

# Daratumumab plus bortezomib and dexamethasone versus bortezomib and dexamethasone in relapsed or refractory multiple myeloma: updated analysis of CASTOR

Andrew Spencer,<sup>1</sup> Suzanne Lentzsch,<sup>2</sup> Katja Weisel,<sup>3</sup> Hervé Avet-Loiseau,<sup>4</sup> Tomer M. Mark,<sup>5</sup> Ivan Spicka,<sup>6</sup> Tamas Masszi,<sup>7</sup> Birgitta Lauri,<sup>8</sup> Mark-David Levin,<sup>9</sup> Alberto Bosi,<sup>10</sup> Vania Hungria,<sup>11</sup> Michele Cavo,<sup>12</sup> Je-Jung Lee,<sup>13</sup> Ajay K. Nooka,<sup>14</sup> Hang Quach,<sup>15</sup> Cindy Lee,<sup>16</sup> Wolney Barreto,<sup>17</sup> Paolo Corradini,<sup>18</sup> Chang-Ki Min,<sup>19</sup> Emma C. Scott,<sup>20</sup> Asher A. Chanan-Khan,<sup>21</sup> Noemi Horvath,<sup>16</sup> Marcelo Capra,<sup>22</sup> Meral Beksac,<sup>23</sup> Roberto Ovilla,<sup>24</sup> Jae-Cheol Jo,<sup>25</sup> Ho-Jin Shin,<sup>26</sup> Pieter Sonneveld,<sup>27</sup> David Soong,<sup>28</sup> Tineke Casneuf,<sup>29</sup> Christopher Chiu,<sup>28</sup> Himal Amin,<sup>30</sup> Ming Qi,<sup>28</sup> Piruntha Thiyagarajah,<sup>31</sup> A. Kate Sasser,<sup>32</sup> Jordan M. Schecter<sup>30</sup> and Maria-Victoria Mateos<sup>33</sup>

<sup>1</sup>Malignant Haematology and Stem Cell Transplantation Service, Alfred Health-Monash University, Melbourne, Australia; <sup>2</sup>Division of Hematology/Oncology, Columbia University, New York, NY, USA; <sup>3</sup>Universitaetsklinikum Tuebingen der Eberhard-Karls-Universitaet, Abteilung fuer Innere Medizin II, Tuebingen, Germany; <sup>4</sup>Unite de Genomique du Myelome, CHU Rangueil, Toulouse, France; <sup>5</sup>Department of Medicine, University of Colorado, Aurora, CO, USA; <sup>6</sup>Clinical Department of Haematology, 1<sup>st</sup> Medical Department, Charles University in Prague, Czech Republic; <sup>7</sup>Department of Haematology and Stem Cell Transplantation, St László Hospital, 3<sup>rd</sup> Department of Internal Medicine, Semmelweis University, Budapest, Hungary; <sup>8</sup>Department of Hematology, Sunderbyn Hospital, Luleå, Sweden; <sup>9</sup>Albert Schweitzer Hospital Department of Internal Medicine, Dordrecht, the Netherlands; <sup>10</sup>Department of Hematology, Careggi Hospital and University of Florence, Italy; <sup>11</sup>Irmandade Da Santa Casa De Misericordia De São Paulo, Brazil; <sup>12</sup>“Seràgnoli” Institute of Hematology, Department of Experimental, Diagnostic and Specialty Medicine, University of Bologna, Italy; <sup>13</sup>Department of Hematology-Oncology, Chonnam National University Hwasun Hospital, Jeollanamdo, South Korea; <sup>14</sup>Winship Cancer Institute, Emory University, Atlanta, GA, USA; <sup>15</sup>St. Vincent's Hospital, University of Melbourne, Australia; <sup>16</sup>Royal Adelaide Hospital, North Terrace, Australia; <sup>17</sup>Hospital Santa Marcelina, São Paulo, Brazil; <sup>18</sup>Fondazione IRCCS Istituto Nazionale dei Tumori, University of Milan, Italy; <sup>19</sup>Seoul St. Mary's Hospital, South Korea; <sup>20</sup>Oregon Health & Science University, Portland, OR, USA; <sup>21</sup>Mayo Clinic Florida, Jacksonville, FL, USA; <sup>22</sup>Instituto do Cancer-Hospital Mae de Deus, Porto Alegre, Brazil; <sup>23</sup>Ankara University, Turkey; <sup>24</sup>Hospital Angeles Lomas, Naucalpan de Juárez y alrededores, México; <sup>25</sup>Ulsan University Hospital, South Korea; <sup>26</sup>Division of Hematology-Oncology, Department of Internal Medicine, School of Medicine, Medical Research Institute, Pusan National University Hospital, Busan, South Korea; <sup>27</sup>Erasmus Medical Center, Rotterdam, the Netherlands; <sup>28</sup>Janssen Research & Development, LLC, Spring House, PA, USA; <sup>29</sup>Janssen Research & Development, Beerse, Belgium; <sup>30</sup>Janssen Research & Development, LLC, Raritan, NJ, USA; <sup>31</sup>Janssen Research & Development, High Wycombe, UK; <sup>32</sup>Genmab US, Inc, Princeton, NJ, USA and <sup>33</sup>University Hospital of Salamanca/IBSAL, Spain

©2018 Ferrata Storti Foundation. This is an open-access paper. doi:10.3324/haematol.2018.194118

Received: March 27, 2018.

Accepted: August 17, 2018.

Pre-published: September 20, 2018.

Correspondence: [aspencer@netspace.net.au](mailto:aspencer@netspace.net.au)

## SUPPLEMENTARY APPENDIX

### Supplementary Methods

Cytogenetic abnormalities were determined at the screening visit prior to randomization by centralized next-generation sequencing. High-risk cytogenetic status was defined as having  $\geq 1$  of the following abnormalities: del17p, t(4;14), or t(14;16); standard-risk cytogenetic status was defined as those who underwent cytogenetic testing and did not meet the high-risk criteria. For t(4;14), translocations were detected via RNA-seq reads fused between immunoglobulin H and *WHSC1* or *FGFR3*. For t(14;16), translocations involved immunoglobulin H and *WWOX*. Tophat-Fusion<sup>1</sup> and deFuse<sup>2</sup> were used for translocation detection. For del17p detection using exome-seq, a  $>50\%$  deletion cutoff of the 17p region was utilized with CNVkit<sup>3</sup> and CNV Radar.<sup>4</sup>

Minimal residual disease (MRD) status was assessed by determining the DNA sequence of immunoglobulin genes for patients at the time of suspected complete response (CR; blinded to treatment group) and at 6 and 12 months after first dose (at completion and 6 months after completion of 8 cycles of bortezomib and dexamethasone [Vd] therapy, respectively). MRD was evaluated on bone marrow aspirate samples that had been prepared with Ficoll using the clonoSEQ<sup>®</sup> assay (Version 1.3; Adaptive Biotechnologies, Seattle, WA, USA) at sensitivities of 0.001% (1 cancer cell per 100,000 nucleated cells or  $10^{-5}$ ) and 0.0001% ( $10^{-6}$ ). To enable for a stringent, unbiased evaluation of MRD, samples from the entire intent-to-treat population that contained  $\geq 1$  million cells were assessed; patients were considered MRD-positive if they had only MRD-positive test results or had no MRD assessment. A minimum cell input equivalent to

the given sensitivity threshold was required to determine MRD negativity (for example, MRD at  $10^{-6}$  required that  $\geq 1$  million cells were evaluated).

### ***Patient Reported Outcomes***

Patient reported outcomes were evaluated in the intent-to-treat population using the EuroQol 5 Dimensions Questionnaire (EQ-5D-5L) and the European Organization for Research and Treatment of Cancer Quality of Life (QoL) Questionnaire Core-30 (EORTC-QLQ-C30). The utility score and visual analog scale were evaluated for EQ-5D-5L. EORTC-QLQ-C30 subscales included the Global Health Status/QoL scale, functional scales (physical, role, cognitive, emotional, and social) and symptom scales (fatigue, pain, and nausea and vomiting). Single-item scores for dyspnea, loss of appetite, insomnia, constipation, diarrhea, and financial difficulties were also evaluated. Least squares mean changes from baseline were calculated for EQ-5D-5L and EORTC-QLQ-C30 using mixed models for repeated measures.

### ***Statistical Analysis***

A total of 498 patients were randomly assigned. Based on an interim analysis after 189 disease progression events had occurred with 7.4 months of follow-up,<sup>5</sup> the independent data and safety monitoring committee recommended that the trial be unblinded early because the prespecified statistical boundary (alpha level of 0.0102) for the primary endpoint was crossed; patients in the control group who had progressed had the option to receive daratumumab monotherapy.

Progression-free survival was compared between treatment groups based on a stratified log-rank test; hazard ratios and 95% confidence intervals were estimated using a stratified Cox regression

model with treatment as the sole explanatory variable; the Kaplan-Meier method was used to estimate the distributions. A stratified Cochran-Mantel-Haenszel chi-square test was used to test treatment differences in overall response rate and rates of very good partial response or better and CR or better. The MRD-negative rates for each treatment group were compared using the likelihood-ratio chi squared test.

## Supplemental Tables

**Table S1. Distribution of Cytogenetic Abnormalities (Next generation Sequencing)**

	<b>D-Vd (n=167)</b>	<b>Vd (n=186)</b>
del17p, n (%)	13 (7.8)	19 (10.2)
t(4;14), n (%)	26 (15.6)	32 (17.2)
t(14;16), n (%)	7 (4.2)	2 (1.1)

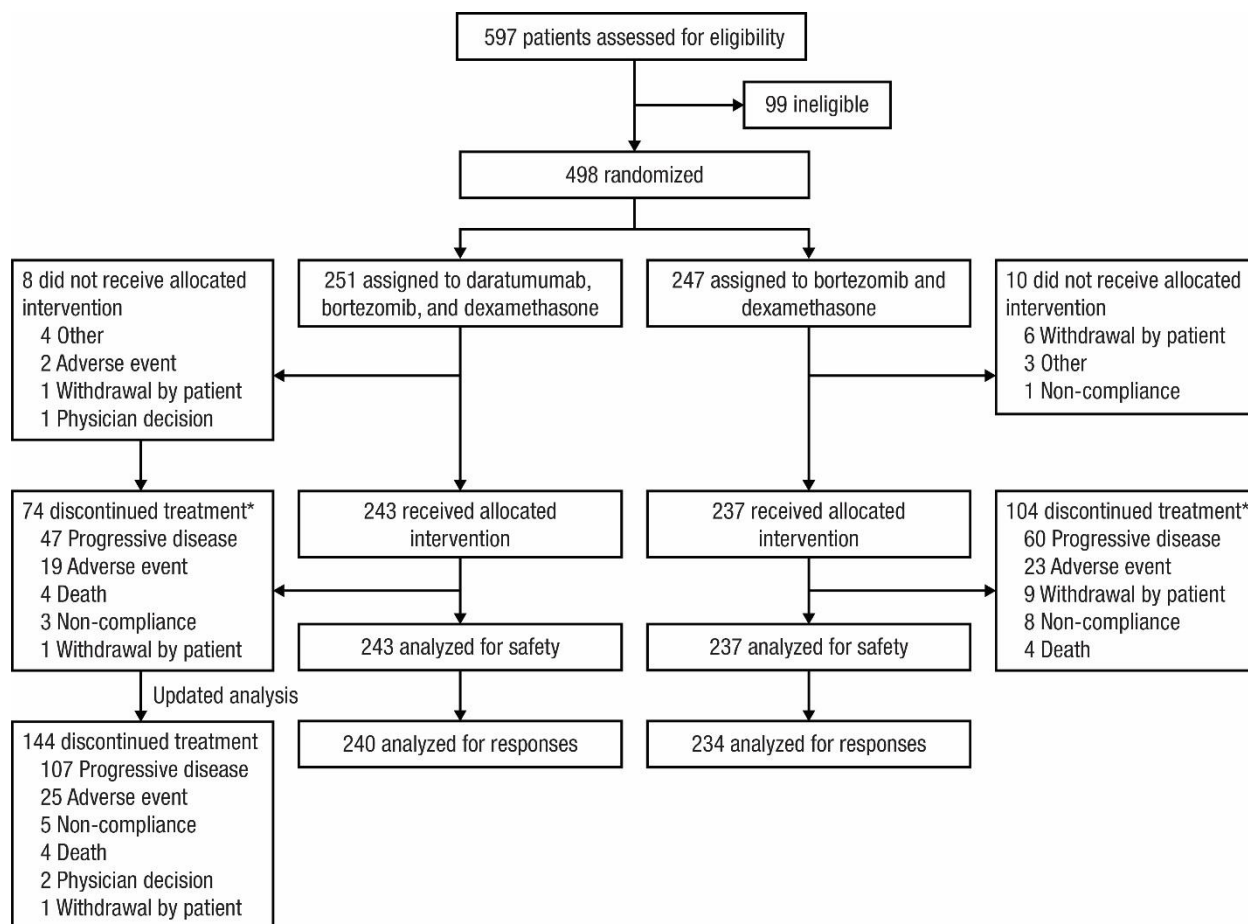
D-Vd, daratumumab plus bortezomib and dexamethasone; Vd, bortezomib and dexamethasone.

**Table S2. Overall Best Confirmed Response in the Response-evaluable Population**

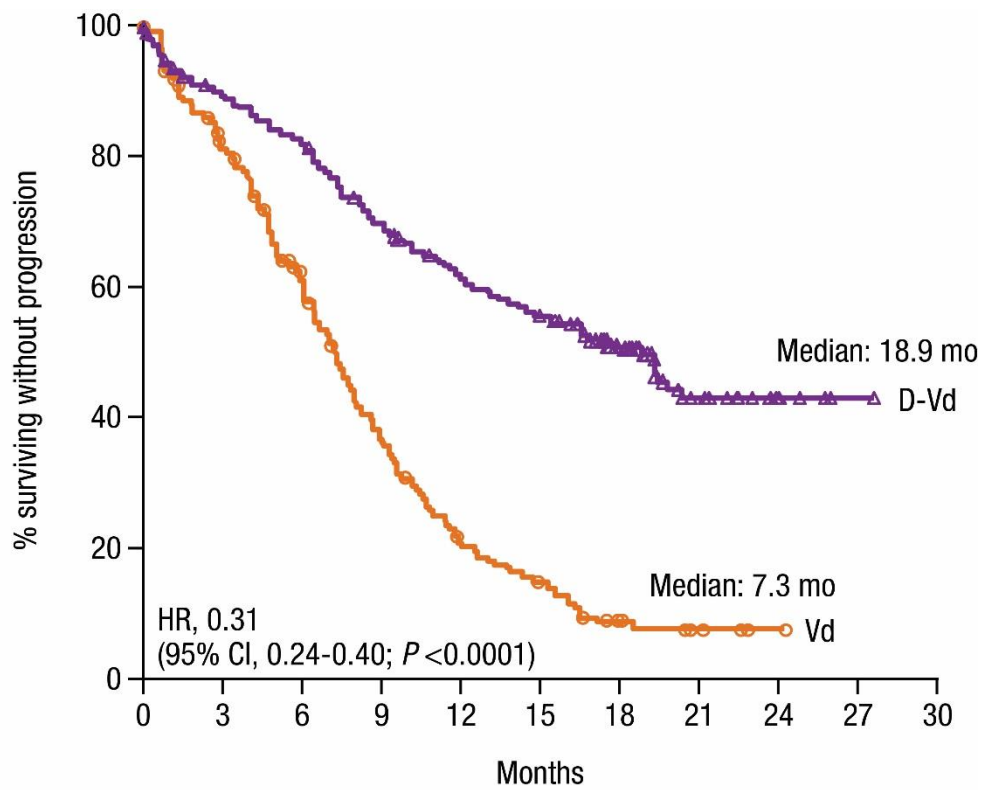
<b>Response, n (%)</b>	<b>D-Vd (n = 240)</b>	<b>Vd (n = 234)</b>	<b>P-value</b>
ORR	201 (83.8)	148 (63.2)	<0.0001
CR or better	69 (28.8)	23 (9.8)	<0.0001
sCR	21 (8.8)	6 (2.6)	
CR	48 (20.0)	17 (7.3)	
VGPR or better	149 (62.1)	68 (29.1)	<0.0001
VGPR	80 (33.3)	45 (19.2)	
PR	52 (21.7)	80 (34.2)	
MR	9 (3.8)	20 (8.5)	
SD	23 (9.6)	47 (20.1)	
PD	5 (2.1)	16 (6.8)	
NE	2 (0.8)	3 (1.3)	

D-Vd, daratumumab plus bortezomib and dexamethasone; Vd, bortezomib and dexamethasone; ORR, overall response rate; CR, complete response; sCR, stringent complete response; VGPR, very good partial response; PR, partial response; MR, minimal response; SD, stable disease; PD, progressive disease; NE, not evaluated.

Data are n (%) based on computerized algorithm.

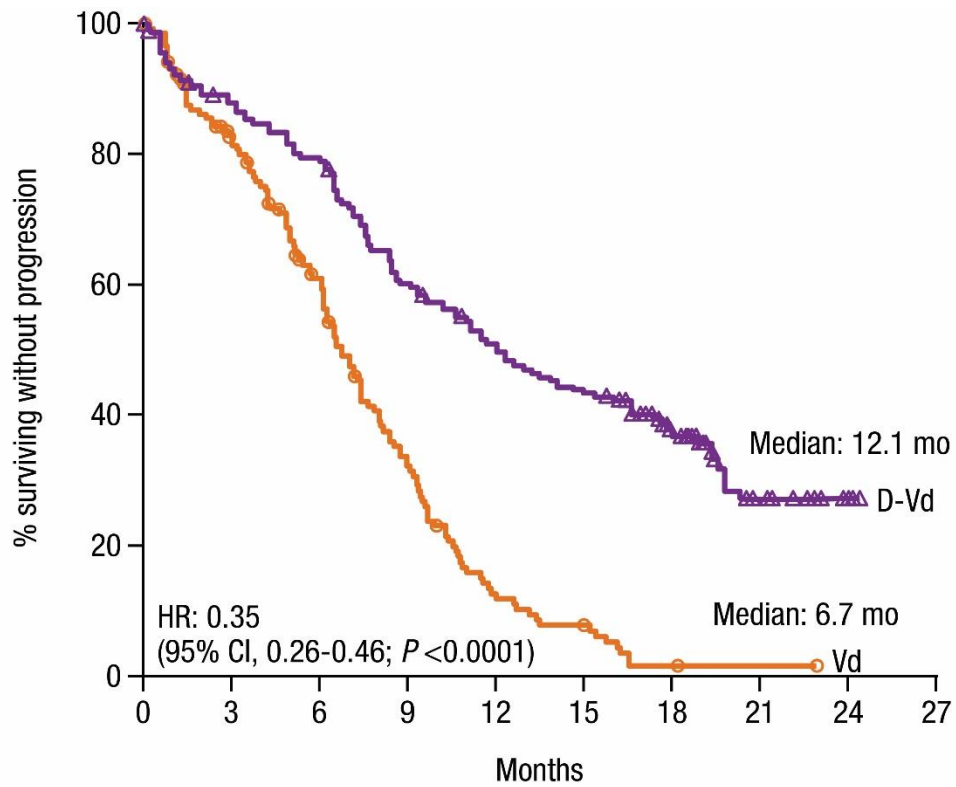


**Figure S1. Trial profile.** \* All patients were to receive 8 cycles of bortezomib and dexamethasone. After Cycle 8, patients in the daratumumab group continued to receive daratumumab monotherapy every 4 weeks, whereas patients receiving only bortezomib and dexamethasone were entered into an observation phase. All patients had discontinued or completed 8 cycles of bortezomib and dexamethasone by the interim analysis.<sup>5</sup> For the updated analysis (clinical cutoff date of January 11, 2017), 99 (41%) patients continued to receive daratumumab monotherapy.



No. at risk											
Vd	219	164	119	71	38	27	11	5	1	0	0
D-Vd	229	196	181	151	131	118	75	28	7	1	0

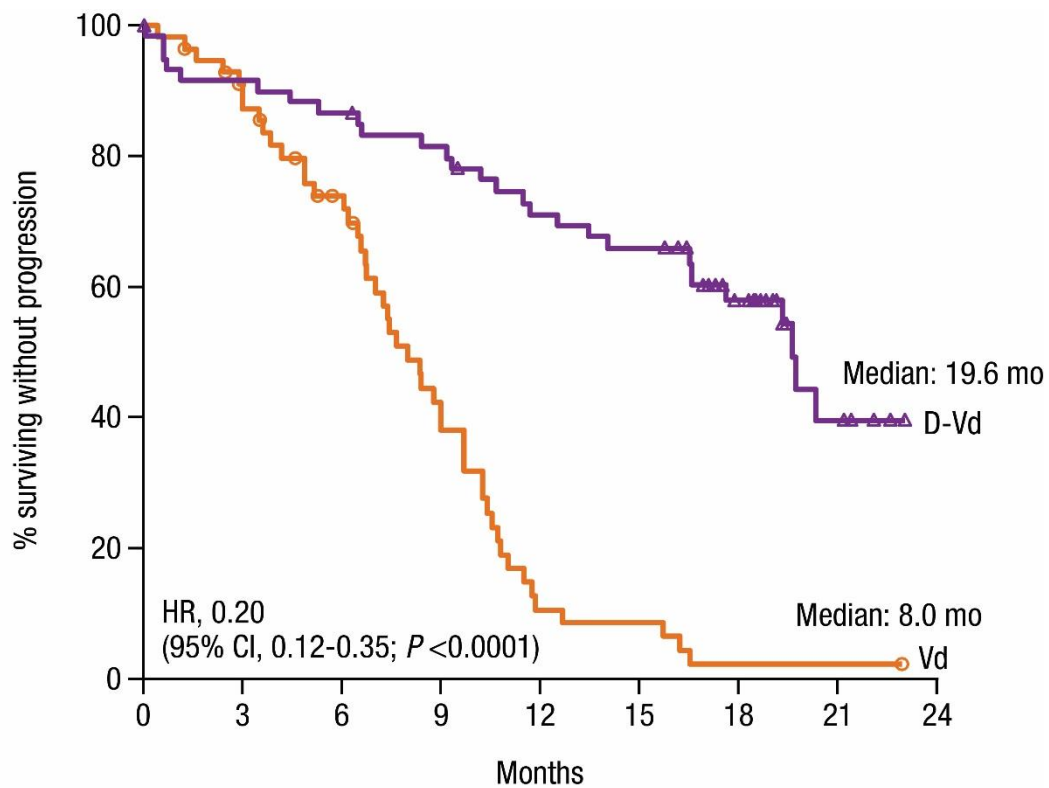
**Figure S2. Progression-free survival among patients who received 1 to 3 prior lines of therapy.** D-Vd, daratumumab plus bortezomib and dexamethasone; Vd, bortezomib and dexamethasone; HR, hazard ratio; CI, confidence interval.



No. at risk		0	3	6	9	12	15	18	21	24	27
Vd	164	119	83	44	16	10	2	1	0	0	
D-Vd	162	137	124	93	76	66	42	16	3	0	

**Figure S3. Progression-free survival based on prior bortezomib exposure.** D-Vd, daratumumab plus bortezomib and dexamethasone; Vd, bortezomib and dexamethasone; HR, hazard ratio; CI, confidence interval.





No. at risk	0	3	6	9	12	15	18	21	24
Vd	57	48	36	20	5	4	1	1	0
D-Vd	62	55	52	48	41	38	24	8	0

**Figure S4. Progression-free survival in patients that received bortezomib in their only line of therapy.** D-Vd, daratumumab plus bortezomib and dexamethasone; Vd, bortezomib and dexamethasone; HR, hazard ratio; CI, confidence interval.

## References

1. Kim D, Salzberg SL. TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. *Genome Biol.* 2011;12(8):R72.
2. McPherson A, Hormozdiari F, Zayed A, et al. deFuse: an algorithm for gene fusion discovery in tumor RNA-Seq data. *PLoS Comput Biol.* 2011;7(5):e1001138.
3. Talevich E, Shain AH, Botton T, Bastian BC. CNVkit: Genome-wide copy number detection and visualization from targeted DNA sequencing. *PLoS Comput Biol.* 2016;12(4):e1004873.
4. Chiu C, Soong D, Spicka I, et al. Next generation sequencing (NGS) methodology for determining cytogenetic risk status in the daratumumab phase 3 CASTOR and POLLUX studies in relapsed or refractory multiple myeloma (RRMM). Presented at: the 22nd Congress of the European Hematology Association (EHA); June 22–25, 2017; Madrid, Spain.
5. Palumbo A, Chanan-Khan A, Weisel K, et al. Daratumumab, bortezomib, and dexamethasone for multiple myeloma. *N Engl J Med.* 2016;375(8):754–766.