Multiple **MY**eloma: an epidemio**LO**gical study using SNII**R**AM **D**atabase

# Treatment pathways for patients with Multiple Myeloma: a real-life study based on the French national claim database from 2014 to 2019

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# Disclosure of interest

*Aurore Perrot*

**Disclosures of interest:**
**Janssen, Amgen, BMS/Celgene, GSK, Takeda and Sanofi**

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# Introduction

*Context and objective*

MYLORD
Multiple **MY**eloma: an epidemio**LO**gical study using SNII**R**AM **D**atabase

**Cohort of patients treated for a Multiple Myeloma (MM) in France**

- **Using French NHI database (SNDS)**
- **40 747 patients from 2014 to 2019, and among them 36 241 for whom treatment history has been identified using an IA algorithm (ATLAS)**
- **The most extensive and exhaustive cohort of MM in France**
- **Methodology and 1st study results presented at EHA congress**

Objective : describe treatment pathway and attrition rates across lines of treatments in MM patients

MYLORD: Multiple mYeloma: an epidemioLOgical study using SNIIRAM Database
NHI: National Health Insurance
SNDS: Système National des Données de Santé

# Methods

*Patients identification and statistics*

## Patients' identification

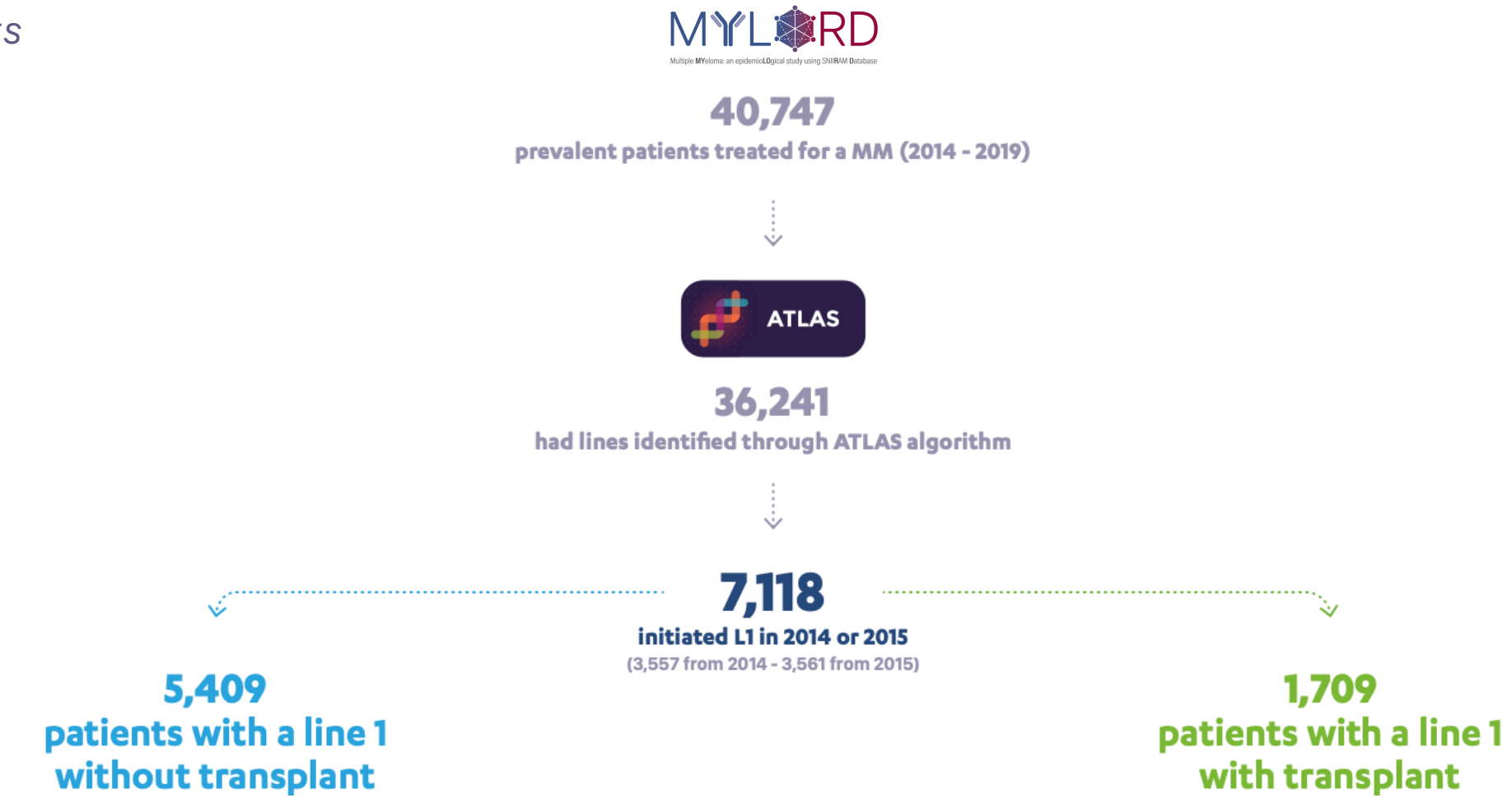
- Using MYLORD cohort
- **Inclusion of patients who initiated a L1 in 2014 or in 2015** to get enough follow-up
- Follow-up until December 31st, 2019 (or death)

## Statistical analyses

- Attrition rate across lines of treatment
- Treatment sequences
- Survival using Kaplan Meier method

# Results

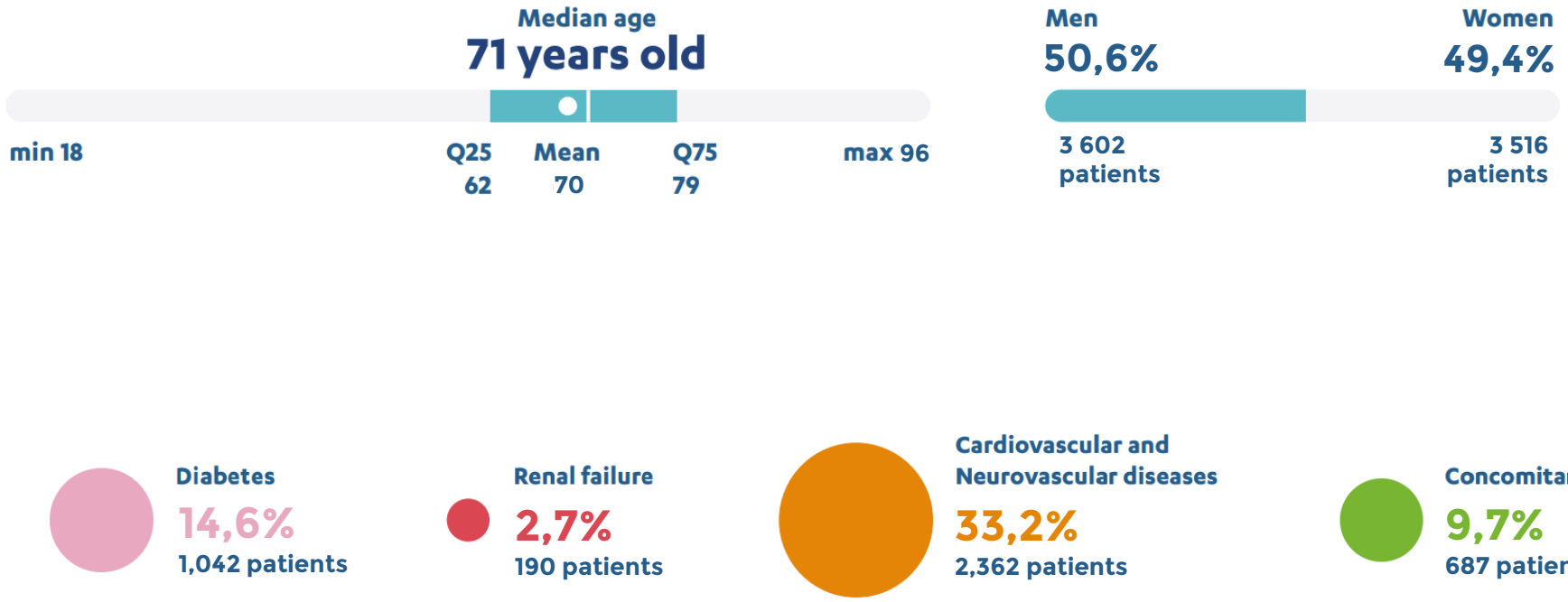
*Cohort of patients*



# Results

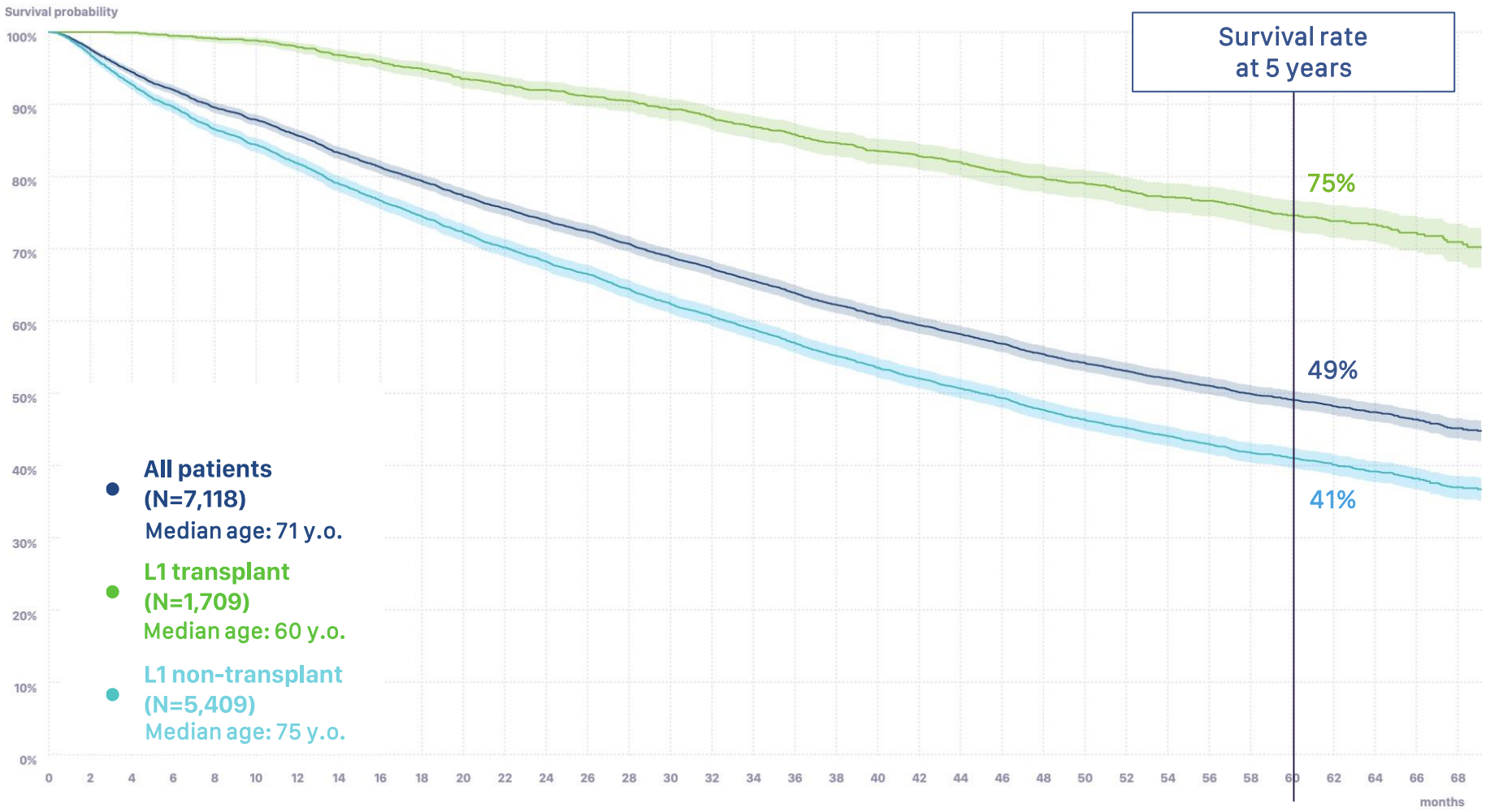
*Patients characteristics*

*N=7 118*



# Results

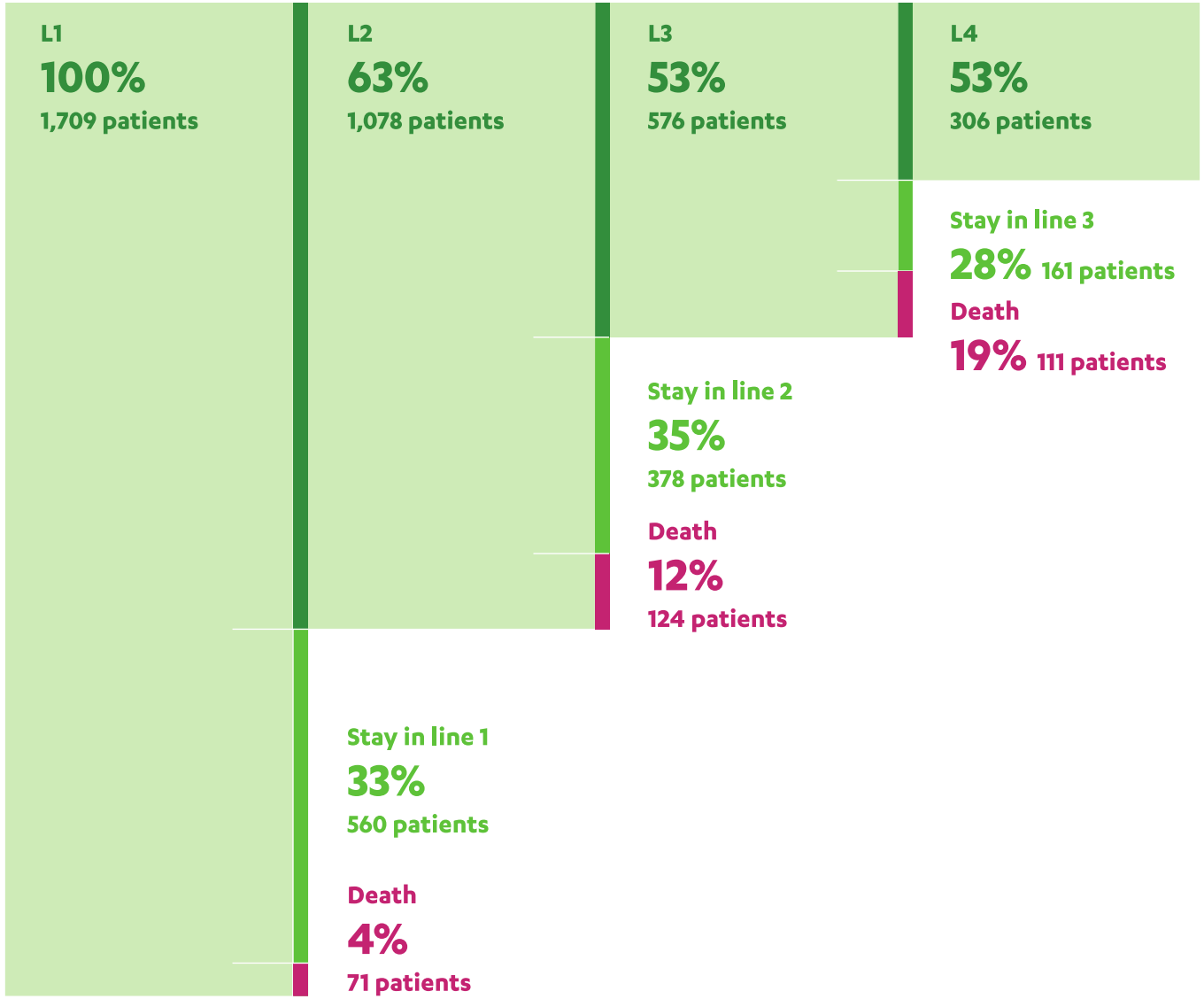
*Survival curves*




Median age are computed at L1 initiation

# Results

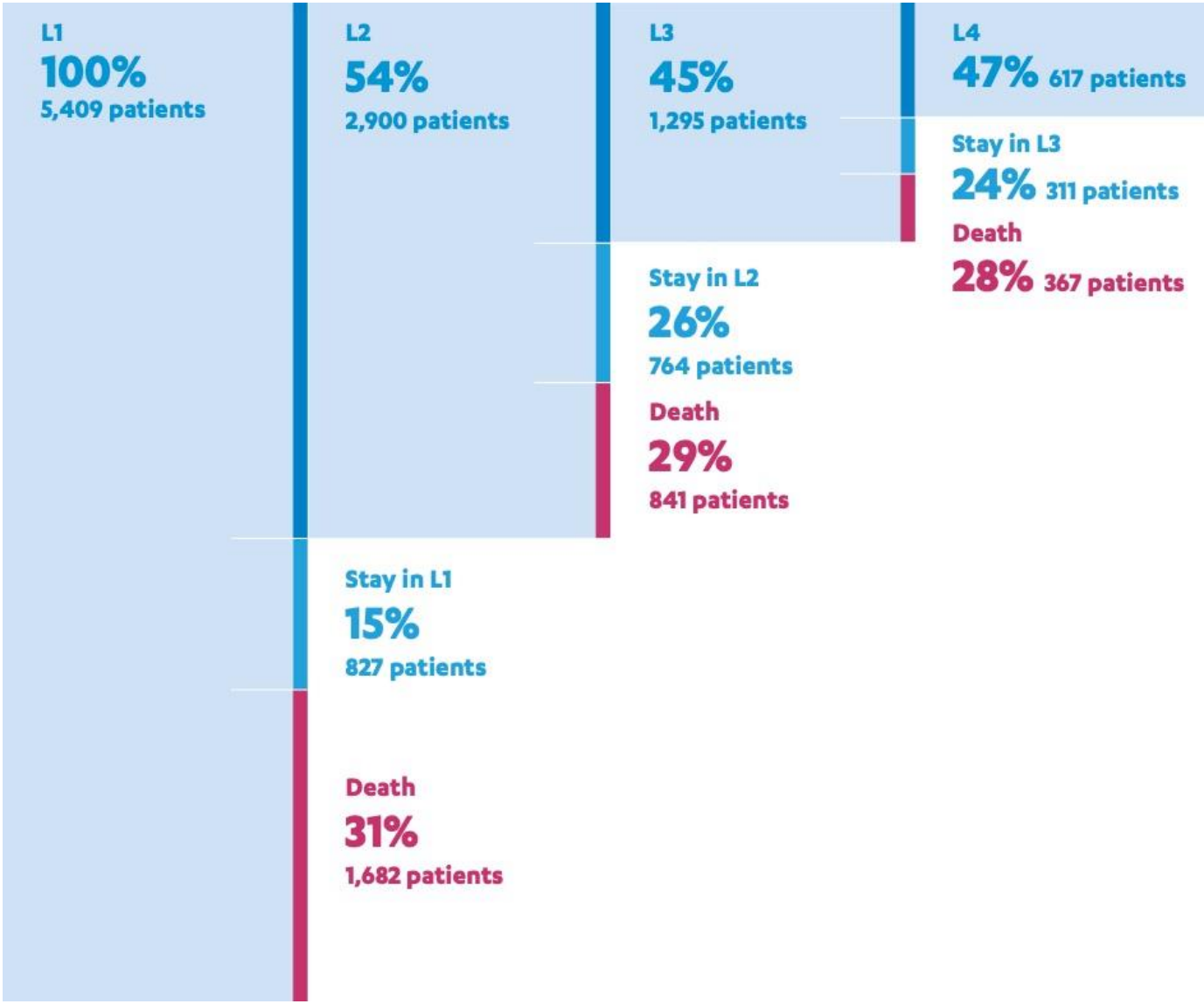
*Treatment lines flow for patients with a* ***line 1 with transplant***




All-cause of deaths are considered in this study

# Results

*Treatment lines flow for patients with a* ***line 1 without transplant***

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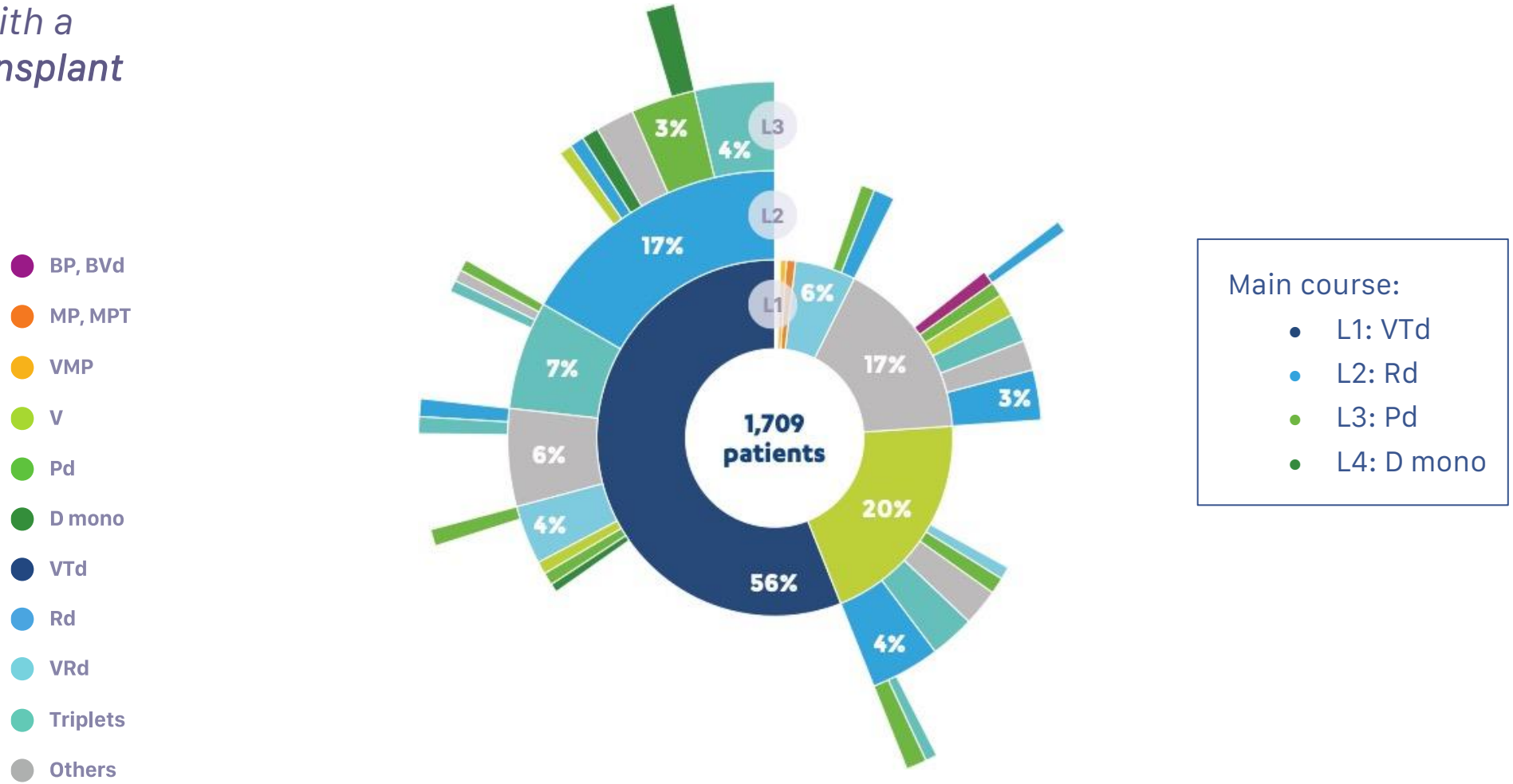
# Results

*Treatment sequences for patients with a* ***line 1 with transplant***



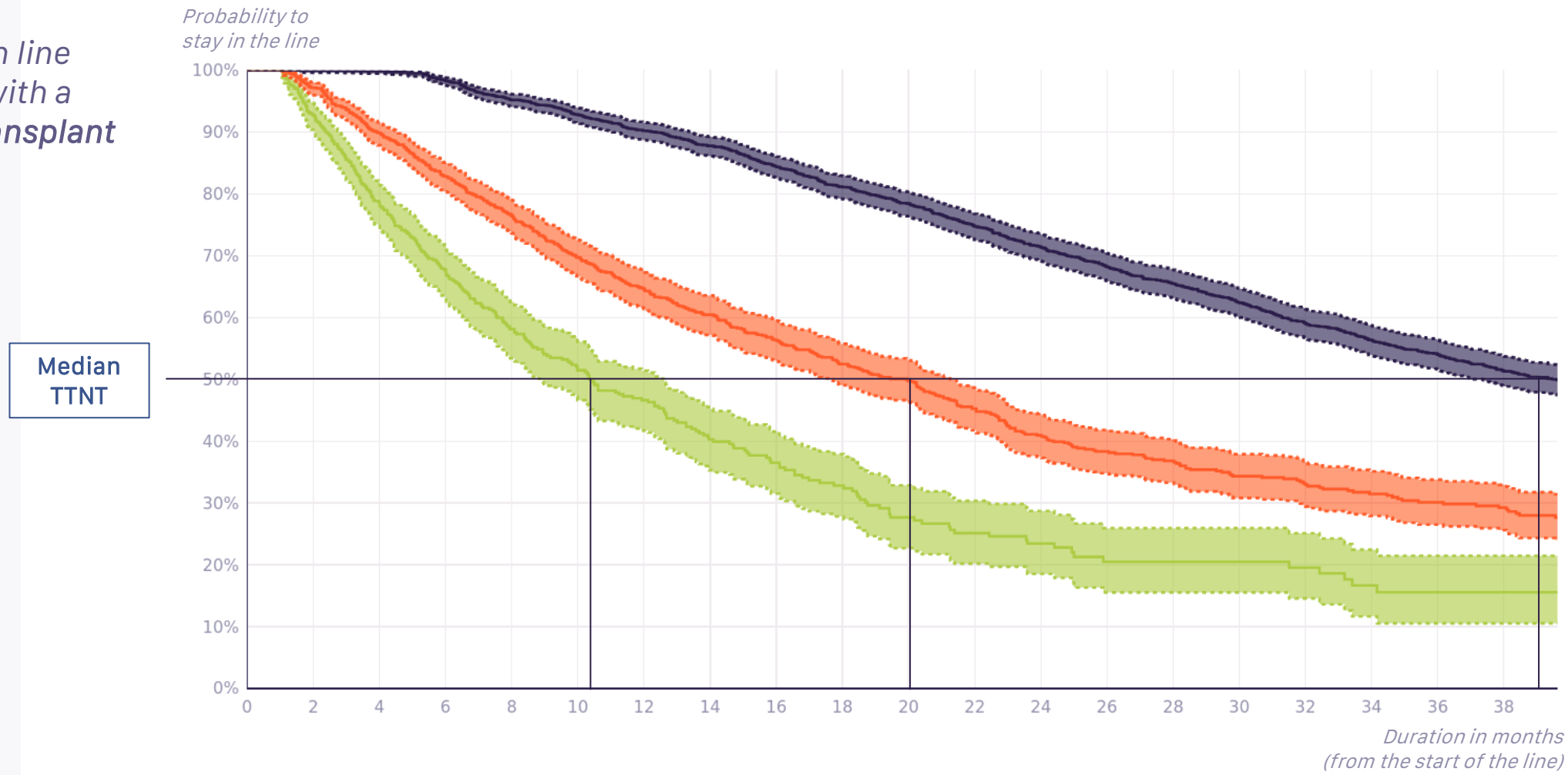

Main course:

- L1: VTd
- L2: Rd
- L3: Pd
- L4: D mono

Triplets: IRd; KRd; DRd; DVd; PVd; DPd; VRd

# Results

*TTNT for each line for patients with a* ***line 1 with transplant***

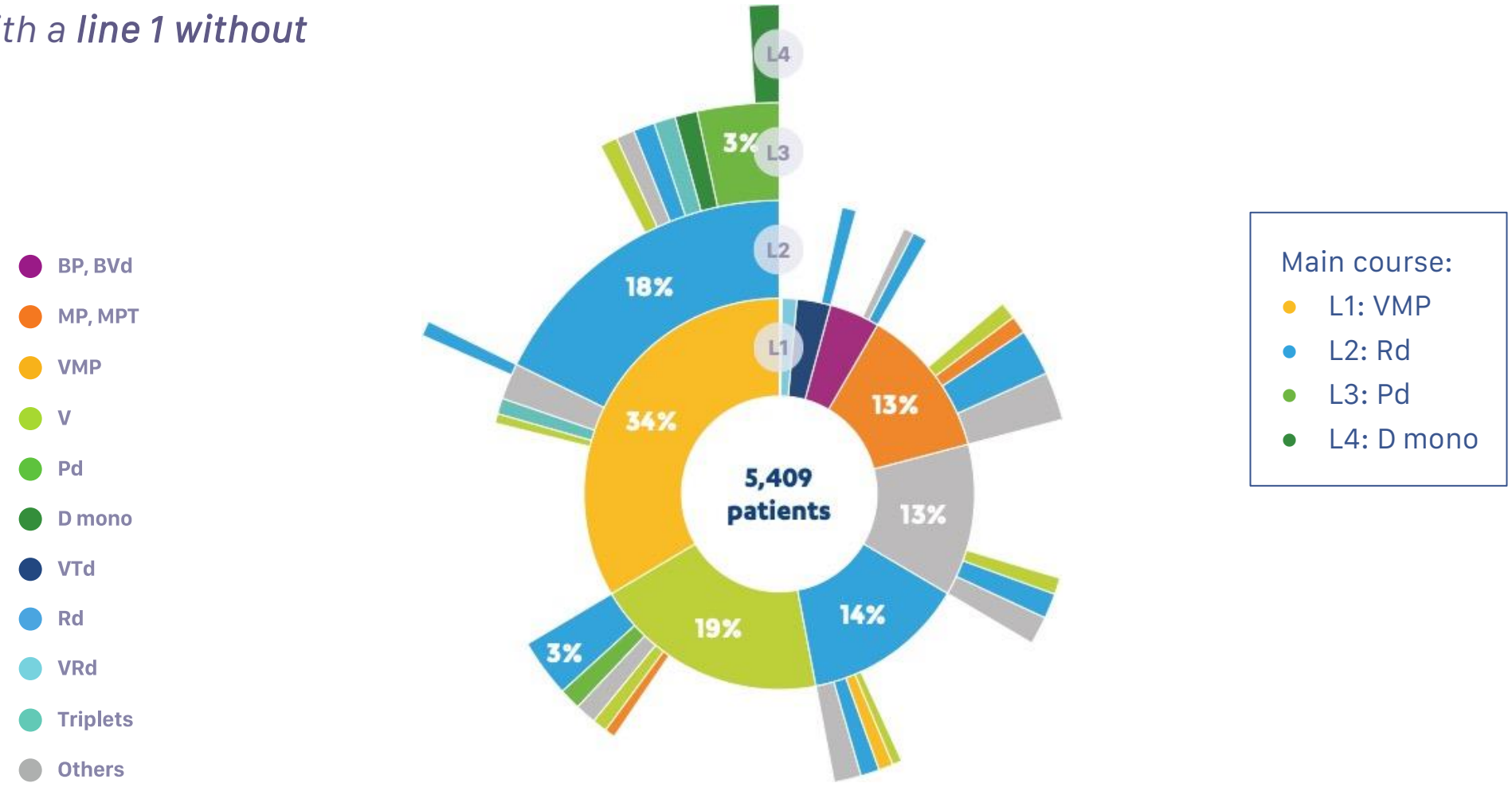



- Line 1
- Line 2
- Line 3

TTNT: Time to Next Treatment

# Results

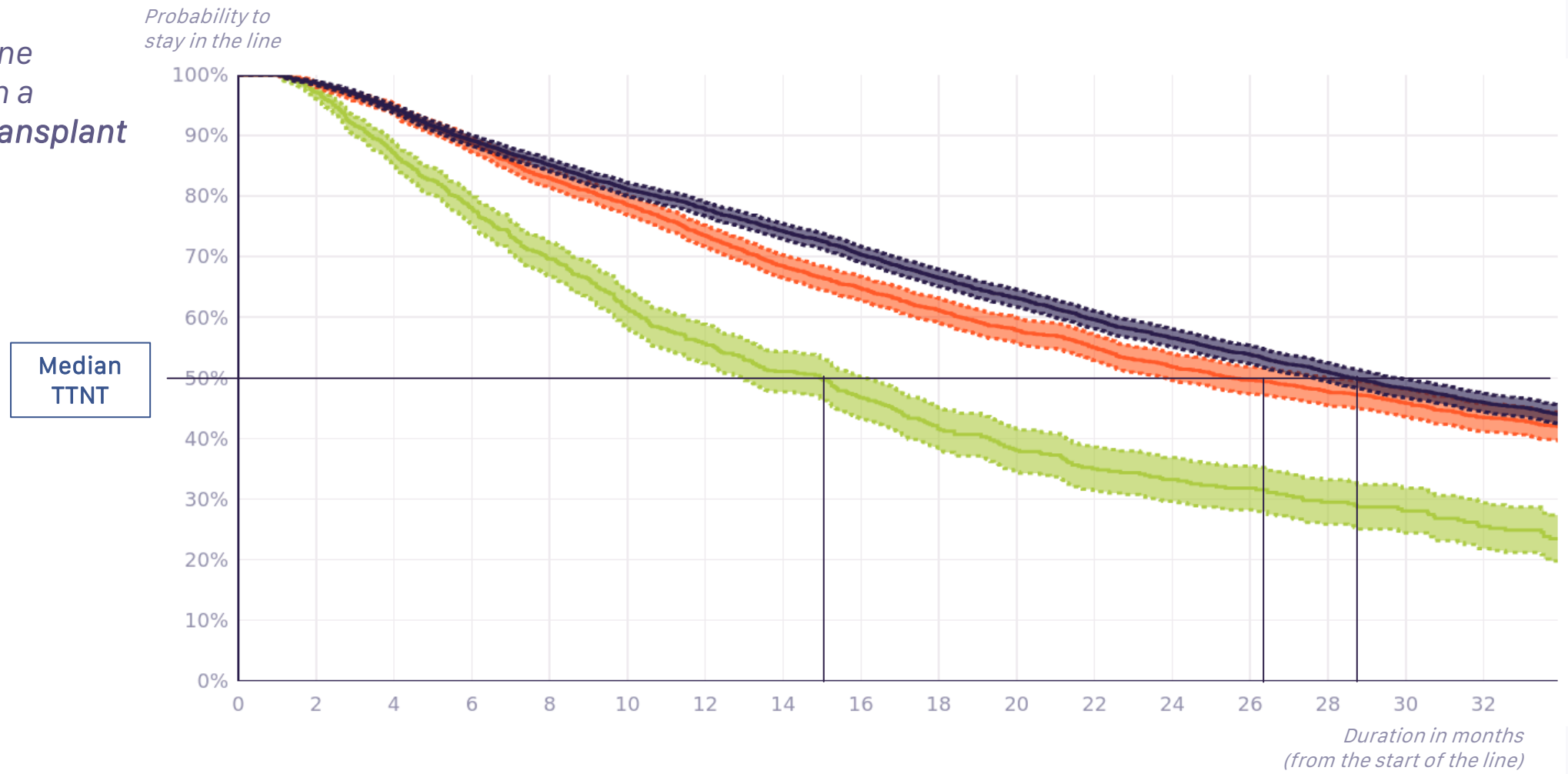
*Treatment sequences for patients with a **line 1 without transplant***




Triplets: IRd; KRd; DRd; DVd; PVd; DPd; VRd

# Results

*TTNT for each line for patients with a* ***line 1 without transplant***




- Line 1
- Line 2
- Line 3

TTNT: Time to Next Treatment

# Conclusion

- Many patients do not have the opportunity to be treated with several lines
  → **Initiate new treatments as early as possible**

- Fast evolving therapeutic landscape
  → **Important role of RWE studies to describe changes and could be used to compare treatment sequences effectiveness**

# Thank you for your attention

# EHA congress 2021

MYLORD EP999

## Epidemiology of multiple myeloma: data from the french national health insurance database (SNDS)


Cyrille Touzeau[1], Marie Pierres[2], Matthieu Javelot[2], Caroline Guilmet[2], Ludovic Lamarsalle[3], Fanny Raguideau[2], Isabelle Borget[4], Vincent Augusto[2], Aurore Perrot[4]

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### Background

Multiple myeloma (MM) is considered as an incurable hematologic disease. Net cancer-specific survival at 5 years after diagnosis of MM was estimated at 47% between 2005 and 2010 in France[a]. Thanks to significant improvements of the MM therapeutic management in the past decades, the overall survival of MM patients tends to increase, and some patients now achieve long-term remission. This directly impacts the dynamic of MM epidemiology. The world age-standardized MM incidence rate in France was estimated at 4.1 per 100,000 PY in 2020, based on extrapolations from available regional data. For the first time, this study provides updated and comprehensive epidemiological data by line of treatments based on the nationwide French National Health Insurance (NHI) databases, called SNDS ("Système National des Données de Santé"). These databases include hospital records, primary and secondary care, and deaths, for 66 million people.

The objective of the study is to estimate incidence, prevalence of MM and mortality of these patients, each year and for each line from 2014 to 2019, based on secondary use of data from the French NIH databases.

### Methods

**Design**

This is a retrospective observational cohort study of MM patients identified through SNDS from 2014 to 2019. To identify patients with MM, a published algorithm[b] was used as a base and was expanded to consider recent evolutions of MM therapeutic management. The rates were standardized using the age distribution to allow international comparison. Treatment lines were re-constructed through ATLAS, an artificial intelligence algorithm adapted on the Smith-Waterman alignment sequence[c].

**Inclusion criteria**

Adult patients affiliated to the General health insurance Scheme (covering around 76% of the French population) were included if they presented either:

- a hospital record with MM diagnosis (ICD-10 C90*), or
- a Long-Term Disease (LTD) status with MM diagnosis (ICD-10 C90*), or
- a treatment with lenalidomide or thalidomide paired with at least 2 protein electrophoresis on serum or urine in less than 4 months after the first delivery of the drug

from January 1st, 2006 to December 31st, 2019.

Data since 2006 are used to define prevalent and incident patients. Incident MM patients were defined as patients without MM information (LTD or hospitalization with MM diagnosis codes or MM treatment) during the 2 years prior to index date. Analysis were conducted only on patients treated and alive on January 1st 2014.

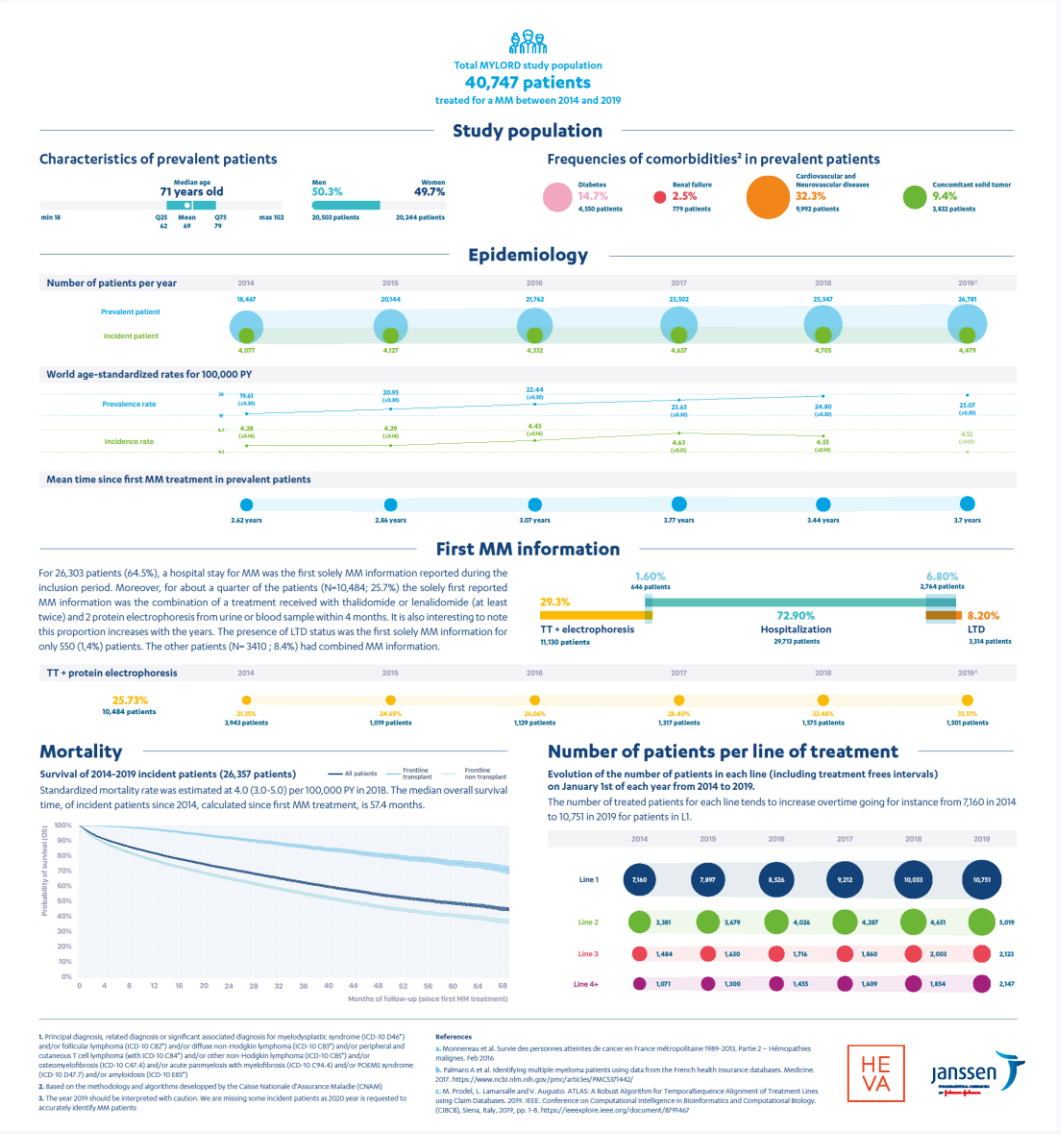
**Exclusion criteria**

- Patients with only ICD-10 C90.1/C90.2/C90.3 and not treated during the follow-up
- Among patients treated with lenalidomide or thalidomide and paired with at least 2 protein electrophoresis, patients with no hospital stay for MM and with a hospital stay for another reason[1].

### Conclusion

This study expands existing epidemiological data on MM patients in France and is the first to present recent nationwide results by line of treatment. Growing prevalence and incidence rates of MM are in accordance with the estimations from French network of cancer registries confirming that the French health insurance databases are a valuable source of data to further study the therapeutic management of MM.


European Hematology Association (EHA), June 9–17 2021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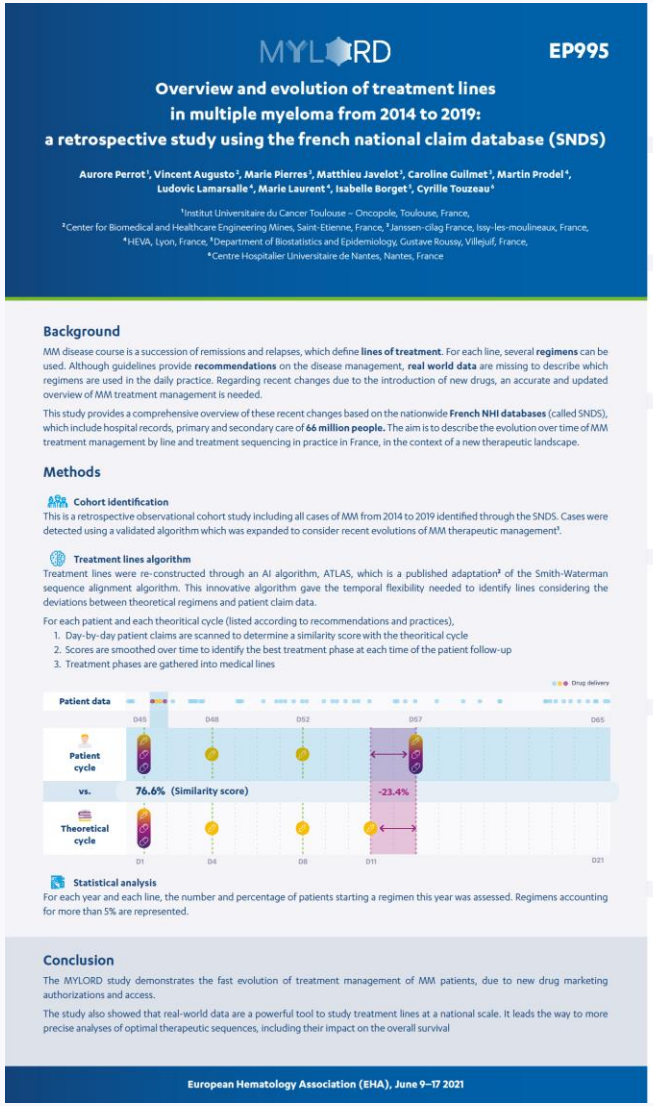

MYLORD EP995

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

Aurore Perrot[1], Vincent Augusto[2], Marie Pierres[3], Matthieu Javelot[2], Caroline Guilmet[3], Martin Prodel[4], Ludovic Lamarsalle[4], Marie Laurent[4], Isabelle Borget[5], Cyrille Touzeau[1]

[1]Institut Universitaire du Cancer Toulouse – Oncopole, Toulouse, France, [2]Center for Biomedical and Healthcare Engineering Mines, Saint-Etienne, France, [3]Janssen-cilag France, Issy-les-moulineaux, France, [4]HEVA, Lyon, France, [5]Department of Biostatistics and Epidemiology, Gustave Roussy, Villejuif, France, [6]Centre Hospitalier Universitaire de Nantes, Nantes, France

## 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 management[1].

**Treatment lines algorithm**

Treatment lines were re-constructed through an AI algorithm, ATLAS, which is a published adaptation[2] 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 theoritical cycle (listed according to recommendations and practices),

1. Day-by-day patient claims are scanned to determine a similarity score with the theoritical 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 each line, the number and percentage of patients starting a regimen this year was assessed. Regimens accounting for more than 5% 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

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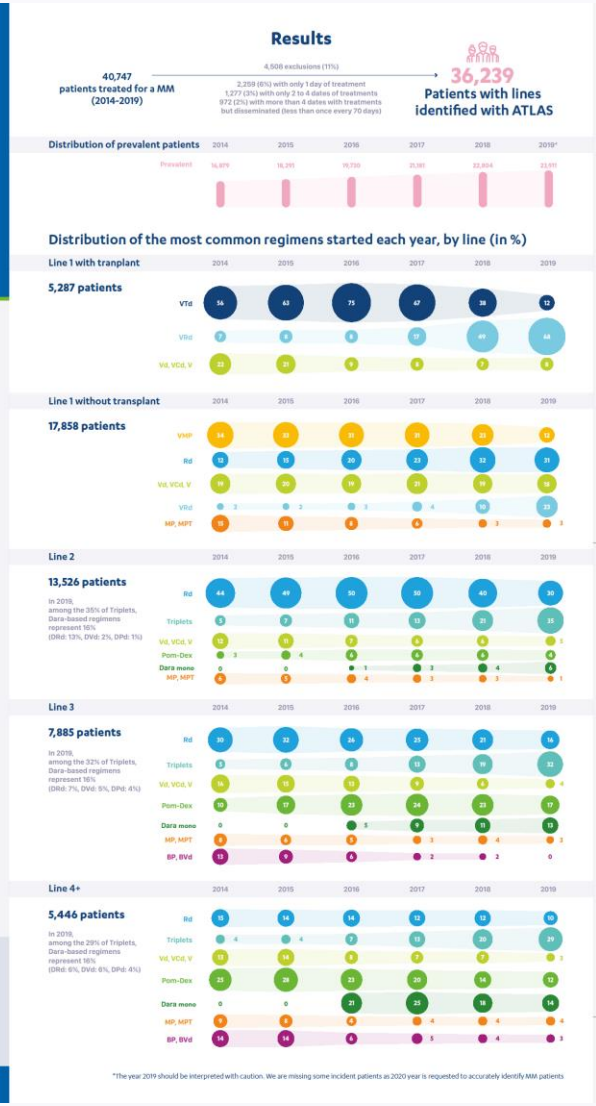

## Results

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 prevalent patients**



**Distribution of the most common regimens started each year, by line (in %)**



*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 mono



**Legend**

Rd
Lenalidomide / low-dose dexamethasone
Triplets
IRd: Isatomib / 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 mono
Daratumumab
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 SNIIRAM Database
**SNDS:** Système National des Données de Santé

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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

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