

Epidemiology and real-world management of Monoclonal Gammopathies patients in Spain based on natural language processing and machine learning techniques, the CIMMA Study.

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Key Takeaway
The CIMMA study is a pioneering initiative in RWE that holds the promise of transforming our understanding of patient journey, disease epidemiology, and treatment patterns in Spain patients diagnosed with monoclonal gammopathies. With preliminary data from 977 patients and the groundbreaking use of NLP and ML technologies, this study offers a different approach and opportunity to deepen our knowledge of MM, sMM-HR, and AL-AMY. This study embodies innovation, highlighting the incredible potential of advanced technology and collaborative research to enhance patient care.

Conclusions
Innovative Methodology and Significant Scale: The CIMMA study represents a novelty as for its large-scale and precise extraction approach of clinical data from EHRs from almost 2 million patients, only on in this first phase. The study provides detailed insights into patient diagnosis, demographics, clinical characteristics, and treatment patterns in real-world clinical practice.

Future Impact on Patient Care: As data processing nears completion, covering thousands of patients, we expect high-quality results that will undoubtedly improve the care and outcomes of patients with MM. The potential impact of this type of research is an innovative approach that will directly benefit numerous patients and guide clinical decision making towards personalized and optimized treatment strategies.

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Poster <https://www.congresshub.com/Oncology/EHA2024/Daratumu/mab/Mateos>

Narrated poster video

Supplementary material

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Disclosures
Natalia Marin Huarte, Angela Garcia, and Miguel Villanueva are employees of J&J Innovative Medicine. Savana Research Group members are employees of Savana Research S.L.

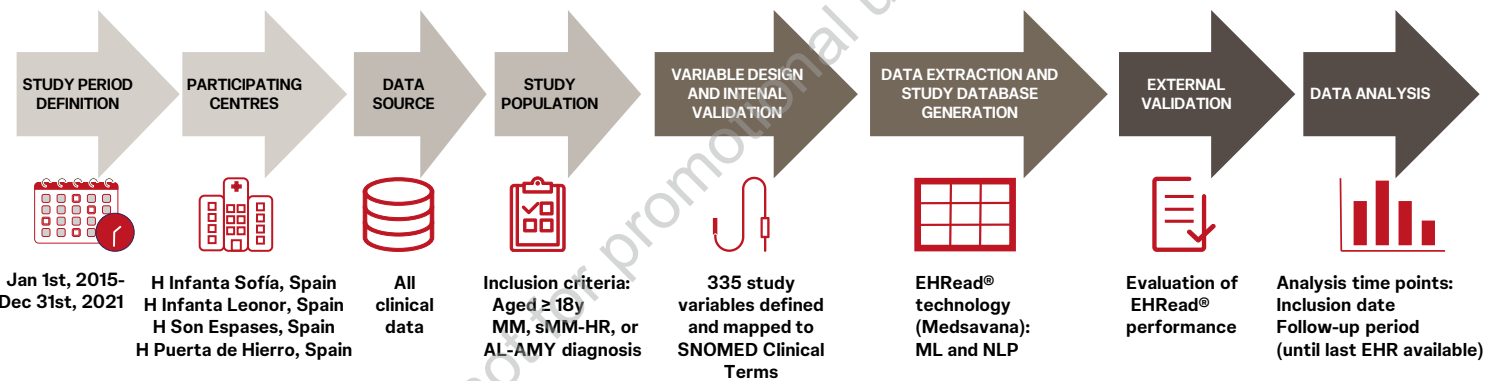
Introduction

The CIMMA study is an initiative to address the challenges of limited real-world evidence in the field of monoclonal gammopathies aiming to describe demographic, clinical, and treatment characteristics of patients with MM, sMM-HR, and AL-AMY in Spain. To achieve this, the study employs natural NLP and ML techniques to extract clinical information from patients' electronic health records (EHRs).

Methods

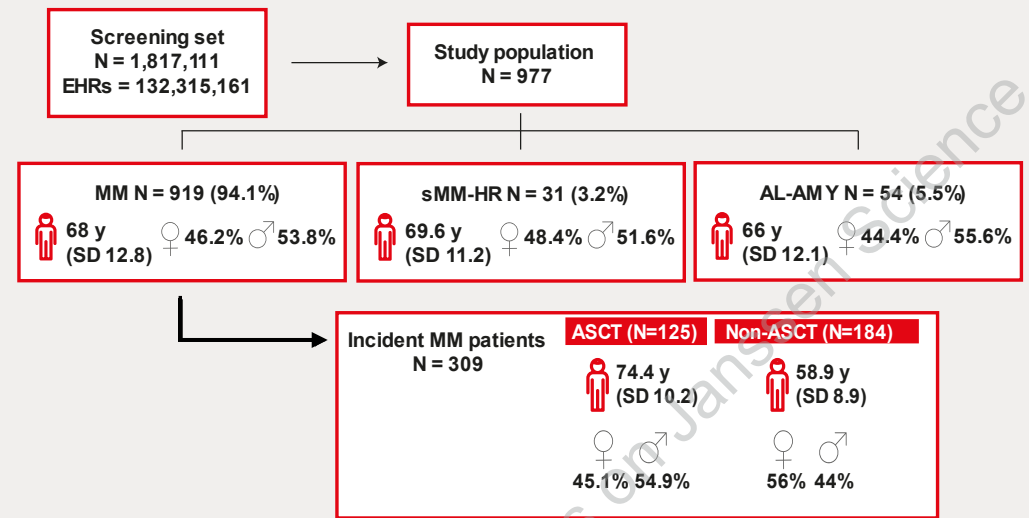
Multicenter, retrospective and observational study based on the secondary use of data included in the EHRs of adult patients diagnosed with monoclonal gammopathies in the period between 2015-2021. This study used EHRRead®, an innovative technology that applies NLP and ML to extract unstructured clinical information from EHRs using SNOMED-CT (Figure 1).

Figure 1: Study design.

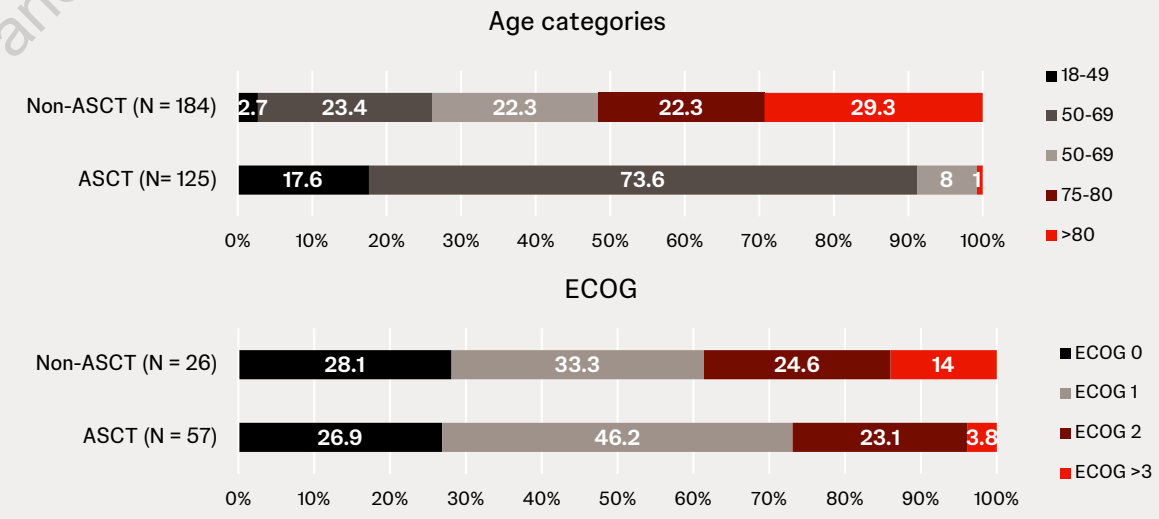


Results

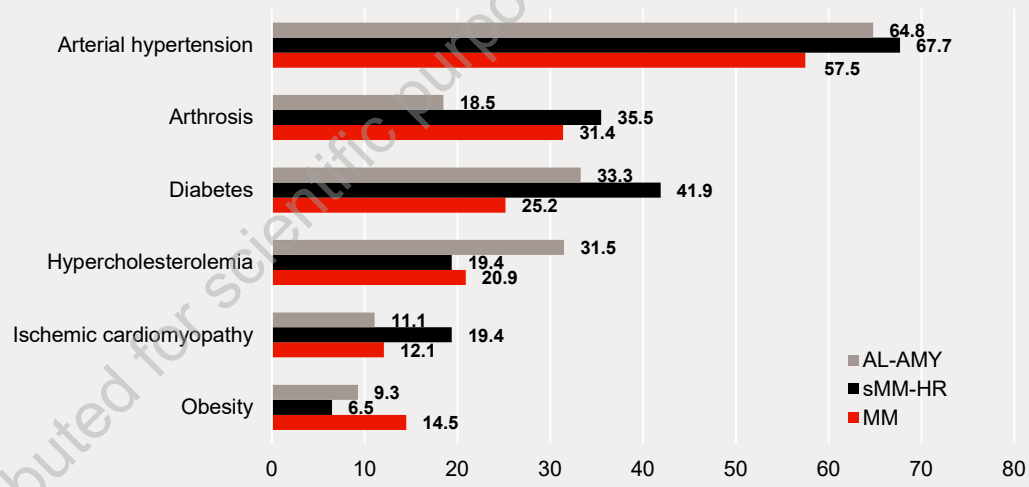
1. Study population Flow Chart



2. Incident MM patients (N = 309) demographics and clinical characteristics at diagnosis (note that for ECOG results, only patients with ECOG mentions in their EHRs are shown)



3. Main comorbidities at index (%)

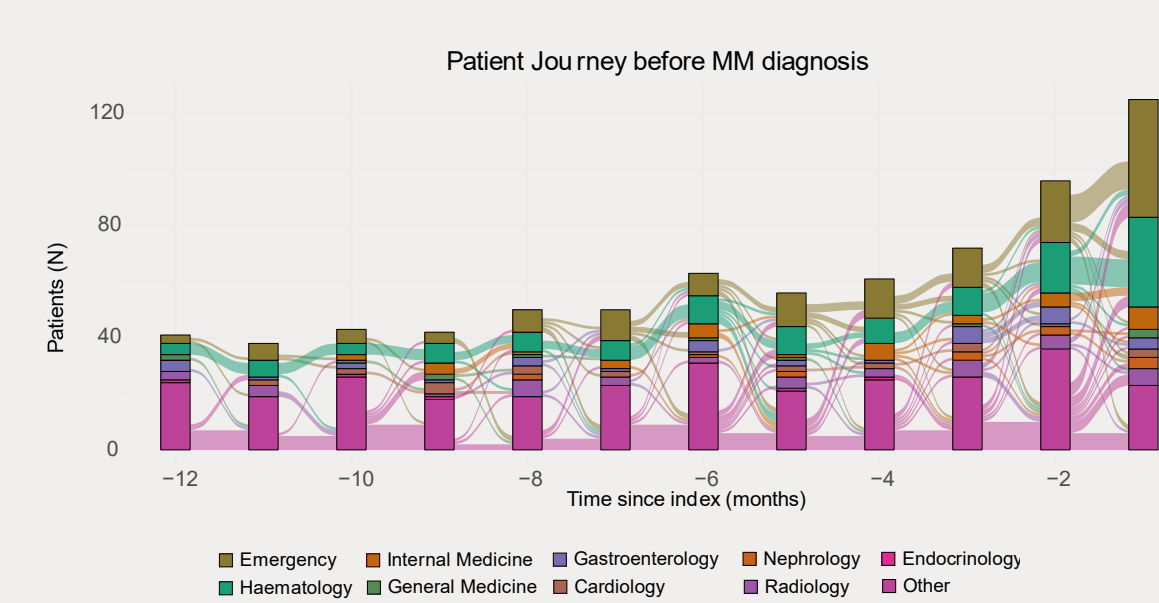


4. Main treatment combinations

	MM	
	ASCT	Non-ASCT
IMiD + PIs ^a	57.7%	18.6%
IMiD ^b	8.9%	36.2%

^aBortezomib+lenalidomide based treatment.
^bLenalidomide based treatment
The most frequent treatment for each group is underlined

5. Patient journey



Abbreviations:

RWE: Real-World Evidence. NLP: Natural Language Processing. ML: Machine Learning. EHR: Electronic Health Records. MM: Multiple Myeloma. sMM-HR: high-risk smoldering myeloma. AL-AMY: light chain amyloidosis. ASCT: Autologous Stem Cell Transplantation. IMiD: Immunomodulatory imide Drugs, PIs: proteasome inhibitors.

Multiple Myeloma