

Overview and evolution of treatment lines in multiple myeloma from 2014 to 2019: a retrospective study using the french national claim database (SNDS)

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Background

MM disease course is a succession of remissions and relapses, which define **lines of treatment**. For each line, several **regimens** can be used. Although guidelines provide **recommendations** on the disease management, **real world data** are missing to describe which regimens are used in the daily practice. Regarding recent changes due to the introduction of new drugs, an accurate and updated overview of MM treatment management is needed.

This study provides a comprehensive overview of these recent changes based on the nationwide **French NHI databases** (called SNDS), which include hospital records, primary and secondary care of **66 million people**. The aim is to describe the evolution over time of MM treatment management by line and treatment sequencing in practice in France, in the context of a new therapeutic landscape.

Methods

Cohort identification

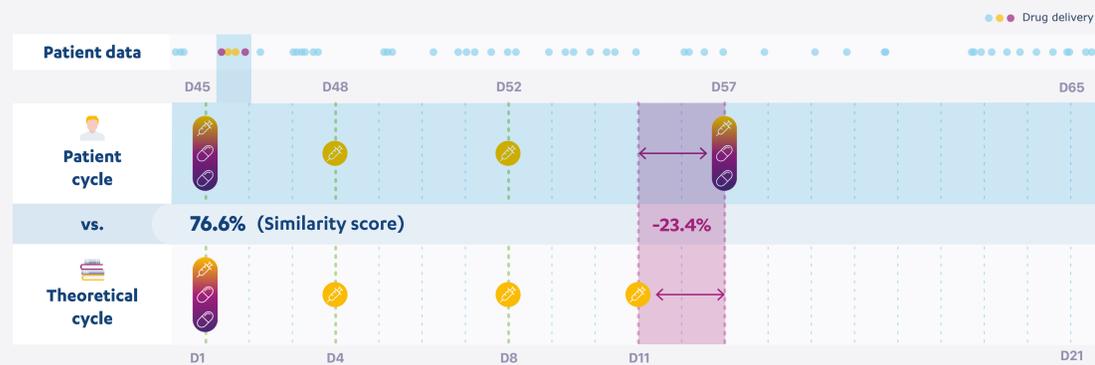
This is a retrospective observational cohort study including all cases of MM from 2014 to 2019 identified through the SNDS. Cases were detected using a validated algorithm which was expanded to consider recent evolutions of MM therapeutic management¹.

Treatment lines algorithm

Treatment lines were re-constructed through an AI algorithm, ATLAS, which is a published adaptation² of the Smith-Waterman sequence alignment algorithm. This innovative algorithm gave the temporal flexibility needed to identify lines considering the deviations between theoretical regimens and patient claim data.

For each patient and each theoretical cycle (listed according to recommendations and practices),

1. Day-by-day patient claims are scanned to determine a similarity score with the theoretical cycle
2. Scores are smoothed over time to identify the best treatment phase at each time of the patient follow-up
3. Treatment phases are gathered into medical lines



Statistical analysis

For each year and for each line, the number and percentage of patients being under a regimen at least one day in the year was assessed. Regimens accounting for more than 5% of the given regimens (at least one year) are represented.

Conclusion

The MYLORD study demonstrates the fast evolution of treatment management of MM patients, due to new drug marketing authorizations and access.

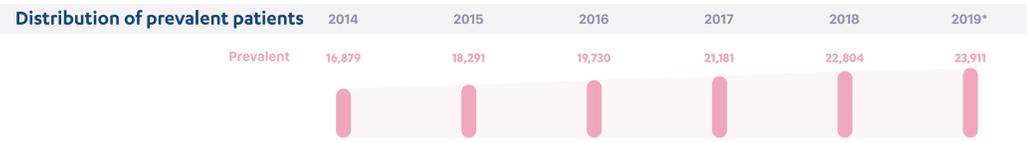
The study also showed that real-world data are a powerful tool to study treatment lines at a national scale. It leads the way to more precise analyses of optimal therapeutic sequences, including their impact on the overall survival

Results

40,747 patients treated for a MM (2014-2019)

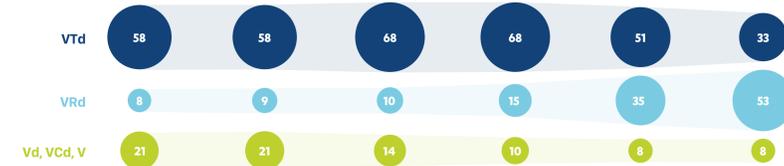
4,508 exclusions (11%)
 2,259 (6%) with only 1 day of treatment
 1,277 (3%) with only 2 to 4 dates of treatments
 972 (2%) with more than 4 dates with treatments but disseminated (less than once every 70 days)

36,239 Patients with lines identified with ATLAS

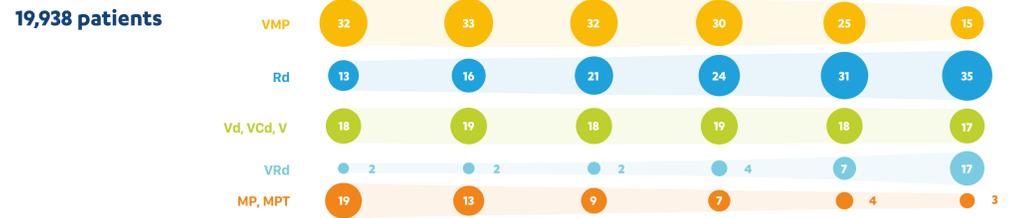


Distribution of the most common regimens by line (in %)

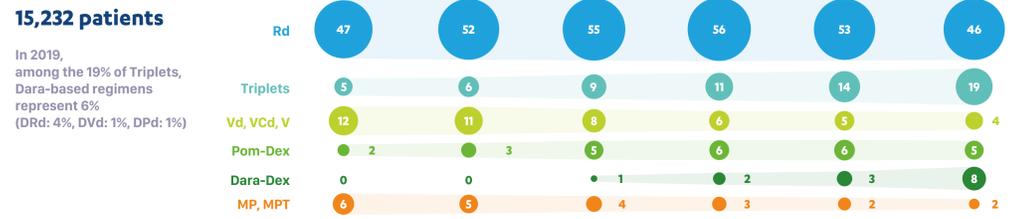
Line 1 with transplant
5,971 patients



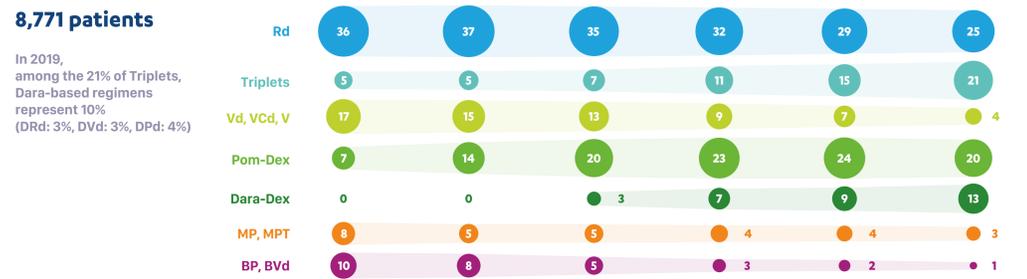
Line 1 without transplant



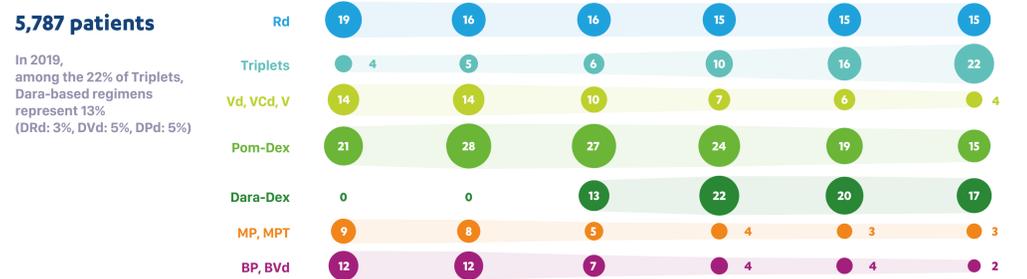
Line 2



Line 3



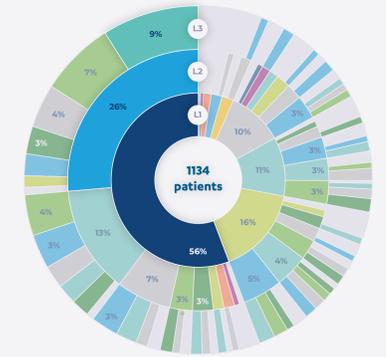
Line 4+



*The year 2019 should be interpreted with caution. We are missing some incident patients as 2020 year is requested to accurately identify MM patients

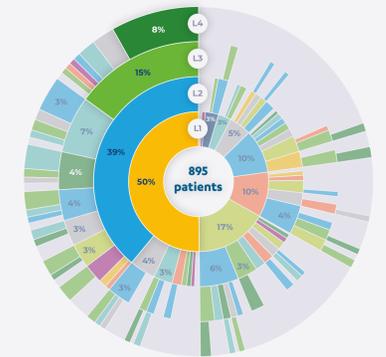
Treatment sequences of all incident patients from 2014 to 2019

With a transplant and who had 3 lines of treatment
 The main course is: L1: VTd, L2: Rd, L3: Triplets



Without transplant who had 4 lines of treatment

The main course is: L1: VMP, L2: Rd, L3: Pom-Dex, L4: Dara-Dex



Legend

- Rd**: Lenalidomide / low-dose dexamethasone
- Triplets**: IRd: Ixazomib / Lenalidomide / Dexamethasone; KRd: Carfilzomib / Lenalidomide / Dexamethasone; DRd: Daratumumab / Lenalidomide / Dexamethasone; DVd: Daratumumab / Bortezomib / Dexamethasone; PVd: Pomalidomide / Bortezomib / Dexamethasone; DPd: Daratumumab / Pomalidomide / Dexamethasone; VRd: Bortezomib / Lenalidomide / Dexamethasone
- VTd**: Bortezomib / Thalidomide / Dexamethasone
- VRd**: Bortezomib / Lenalidomide / Dexamethasone
- Vd, VCd, V**: Vd: Bortezomib / Dexamethasone; VCd: Bortezomib / Cyclophosphamide / Dexamethasone; V: Bortezomib monotherapy
- Pom-Dex**: Pomalidomide / Dexamethasone
- Dara-Dex**: Daratumumab / Dexamethasone
- VMP**: Bortezomib / Melphalan / Prednisone
- MPT, MP**: MP: Melphalan / Prednisone; MPT: Melphalan / Prednisone / Thalidomide
- BP, BVd**: BVd: Bendamustine / Bortezomib / Dexamethasone; BP: Bendamustine / Prednisone

Glossary

- AI**: Artificial Intelligence
- ATLAS**: Analysis of Treatment Lines using Alignment of Sequences
- MM**: Multiple Myeloma
- NHI**: National Health Insurance
- MYLORD**: Multiple myeloma: an epidemiological study using SNIRAM Database
- SNDS**: Système National des Données de Santé

References

1. C. Touzeau, M. Pierres, M. Javelot, C. Guilmet, L. Lamarsalle, F. Raguideau, I. Borget, V. Augusto, A. Perrot, "Epidemiology of multiple myeloma: data from the french national health insurance database (SNDS)", 2021 European Hematology Association (EHA), June 9-17 2021
2. M. Prodel, L. Lamarsalle and V. Augusto, "ATLAS: A Robust Algorithm for Temporal Sequence Alignment of Treatment Lines using Claim Databases," 2019 IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), Siena, Italy, 2019, pp. 1-8. <https://ieeexplore.ieee.org/document/8791467>