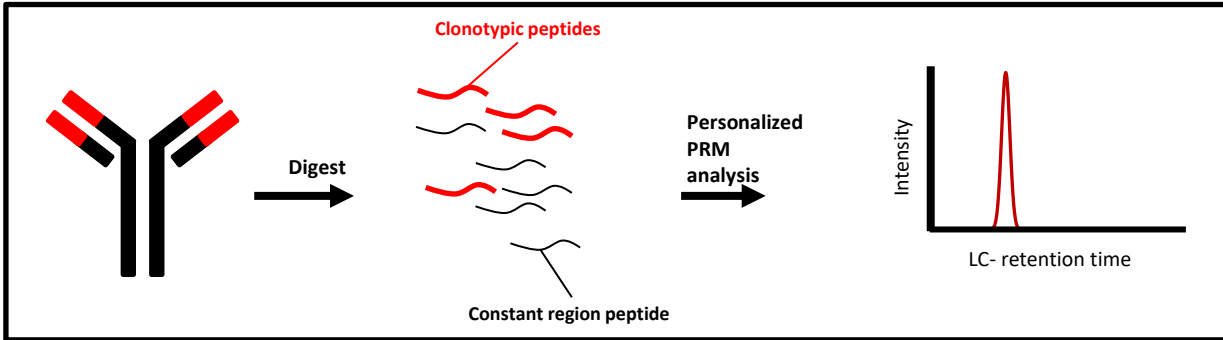


Constant region

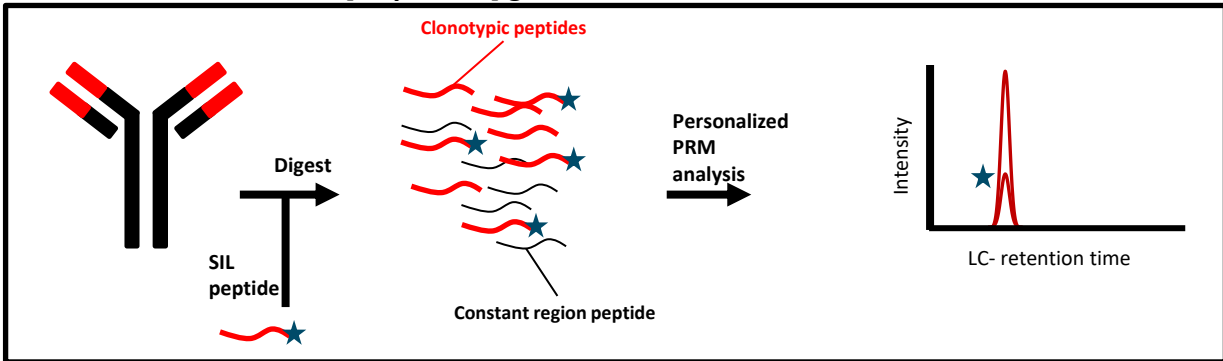


MS-MRD approach

Qualitative assessment : MRD +/-

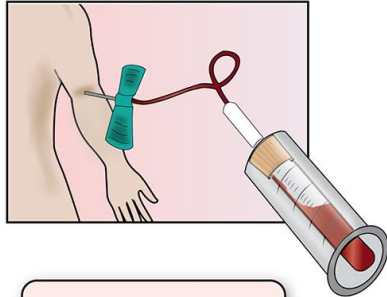


Quantitative assessment: [M-protein] g/L



MS-MRD vs. NGS-MRD

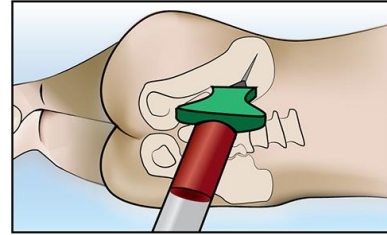
MS-MRD



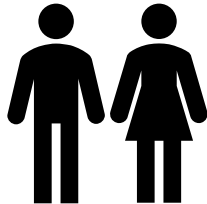
M-protein based

VERSUS

NGS-MRD



Myeloma cell based



n=41

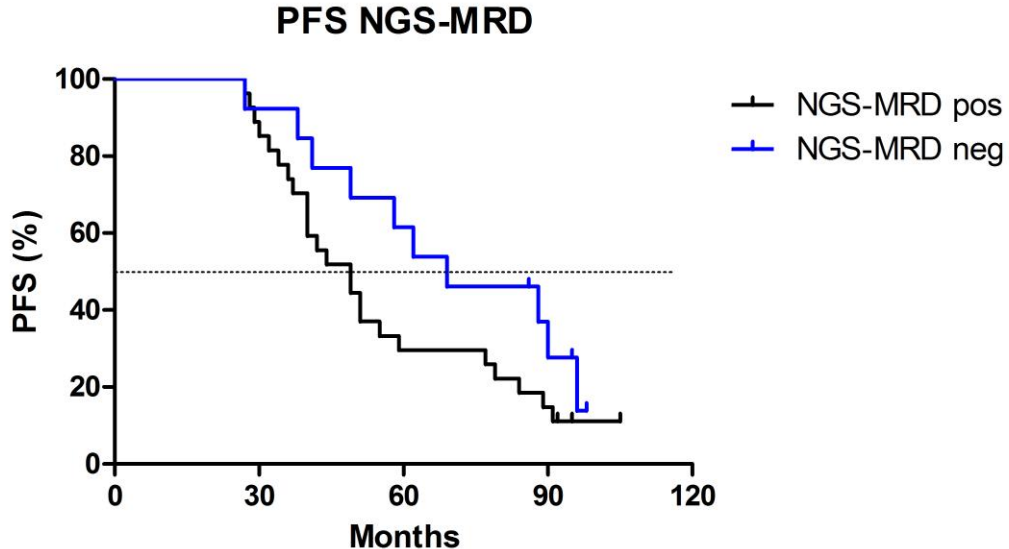
- ✓ Survival data
- ✓ NGS-MRD data
- ✓ Frozen sera for MS-MRD
- ✓ Sera available at 3 time points:
 - Screening*
 - Pre-Maintenance therapy*
 - Post-Maintenance therapy*

NGS-MRD vs. MS-MRD

- PFS comparison between NGS-MRD and MS-MRD during therapy

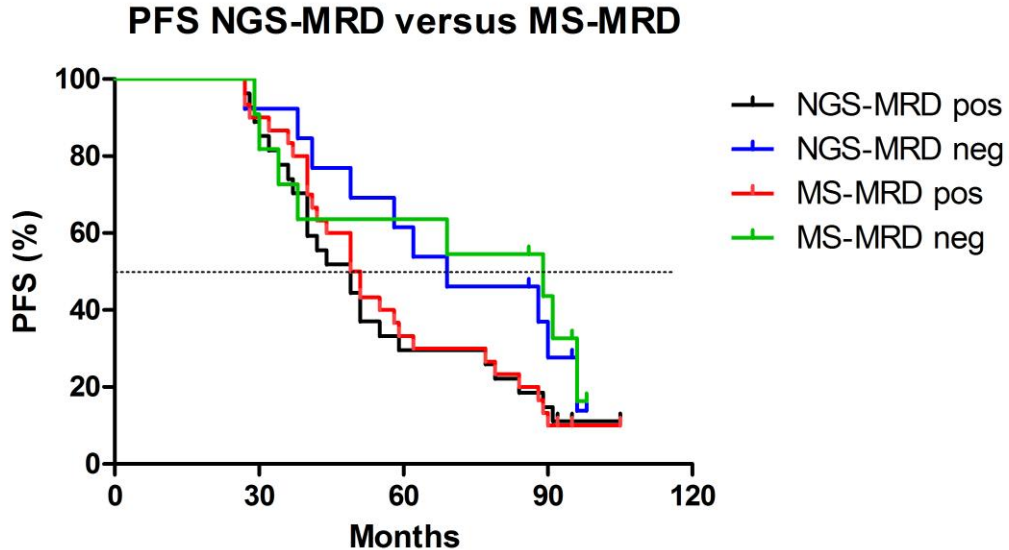
NGS-MRD vs. MS-MRD

- PFS comparison between NGS-MRD and MS-MRD during therapy



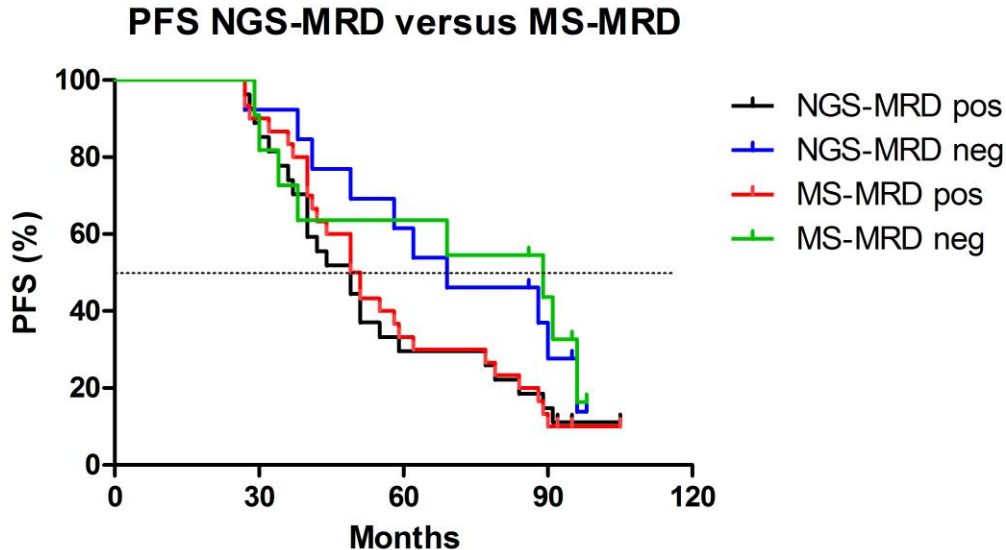
NGS-MRD vs. MS-MRD

- PFS comparison between NGS-MRD and MS-MRD during therapy



NGS-MRD vs. MS-MRD

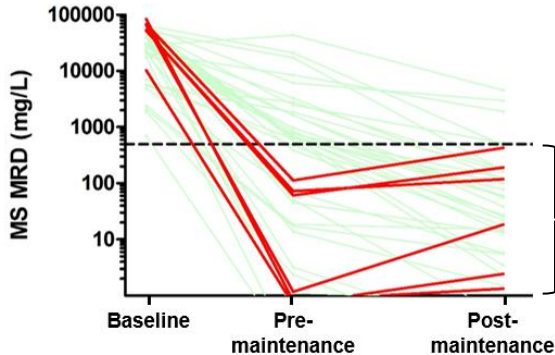
- PFS comparison between NGS-MRD and MS-MRD during therapy



NGS-MRD in bone marrow and MS-MRD in blood have similar prognostic value

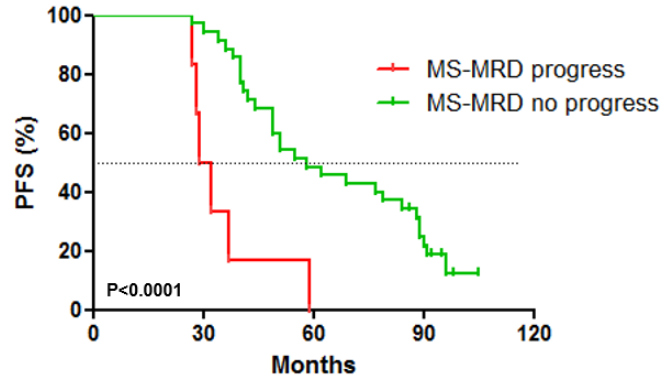
MS-MRD for dynamic monitoring

- Quantitative MS-MRD to monitor disease progression

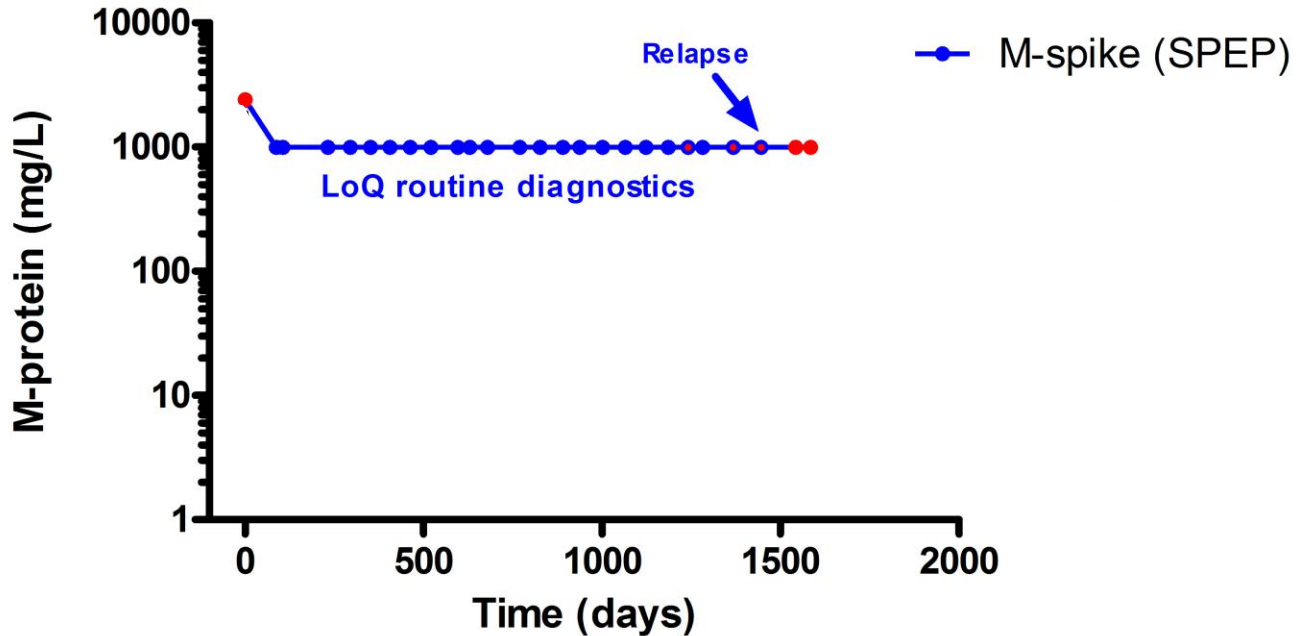


Red lines: (early) relapse detected during maintenance therapy

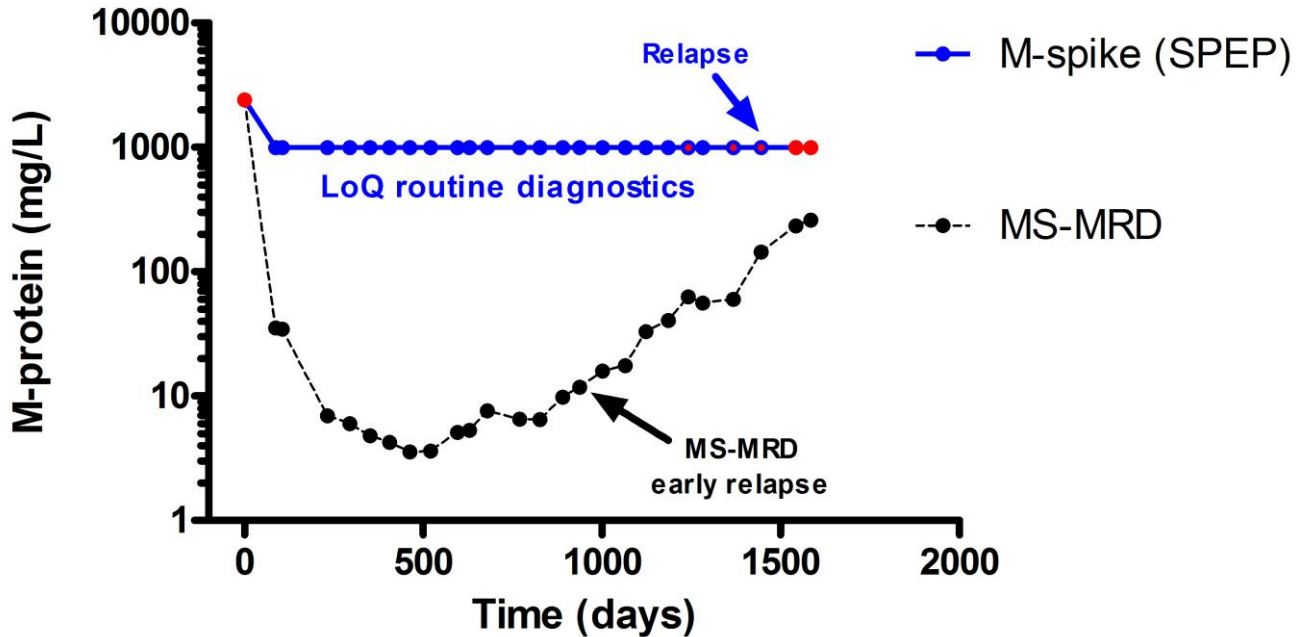
- Early relapse detected in 6 patients
- Strongly correlated with poor-prognosis



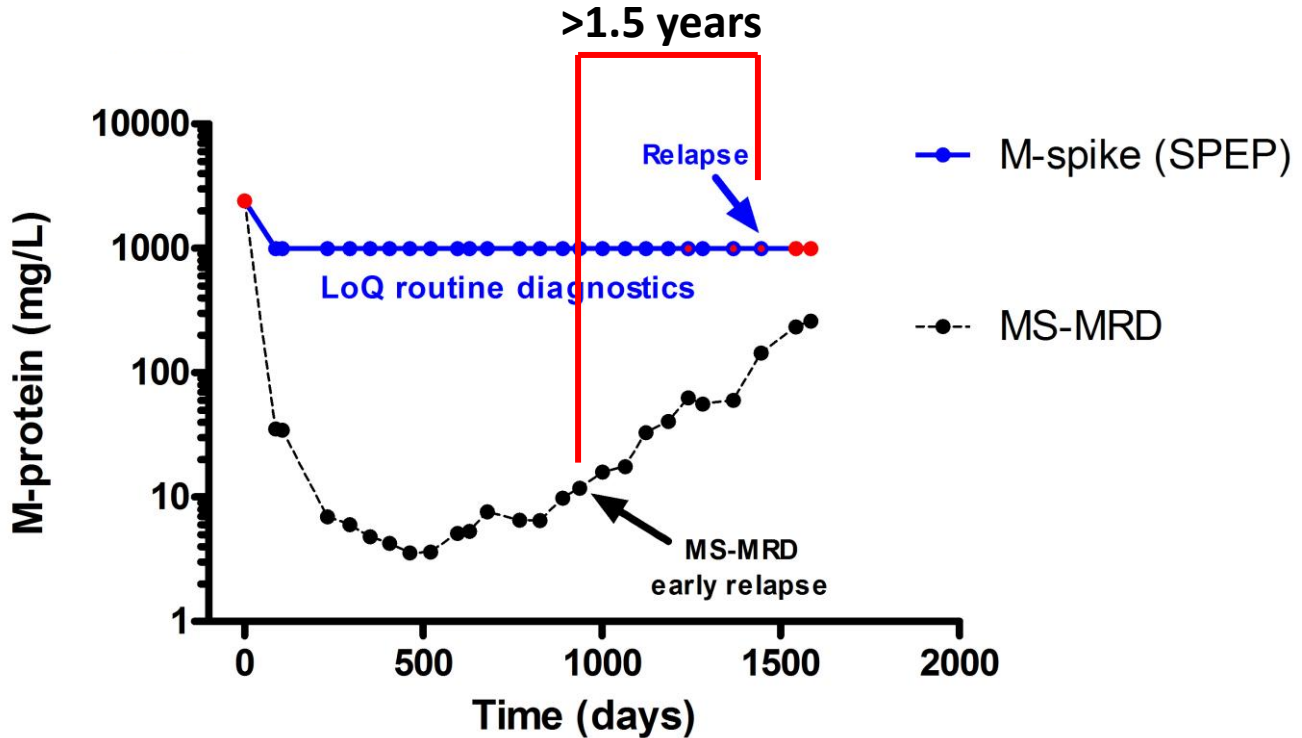
MS-MRD for dynamic monitoring



MS-MRD for dynamic monitoring



MS-MRD for dynamic monitoring

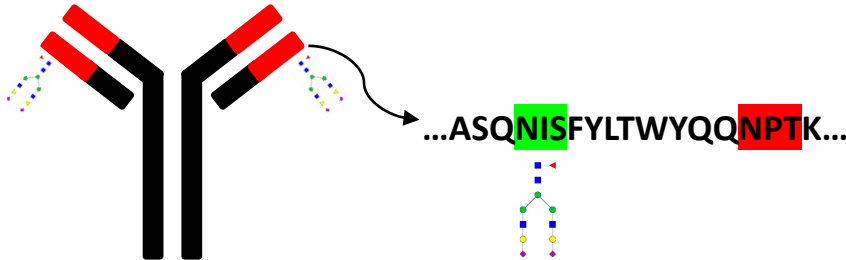


M-protein Fab N-glycosylation

N-linked glycosylation motif



X= any amino acid except proline

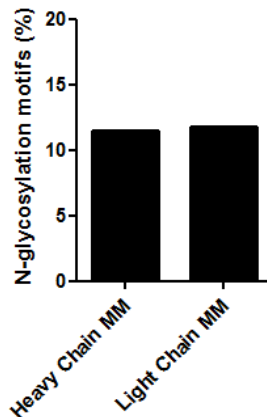
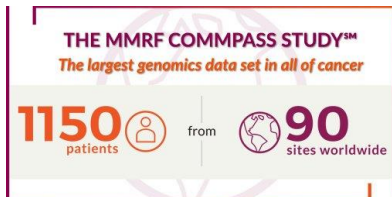


- Somatic hypermutations in the M-protein variable region can lead to *de novo* N-glycosylation sites
 - Possibly clinically relevant
- Organ damage, disease progression*
- Extra layer of personalized biomarker

Increase in M-protein Fab N-glyco sites

- Genomic screening for *de novo* Fab N-glycosylation sites

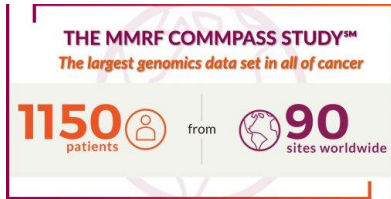
MM patients



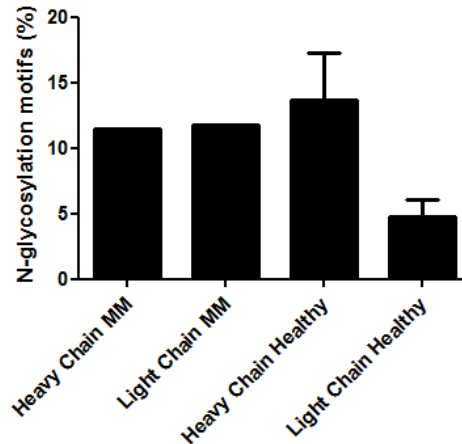
Increase in M-protein Fab N-glyco sites

- Genomic screening for *de novo* Fab N-glycosylation sites

MM patients



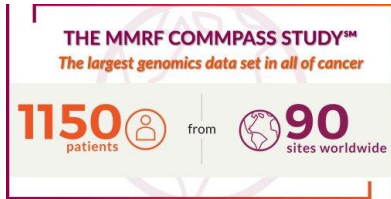
Healthy individuals



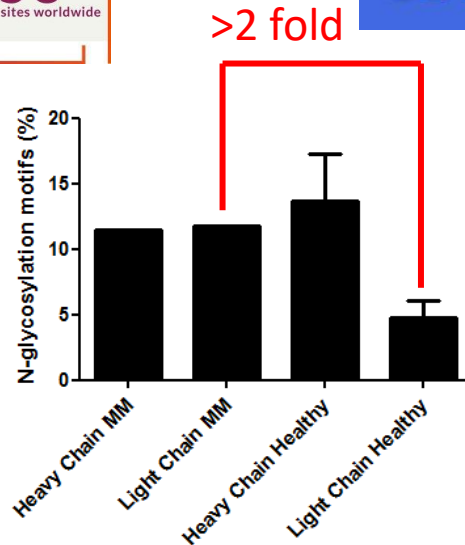
Increase in M-protein Fab N-glyco sites

- Genomic screening for *de novo* Fab N-glycosylation sites

MM patients

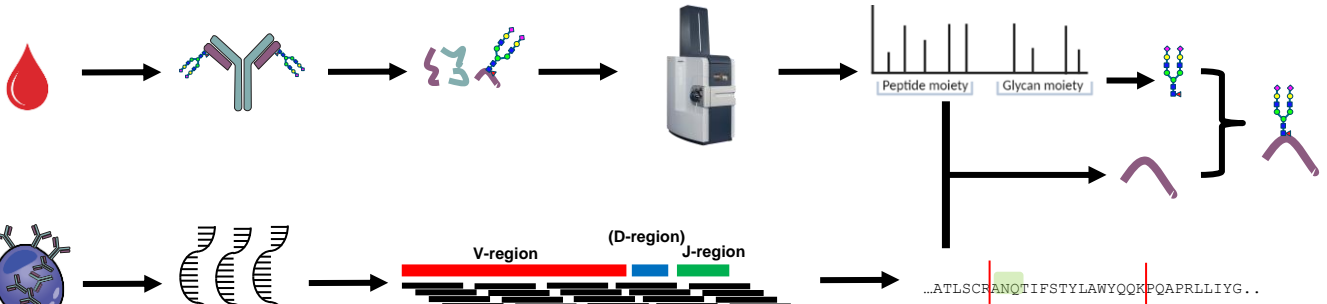


Healthy individuals



Glycoproteogenomics

Glycoproteomics



Genomics



Applied to a cohort of 41 MM patients

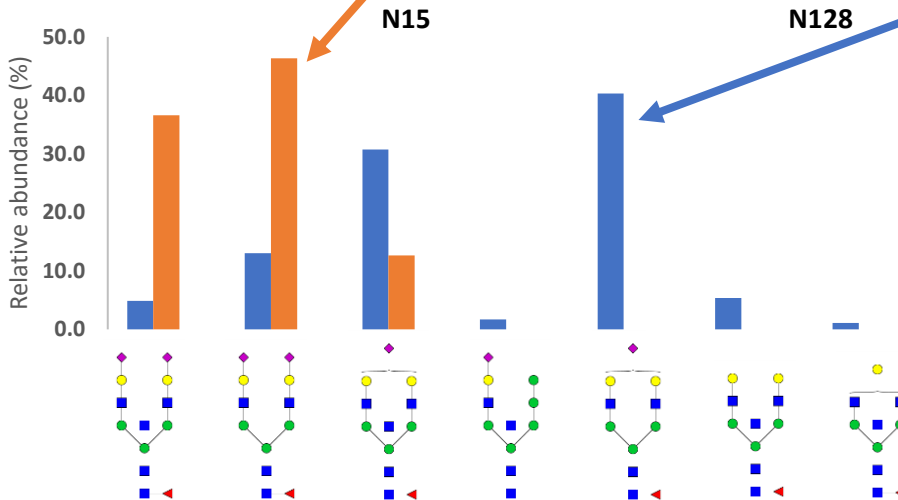
7/41 had a *de novo* N-glycosylation site in their M-protein

Glycoproteogenomics

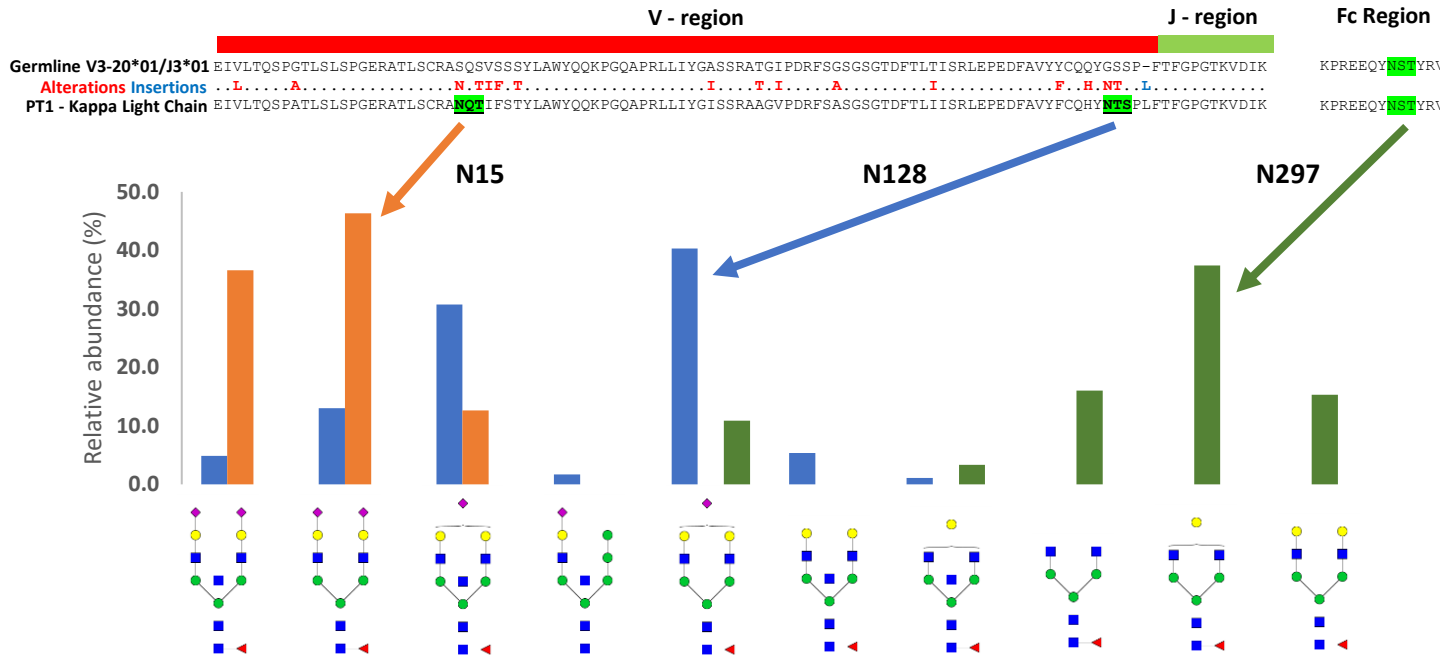
V - region

J - region

Germline V3-20*01/J3*01 EIVLTQSPFGLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSDTFTLTISRLEPEDFAVYYCQQYGSSP-FTFGPGTKVDIK
 Alterations Insertions . . L . . . A N . T I F . T I . . T . I . A I . . F . . H . N T . . L
 PT1 - Kappa Light Chain EIVLTQSPATLSPGERATLSCRAN¹⁵IFSTYLAWYQQKPGQAPRLLIYGISSRAAGVDRFSASGSGDTFTLIISRLEPEDFAVYFCQHY¹²⁸PLPTFGPGTKVDIK



Glycoproteogenomics



Conclusions

Personalized MS methods in blood introduce a new era in M-protein diagnostics

MS-MRD in blood

- Personalized diagnostic to monitor MRD In the blood of patients with MM
- Similar prognostic value as NGS-MRD in bone marrow
- Enables dynamic monitoring for early relapse detection

Glycoproteogenomics

- Increased de novo N-glycosylation in M-proteins of patients with MM
 - Enables detailed glycoprofiling of de novo glycosites
 - Opens possibilities to study clinical value/pathogenicity of M-protein fab glycosylation
 - Possible integration with diagnostic workflows for also other diseases
- WES/WGS/RNA-seq → Glycosite-ID → Glycoproteomics

Acknowledgements

Radboudumc

Dr. Sandra Croockewit (Hematology)
Dr. Jolein Gloerich (Laboratory Medicine)
Prof. Alain van Gool (Laboratory Medicine)
Dr. Patricia Groenen (Pathology)
Dr. Hans Jacobs (Laboratory Medicine)
Prof. Irma Joosten (Laboratory Medicine)
Jenneke Keizer-Garritsen (Laboratory Medicine)
Prof. Dirk Lefeber (Laboratory Medicine)
Merel Post (PhD student)
Dr. Blanca Scheijen (Pathology)
Dr. Hans Wessels (Laboratory Medicine)
Charissa Wijnands (PhD student)

Erasmus MC

Universitair Medisch Centrum Rotterdam

Erasmus

Dr. Annemiek Broijl (Hematology/HOVON)
Dr. Mark van Duin (Hematology)
Dr. Martijn van Duijn (Neurology)
Dr. Theo Luidier (Neurology)
Somayya Noori (PhD student)
Dr. Henk Russcher (Clinical Chemistry)
Dr. Yolanda de Rijke (Clinical Chemistry)
Prof. Pieter Sonneveld (Hematology/HOVON)
Marina Zajec (PhD student)

ThermoFisher
SCIENTIFIC



Prof. Niels vd Donk (Hematology)
Kristine Frerichs (PhD student)
Christy Verkleij (PhD student)
Prof. Sonja Zweegman (Hematology)



Prof. Hervé Avet-Loiseau
Dr. H el ene Caillon
Dr. Jill Corre
Dr. Thomas Dejoie



Dr. Melissa B arenf anger



NL Health~Holland

