PA-482

Understanding Specific Treatment Sequences in Multiple Myeloma Dependent on the Treatment Received in Second Line: Survey Data from 141 International Clinicians

Joshua Richter,[1] James Farrell,[2] Didem Aydin,[3] Colin Burke,[4] Daniel Comoroda[5]

[1]Mount Sinai, New York, USA; [2]Pfizer Ltd, Dublin, Ireland; [3]Pfizer Ltd, Istanbul, Türkiye; [4]Lumanity, London, UK; [5]Lumanity, NJ, USA

Objectives

- How to appropriately sequence the MM treatment options in a clinician's armamentarium depends on many factors including the previous treatments received by the patient
- This study aimed to quantify the current practice for 2L to 4L MM treatment

Conclusions

- There is significant variance in the approach to treating patients with 2L to 4L MM across, and even within countries
- This study extends existing literature[3] by generating bespoke sequences dependent on prior treatments received. These can be used to identify the average sequences and understand how different regimens are being sequenced in real-world clinical practice
- The complexity of European sequences and lower uptake of BCMA and GPRC5D targeted agents is likely linked to funding and availability of treatment options and there could be opportunity for European clinicians to leverage the experience of their US colleagues to simplify treatment class selection and sequencing
- Canadian sequences are presented in the **supplementary material** and are complex even at the class level

Electronic Poster and Supplementary Material

Please scan this Quick Response (QR) code with your smartphone app to view this poster. If you do not have a smartphone, access the poster via the internet at: https://scientificpubs.congressposter.com/p/qjz1yky8wl5i8qgy

References: **1.** Dimopoulos MA, et al. Nat Rev Clin Oncol 2025; 22:680-700. **2.** Kumar SK, et al. J Natl Compr Canc Netw 2025; 23:132-140. **3.** Costa LJ, et al. Leukemia 2025;39:543-554.

Acknowledgments: The study was sponsored by Pfizer. Editorial services provided by Nucleus Global were funded by Pfizer.

Disclosures: JR reports consultant/advisory board: Janssen, BMS, Pfizer, Karyopharm, Sanofi, Takeda, Genentech, Abbvie, Regeneron, Forus, Menarini and speakers bureau: Janssen, BMS, Sanofi, Adaptive Biotechnologies, JF and DA report employment and stock ownership at Pfizer. CB and DC report employment by Lumanity who received study funding from Pfizer.

Contact: james.lawless-farrell@pfizer.com

Presented at the 2025 IMS Annual Meeting
September 17-20, 2025 | Toronto, ON, Canada

Background

- There are many treatment combinations for relapsed/refractory multiple myeloma (RRMM) comprising 7 main classes: immunomodulatory drugs (IMiDs), proteasome inhibitors (PIs), anti-CD38 antibodies (CD38), exportin-1 inhibitors (XPO1) and agents targeting B-cell maturation antigen (BCMA), G protein-coupled receptor class C group 5 member D (GPRC5D) or Signalling Lymphocytic Activation Molecule F7 (SLAMF7). Many are often combined with steroids such as dexamethasone (dex) or chemotherapy agents like cyclophosphamide (cyclo)
- Guidelines exist to support treatment choice (EHA-EMN[1], NCCN[2]), but limited data exists on which sequences are most commonly being used in real-world practice

Methods

- This cross-sectional survey (January 2025 to March 2025) included data from 141 hematologists, oncologists, and onco-hematologists across 5 countries: United States (US, n=49), United Kingdom (UK, n=28), Canada (CA, n=29), France (FR, n=24), and the Netherlands (NL, n=11)
- Physicians were recruited if they met the following criteria: 1) practiced medicine for 3-30 years, 2) ≥60% of time spent in direct patient care, 3) responsible for treating MM patients, and 4) ≥10 patients with MM treated per year
- Respondents estimated the percentage of patients they prescribed each treatment regimen in 1L through 4L. Treatment regimens in 3L and 4L were reported separately based on treatments used in 2L and 3L, respectively
- In the US the sequences are less complex at the drug class level, but more complex when individual agents are considered. US sequences show higher uptake and utilisation of newer agents from the BCMA and GPRC5D targeted classes

Results

- Across countries, a total of 18,671 unique sequences from 2L to 4L were reported (**Table 1**) with the most unique sequences coming from the US (12,185 sequences) and smallest number from the NL (837). In 2L, the number of different regimens was generally similar, from 24 in the NL to 39 in the UK and FR. When filtering by regimens reported by ≥5% of respondents (to avoid infrequently used regimens), the number of 2L options ranged from 4 (UK) to 8 (FR / NL)
- The figures show the most used 2L drug class combinations for European countries (**Figure 1**) and the US (**Figure 2**) and the treatment sequences for the European countries (**Figure 3**) and for the US (**Figure 4**) grouped and re-weighted by drug class to aid in presentation

Figure 1. European 2L options with 5% filter by drug class

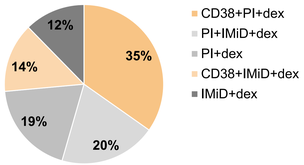


Figure 2. US 2L options with 5% filter by drug class

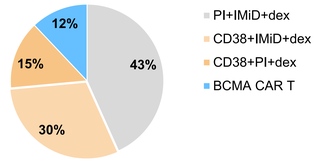


Table 1. Number of sequences from full survey and when limited to combinations indicated for 5% or more

Country	2L combinations	Sequences (2L→4L)
All	40	18,671
UK	39	4757
FR	39	1737
US	35	12,185
CA	35	2269
NL	24	837
	With 5% Filter	
Country	**2L combinations**	**Sequences (2L→4L)**
FR	8	232
NL	8	154
CA	7	244
US	6	161
UK	4	125

CD38+-dex/cyclo	SLAMF7+dex	BCMA bsAb	XPO1+dex	IMiD+-dex/cyclo	PI+cyclo+dex
CD38+PI+dex	SLAMF7+ImiD+dex	BCMA CAR T	XPO1+PI+dex	PI+-dex/cyclo	Other
CD38+IMiD+dex	SLAMF7+PI+dex	BCMA ADC	GPRC5D	PI+IMiD+dex	

Figure 3. European sequences

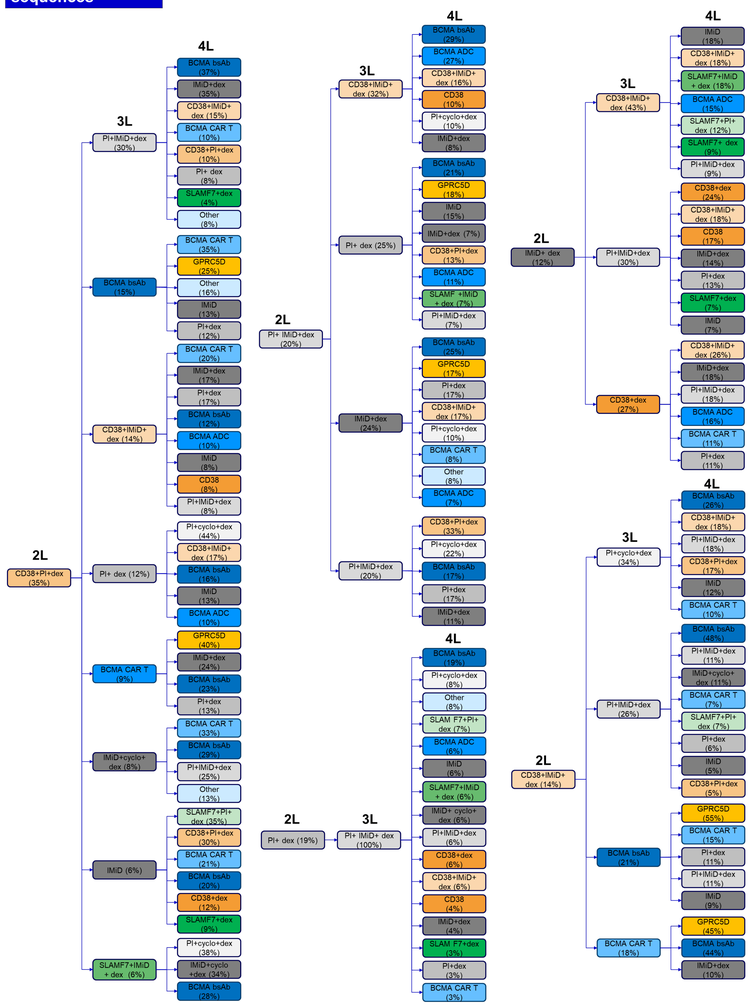
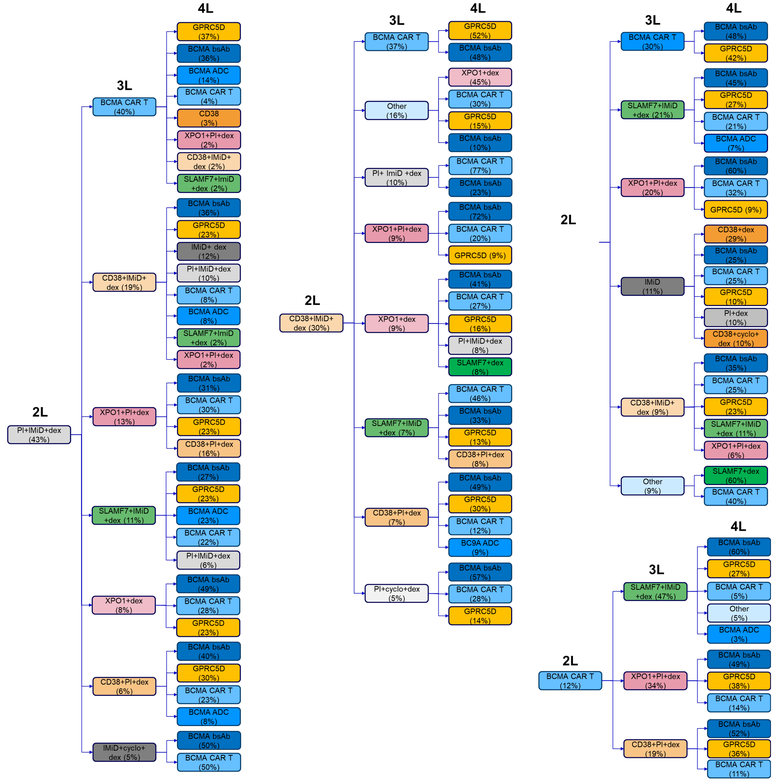
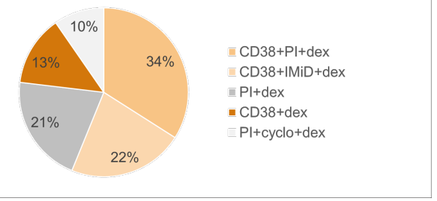


Figure 4. US sequences



Supplemental Figure 1. Canadian 2L options with 5% filter by drug class



Supplemental Figure 2. Canadian 2L options and sequences by drug class with 5% filter