

### INTRODUCTION

- Myelodysplastic syndromes (MDS) are characterized by clonal myeloproliferation arising from malignant progenitor cell clones that have multiple genetic abnormalities.<sup>1</sup>
- Patients with red blood cell (RBC) transfusion-dependent (TD), lower risk MDS (LR-MDS) that has relapsed or is refractory to erythropoiesis-stimulating agents (ESAs) have limited treatment options. New approaches are needed.
- Higher telomerase activity, overexpression of human telomerase reverse transcriptase (hTERT) and shorter telomeres predict for shorter overall survival in LR-MDS.<sup>2, 3</sup>
- Imetelstat is a 13-mer lipid-conjugated oligonucleotide that specifically targets the RNA template of human telomerase and is a potent, first-in-class competitive inhibitor of telomerase enzymatic activity<sup>4, 5</sup> (Figure 1). It has disease-modifying potential to selectively kill malignant stem and progenitor cells enabling normal blood cell production (Figure 2). <sup>6,7</sup>
- IMerge (MDS3001, NCT02598661) is a Phase 2/3 global study of imetelstat for red blood cell (RBC) transfusion dependent (TD), non-del(5q) patients with ESA-R/R LR-MDS. Phase 2 results indicated that imetelstat achieved durable transfusion independence (TI) with a manageable safety profile.<sup>8</sup> With a median follow-up of 24 months for Phase 2, 42%, 32% and 29% of 38 patients achieved  $\geq$ 8-week (w),  $\geq$ 24-w and 1-year (y) TI, respectively.<sup>9</sup>

#### Figure 1. Imetelstat binds to the RNA template as a competitive inhibitor to prevent maintenance of telomeres

Figure 2. Imetelstat selective killing of malignant stem and progenitor cells enabling normal blood cell production



# **OBJECTIVES**

• To evaluate clinical efficacy of imetelstat in molecularly defined subtypes based on cytogenetic and mutation profiles.

### METHODS

- Bone marrow aspirates from screening were used for cytogenetic analysis by karyotyping.
- Peripheral blood samples were collected to analyze mutations by next-generation sequencing using the Illumina TruSight Myeloid Panel of 54 genes.
- Correlation analyses between molecular profiles and clinical efficacy, including TI ≥8-w,  $\geq$ 24-w,  $\geq$ 1-y, and hematologic improvement-erythroid (HI-E) response per International Working Group 2006 guidelines, were performed for patients in the Phase 2 part of IMerge study.

# EFFICACY OF IMETELSTAT IS INDEPENDENT OF MOLECULAR SUBTYPES IN HEAVILY TRANSFUSED NON-DEL(5Q) LOWER RISK MDS (LR-MDS) RELAPSED/REFRACTORY (R/R) TO ERYTHROPOIESIS STIMULATING AGENTS (ESA)

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### RESULTS

#### Table 1. Durable TI, hematologic improvement with imetelstat treatment

Parameters	n = 38					
8-week TI, n (%)	<b>16 (42)</b>					
Time to onset of 8-week TI, weeks, median (range)	8.3 (0.1-40.7)					
Duration of TI, weeks, median (95% CI) <sup>a</sup>	<b>88.0 (23.1 – 140.9*)</b>					
Cumulative duration of TI ≥ 8 weeks <sup>b</sup> , median (95% CI) <sup>a</sup>	92.3 (42.9, 140.9)					
Hb rise ≥ 3.0 g/dL during TIc, n (%)	12 (32)					
24-week TI, n (%)	<b>12 (32)</b>					
Hb rise ≥ 3.0 g/dL during TI <sup>c</sup> , n (%)	11 (29)					
HI-E per IWG 2006, n (%)	<b>26 (68)</b>					
≥1.5 g/dL increase in Hb lasting ≥ 8 weeks <sup>d</sup> , n (%)	13 (34)					
Transfusion reduction by ≥ 4 units/8 weeks, n (%)	26 (68)					
Duration of HI-E, weeks, median (95% CI) <sup>a</sup>	<b>92.7 (37.1, 149.4)</b> )					
Major and Minor Response per IWG 2018 Major response: 16-week TI, n (%) Minor response: ≥ 50% transfusion reduction/16 weeks, n (%)	<b>14 (37)</b> 21 (55)					

#### Figure 3. Mutation profile and risk groups vs clinical response (N=31 with sequencing data for mutations)

IPSS																
Cytogenetics																
SF3B1																
SRSF2																
TET2																
DNMT3A																
ASXL1																
TP53																
RUNX1																
КІТ																
NRAS																
JAK2																
MPL																
#of Mutation	0	2	1	3	2	2	4	0	1	3	1	3	1	1	3	2
≥8-week TI																
≥24-week TI																
≥ 1 year TI																
HI-E response																

# cytogenetic risk (B) groups



### Figure 5. Clinical response was independent of mutation status (A), or mutations in genes involved in different biological functions (B)



38 patients with non-del(5a) LR MDS R/R to ESA Clinical cutoff for analyses: 4 Feb 2020 Kaplan Meier method: <sup>b</sup> Cumulative Duration of TI  $\geq$  8 weeks is defined as the sum of all periods of  $TI \ge 8$  weeks during the <sup>2</sup> Maximum Hb rise of  $\geq 3g/dL$  from pretreatment level (pretreatment level defined as mean Hb / 8 <sup>d</sup> All patients also achieved 8-week TI. CI, confidence interval; Hb, hemoglobin HI-E, hematologic improvement-erythroic IWG 2006, International Working Group Response Criteria 2006: TI. Transfusion Independence

\*Longest TI > 2.7 years





### Figure 6. HI-E response was seen in patients with different SF3B1 hot spot mutations, durable TI was observed in patients with all SF3B1 hot spot mutations except K666R



## **SUMMARY**

- with all hot spot mutations (Fig. 6).

### CONCLUSIONS

Imetelstat demonstrated clinical efficacy across different molecularly defined subgroups of heavily transfused LR-MDS ESA-R/R patients, including those with poor prognosis, who have limited treatment options.

## REFERENCES

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### **CONTACT INFORMATION**



Imetelstat treatment showed meaningful and durable TI in 38 heavily TD, non-del(5q), HMA/Len naïve, LR-MDS patients with substantial increase in hemoglobin (**Table 1**).

• No statistically significant difference in response rate was observed in patients between IPSS low and Int-1 risk group or between very good/good and int poor cytogenetic risk groups, though a high rate of TI and HI-E was observed in the poor risk group (Fig. 4).

• Of 31/38 patients with baseline mutation data, 28 (90.3%) patients had at least one mutation, among which 15 (53.6%), 8 (28.6%) and 5 (17.9%) patients had 1, 2 and  $\geq 3$ mutations, respectively. 3 patients had no mutation detected (Fig. 3). Clinical response was independent of mutation status, or number of mutations (Fig. 5).

• The most frequently mutated gene was SF3B1 (87.1%, n=27), consistent with the predominance of ring sideroblast phenotypes (n=23). SF3B1 hot spot mutations were detected: 3 (11.1%) E622D, 3 (11.1%) R625C/L, 4 (14.8%) H662Q, 4 (14.8%) K666R, 12 (44.4%) K700E and 1 (3.7%%) G740E, respectively. Durable TI was observed in patients with these hot spot mutations except K666R, and HI-E response was seen in patients

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• IMerge (MDS3001): <u>https://www.geron.com/patients/imerge-study</u> ClinicalTrials.gov Identifier:NCT02598661; Email <u>mds3001-info@geron.com</u>

