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DOI:
10.1182/bloodadvances.2023010098

Document Version
Publisher's PDF, also known as Version of record

Citation for published version (Harvard):
Schulz, E, Aplan, PD, Freeman, SD & Pavletic, SZ 2023, 'Towards a Conceptualization of Measurable Residual Disease in Myelodysplastic Syndromes', *Blood Advances*. https://doi.org/10.1182/bloodadvances.2023010098

blood advances

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Towards a Conceptualization of Measurable Residual Disease in Myelodysplastic Syndromes

Tracking no: ADV-2023-010098R1

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Abstract:
Approximately 90% of patients with myelodysplastic syndromes (MDS) have somatic mutations in the malignant cells that are known or suspected to be oncogenic. The genetic risk-stratification of MDS has evolved substantially by the introduction of the clinical-molecular International Prognostic Scoring System (IPSS-M) that establishes next-generation sequencing at diagnosis as a standard of care. Furthermore, the International Consensus Classification (ICC) of myeloid neoplasms and acute leukemias has refined MDS diagnostic criteria with the introduction of a new myelodysplastic syndrome/acute myeloid leukemia (MDS/AML) category. Monitoring measurable residual disease (MRD) has historically been used to define remission status, improve relapse prediction, and determine the efficacy of antileukemic drugs in patients with acute and chronic leukemias. However, in contrast to leukemias, assessment of MRD including tracking of patient-specific mutations has not yet been formally defined as a biomarker for MDS. This article summarizes current evidence and challenges, and provides a conceptual framework for incorporating MRD into the treatment of MDS and future clinical trials.

Conflict of interest: COI declared - see note

COI notes: E.S.: Amgen (Honoraria). P.D.A.: No conflict of interest. S.Z.P.: No conflict of interest.

Preprint server: No;

Author contributions and disclosures: Conception of the work: E.S., S.Z.P; Interpretation of Data: E.S., S.F., P.D.A., S.Z.P; Drafted the manuscript: E.S., S.F., P.D.A., S.Z.P. All authors have seen and approved the manuscript being submitted.

Non-author contributions and disclosures: No;

Agreement to Share Publication-Related Data and Data Sharing Statement: N/A

Clinical trial registration information (if any):

Towards a Conceptualization of Measurable Residual Disease in Myelodysplastic Syndromes

Short title

MRD in MDS

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Author contributions

All authors researched the data for the article and made a substantial contribution to the discussion of the content. ES wrote the first draft, and all authors reviewed and edited the manuscript before submission.

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The views expressed in this work do not represent the official views of the National Institutes of Health or the United States Government.

Key words

Myelodysplastic syndrome; measurable residual disease; acute myeloid leukemia; stem cell transplantation; response criteria.

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Manuscript Data

Word counts

Abstract – 160

Text – 5163

Figures – 2

Tables – 2

Supplemental material – 4 Tables

References – 118

Abstract

Approximately 90% of patients with myelodysplastic syndromes (MDS) have somatic mutations in the malignant cells that are known or suspected to be oncogenic. The genetic risk-stratification of MDS has evolved substantially by the introduction of the clinical-molecular International Prognostic Scoring System (IPSS-M) that establishes next-generation sequencing at diagnosis as a standard of care. Furthermore, the International Consensus Classification (ICC) of myeloid neoplasms and acute leukemias has refined MDS diagnostic criteria with the introduction of a new myelodysplastic syndrome/acute myeloid leukemia (MDS/AML) category. Monitoring measurable residual disease (MRD) has historically been used to define remission status, improve relapse prediction, and determine the efficacy of antileukemic drugs in patients with acute and chronic leukemias. However, in contrast to leukemias, assessment of MRD including tracking of patient-specific mutations has not yet been formally defined as a biomarker for MDS. This article summarizes current evidence and challenges, and provides a conceptual framework for incorporating MRD into the treatment of MDS and future clinical trials.

Introduction

Measurable residual disease (MRD), the detection of residual malignant cells during complete hematologic remission, allows for disease monitoring and is the most important predictor of survival for acute leukemias. [1-3] Although myelodysplastic syndromes (MDS) are considered malignant preleukemic myeloid neoplasms and may share many features with subtypes of acute myeloid leukemia (AML), MRD has not yet been effectively applied as a biomarker in MDS. [4-8]

MDS are a heterogeneous group of biologically and clinically distinct sub-entities characterized by ineffective and dysplastic hematopoiesis; therefore, standardizing clinical response criteria has been difficult. [8] The most recently proposed International Working Group (IWG) 2023 response criteria for higher risk MDS is the first to consider MRD status as an exploratory endpoint and recommends its reporting as a response category. [9] However, the IWG 2023 criteria do not provide details about the application of MRD testing or a formal definition of MRD response.

The available evidence shows that MRD assessment in MDS is likely to be context-dependent and influenced by biological and clinical prognostic factors like genetic subtype, disease stage, and treatment strategy. Furthermore, analytical performance and applicability (subgroup versus general testing) of diagnostic tests as well as timepoints and sample sources are important and must be considered in the assessment of MRD in MDS. Widespread implementation of MRD diagnostics in MDS is currently limited by cost and proven clinical utility.

We propose that MRD can be an important biomarker in MDS, which would allow for pharmacodynamic assessment, prediction of survival, disease monitoring and treatment decision making. In this manuscript, we will first review methodologic considerations, such as multiparametric flow cytometry (MFC) versus next generation sequencing (NGS) as well as bone marrow (BM) versus peripheral blood (PB) as source material. We will next consider MRD in the

context of clonal hematopoiesis (CH) and for the different clinical settings of non-intensive treatment of older or frail MDS patients, and allogeneic hematopoietic cell transplantation (HCT). Finally, we will consider open questions and prospects for the future, including emerging technologies and efforts toward standardization of MRD evaluation.

Methodologic Considerations

Multiparametric Flow Cytometry or Next Generation Sequencing

MFC-MRD, which is considered technically difficult to standardize but has a short turnaround time, quantifies MRD as progenitor cells that express a leukemia-associated or different from normal aberrant immunophenotype (LAIP/DfN), identified in approximately 90% of AMLs but probably less frequently in MDS. [3,10] MFC-MRD has a limit of detection (LOD) of 0.1% to 0.01% (10^{-3} to 10^{-4}) although higher sensitivities (10^{-5} to 10^{-6}) are reported for leukemic stem cell (LSCs) detection by immunophenotypic aberrant hematopoietic stem cell populations. [11] MFC assessment of different from normal 'dysplastic' maturation[12-14] could supplement MFC-MRD quantitation of aberrant blast or stem cells (**Figure 1**). [15] However interpretation of MFC-MRD in MDS may be limited by residual CH-related changes of hematopoietic cells as well as the challenge of discriminating between lower risk dysplastic clones and leukemic blasts. [16,17]

MFC has been used as an MRD test for MDS in a few studies that included high-risk MDS patients in older AML cohorts. [16,18] Evidence from non-intensive treatment trials in AML patients ineligible for HCT shows a significantly higher relapse risk for MFC-MRD positive patients. [19-22] In the peri-transplant setting, tracking of leukemic blasts could be accomplished by MFC-MRD, [23,24] but few studies have examined this approach outside of AML treatment. [25-28]

The genetic landscape of MDS has been studied and reviewed in detail by several authors. [7,29-32] About 90% of MDS patients will have at least one oncogenic lesion but no single mutation is pathognomonic for MDS. [29,30,32] As recurrent hotspot mutations and gene fusions that are detectable by real-time quantitative polymerase chain reaction (qPCR) are less frequent in

MDS compared to AML, an alternate approach, such as targeted error-corrected NGS is possibly the most useful method for MRD assessment in MDS. [6,32-36] However, no single MRD method has perfect sensitivity and specificity in MDS.

NGS-MRD also has several known limitations that have to be addressed prior to broader application in MDS. [37] From a technological perspective, the two most important limitations are the standardization of the bioinformatics analysis platform and the intrinsic error rate due to rare events in a given sample interfering with the clear discrimination of the target from noise. [3,36] Due to its intrinsic error rate, conventional NGS now commonly used at diagnosis of MDS/AML has a LOD of about 2% to 5% variant allele frequency (VAF). [35,36] Although a positive MRD test result above this LOD during complete remission (CR) could be useful prognostically, a deeper LOD is needed to give a meaningful discrimination of relapse risk between positive and negative tests in most instances. Technical advancements like molecular tagging (unique molecular identifiers, UMI) and duplex sequencing allow for error-correction leading to LODs far below 0.1% that are mainly determined by the amount of input DNA/ number of cells and costs. [35,36]

From a biological point of view, results of NGS-MRD do not provide the full picture of MDS/AML defined by clonal diversity and evolution with sometimes indetermined potential due to CH (**Figure 2**). [38-40] Consequently, distinguishing between residual hematopoietic stem cells (HSCs) carrying clonal mutations of no pathogenic significance and LSCs by NGS-MRD is challenging. Furthermore, the ability of tracking MRD by NGS is also limited in MDS with germline predisposition when no additional genetic markers are present because germline mutations are noninformative for MRD (**supplementary Table 1**). [3-5] Fundamentally, two approaches of target selection in NGS-MRD can be distinguished – sequencing of predefined target panels versus patient-specific mutation monitoring, but to date it is unknown which approach is superior. This is a moving target, and the decision will depend on a fine balance between costs versus additionally acquired information and evidence related to outcome benefit.

Source Material: Bone Marrow or Peripheral Blood

Studies in AML patients demonstrated a comparable clinical impact of MRD testing between PB and BM aspirate specimens. [41-45] PB as a source for MRD testing may be more suitable than BM in MDS because PB is generally more informative about CH, is not affected by dilution or fibrosis, and is more easily accessible thereby showing greater consistency in addition to lower cost for serial examinations. However, sensitivity is considered to be about 1 log lower in PB and there are concerns about the accurate quantification of the myeloid clonal burden during phases of neutropenia and concurrent relative lymphocytosis. [3,46] MRD testing is most useful in patients who reach complete remission (CR) and show no morphological signs of the underlying disease. However, in cases where patients do not recover hematopoiesis due to drug toxicity or limited stem cell reserve, skewed lymphoid to myeloid cells ratio may be a relevant problem. [46] In a research context, precise calculations of VAF of somatic mutations could be crucial for monitoring the pharmacodynamics of new drugs in refractory patients who fail to achieve CR. Until prospective studies confirm that PB can effectively replace BM in MRD testing for MDS and that both molecular and flow cytometric testing yield comparable results in PB, BM should continue to be regarded as the current gold standard. Circulating cell-free tumor DNA could provide an alternative MRD target in PB during the phase of neutropenia. [47,48]

The European LeukemiaNet (ELN) MRD working party actively pursues the goal of standardization and published a detailed consensus document in 2021 updating the recommendations on MRD in AML. [3,49] The currently recommended MRD threshold that has been established by prospective trials for AML in first CR is 1 in 1,000 cells (0.1%; 10^{-3}). We propose that the ELN MRD recommendations on optimized technical requirements, minimal detection limit and standardized reporting should also be implemented in the MRD assessment of MDS (**supplementary Table 1**).

Clonal Hematopoiesis of Indeterminate Potential and Clonal Cytopenia of Undetermined Significance

The prevalence of CH is generally age-related and its detection is assay dependent. [50-52] When sensitivity of sequencing reaches approximately 1% VAF, 85% of persons with an age of 80 years or older will have age-related CH. [53] CH of indeterminate potential (CHIP), defined by somatic mutations with a VAF of 2% or higher, and clonal cytopenia of undetermined significance (CCUS), defined by CHIP with persistent cytopenia, are potentially preneoplastic states and inherent features in the pathogenesis of MDS. [4,5,53-55] However, the occurrence of somatic mutations in CH, CHIP and CCUS are stochastic events and the kinetics of clone growth leading to progression to MDS/AML is unpredictable in most cases (**Figure 2**). [38-40,56-58] Complicating matters, copy number alterations, independently or co-occurring with single nucleotide variants, have also been shown to play an important role in leukemogenesis. [59,60]

The number, combinations and VAFs of somatic mutations show a strong association with progression from CCUS to myeloid neoplasm. [38,50,61-63] CH is a risk factor for therapy-related myeloid neoplasms in patients who received cytotoxic treatment for primary malignancies. [64-67] CH involving somatic mutations in *TP53* and *PPM1D* is common in patients developing therapy-related MDS. [65,67-69] Recent evidence suggests that also thalidomide analogs like lenalidomide provide a growth advantage to *TP53* mutated hematopoietic stem cells (HSCs). [67] Longitudinal measurements of mutant driver genes and clone size may allow for early identification of progression into MDS. However, there is currently insufficient evidence to suggest that monitoring of CH or CCUS could be beneficial for high-risk populations such as individuals with somatic *TP53* mutations that received cytotoxic therapy. Reduction in cost and further improvements in sequencing and data analyses could lead to clone-specific targeted interventions as part of a secondary prevention.

Studies in AML and MDS patients suggest that persistence of CH, especially somatic mutations in one or more of the *DTA* (*DNMT3A*, *TET2*, *ASXL1*) genes, during CR after chemotherapy or before HCT is not associated with increased risk of relapse.[3,70-73] It is important to bear in mind that only AML entities that are characterized by certain driver mutations (*NPM1*, bZIP in-frame mutated *CEBPA*) or gene fusions (*CBFB::MYH11*, *RUNX1::RUNX1T1*) are typically cured without allogeneic HCT, presumably because their LSCs are chemotherapy-sensitive.[49] AML with adverse risk genetic abnormalities including mutated *TP53* and myelodysplasia-related gene mutations or cytogenetic abnormalities, whether primary or secondary, should receive HCT as part of their therapy.[49] Recipient's CH should disappear after HCT which can be tracked by MRD testing but the timepoint at which residual *DTA* mutations should not be detected after transplantation is not established.[42,47,74,75] Additionally, donor-derived CH must be carefully excluded especially if untargeted NGS is used for MRD monitoring.[76,77] A retrospective NGS-MRD study of 131 AML patients who underwent HCT showed that residual *DTA* mutations had no prognostic significance at day 90 and day 180 after HCT.[71] This study indicated that kinetics — an increase in VAF of *DTA* mutations between two timepoints – may be a better prognosticator of relapse.[78] In the future, serial single-cell sequencing analyses will likely provide an answer to which mutations or combinations of mutations of residual CH have an impact on clinically relevant endpoints.[79,80]

Clinical Considerations

Adapting the MRD assessment approach based on treatment goals together with considerations of cost and inconvenience is reasonable. Since effective treatment options are currently lacking for most MDS patients who are not eligible for HCT, MRD testing may not be justified for the majority of "real world" patients receiving palliative treatment outside of clinical trials. The subsequent sections will explore various clinical scenarios that may have different implications for MRD results.

Non-intensive Treatment of MDS

Cytogenetic response, a complete or partial disappearance of chromosomal abnormalities, was introduced as a response criterion for MDS by the IWG in 2000 to enable prospective evaluation and comparability between clinical trials although no data were available at that time to support a relationship between cytogenetic response and clinical outcome. [81] Since then, most clinical trials that have included cytogenetic response criteria as an endpoint have demonstrated this association. [8] We argue that defining MRD criteria for MDS is necessary for the same reasons that cytogenetic response criteria were established, to ensure successful clinical research and clear comparisons between trials.

Regular MRD assessment of MDS patients who are not transplant eligible should currently be focused on clinical research. With the exception of hypoplastic MDS or MDS with less than 5% BM blasts and isolated 5q deletion (MDS-del[5q]), treated with immunosuppressive agents or lenalidomide, respectively, most patients with low-risk MDS will initially receive supportive care when they need treatment because of cytopenia. [7]

We advocate that reporting MRD responses is important for understanding the efficacy of investigational new drugs. One example is the phase 2 portion of the MDS3001 study, which evaluated the efficacy of imetelstat, a competitive inhibitor of telomerase activity, in 57 red blood cell (RBC) transfusion-dependent patients with lower-risk MDS. [82] Treatment with imetelstat resulted in a clinically meaningful 37% reduction in the 8-week RBC transfusion dependence rate. It should be emphasized here that the reduction of the VAF of somatic *SF3B1* mutations correlated with transfusion independence suggesting that *SF3B1* VAF could be a surrogate molecular marker that predicted response (prolonged transfusion independence).

Residual mutations of CH further complicate MRD analysis following non-intensive therapies because they represent the remaining founder clone with residual hematopoietic potential that cannot be eradicated without the use of HCT thus far. [39,83] An improvement in

treatment efficacy targeting culprit subclones would make MRD testing more attractive as a surrogate marker for PFS. Since it is biologically implausible that increasing VAF of mutations paralleling progression of subclones would not influence critical outcomes, [84] incorporating MRD analysis in response criteria and in definitions of progressive disease seems to be a reasonable goal.

This premise would also apply to future drugs with a mechanism of action that causes differentiation of neoplastic cells into normal blood cells instead of eradication, thereby improving suboptimal hematopoiesis but potentially not leading to a reduction in clonal burden. Only after studying such associations we can learn about the role of MRD and clinical benefit. Consequently, MRD assessment should be incorporated into the design of clinical trials investigating new agents for the treatment of MDS, while implementing recommendations of the US Food and Drug Administration on regulatory considerations for the use of MRD as a surrogate efficacy end point. [85]

HSCs with del(5q) are selectively resistant to lenalidomide. Tehranchi et al. showed that, similar to a molecular MRD measurement, the 5q deletion remained detectable in all patients with MDS-del(5q) by fluorescence in situ hybridization of sorted CD34+, CD38-/low, CD90+ HSCs at the time of CR during lenalidomide treatment, even in patients with complete cytogenetic response (CCyR). [86] A retrospective analysis of the phase 2 MDS-003 and the phase 3 MDS-004 studies showed that 103/181 (57%) patients achieved a cytogenetic response with lenalidomide of whom 84/103 (81.6%) also achieved RBC transfusion independence at ≥ 26 weeks. [87] The case of lenalidomide and MDS-del(5q) is a good example demonstrating that MRD testing on the one hand shows the efficacy of specific treatment at the genetic level and on the other hand provides evidence that a cure in the strict sense is not possible because the malignant stem cell is not eradicated.

Patients with low-risk MDS-del(5q) who are treated with lenalidomide have a median AML-free survival of approximately 3.5 years. [87] Transplant eligible patients may benefit from early detection of subclonal *TP53* mutations at diagnosis and regular monitoring during lenalidomide treatment. [67,88-91] In a prospective multicenter study of the German MDS study group involving 67 MDS-del(5q) patients, median overall survival (OS) was significantly different between patients with (N=59) and without (N=8) a *TP53* mutation at diagnosis (3.55 years versus not reached; P=0.002). [89] As the expansion of a *TP53* subclone is associated with treatment failure and progression during treatment with lenalidomide, *TP53* MRD testing would allow better stratification of patients for early HCT or clinical trials. [90]

High-risk MDS is treated with hypomethylating agents (HMA) and response is associated with the number and type of somatic mutations. [43,84,92-95] The decrease in VAF of certain high-risk or clearly transforming mutations indicating partial or complete elimination of subclones is associated with better PFS after treatment with HMAs such as azacitidine or decitabine, alone or in combination with other drugs, in several cohort studies (**Table 1; supplementary Table 2**). There seems to be a strong concordance between molecular and clinical responses but the exact threshold of mutation clearance indicating highest outcome difference during treatment with HMAs is not known. VAF thresholds of 1% and 5% have been described to be meaningful in this setting and have to be put in context of baseline risk groups such as *TP53*. [83,84,96]

Treatment response is usually short-lived with currently available agents, which may explain why MRD assessment has not been useful in the palliative setting of high-risk MDS in routine care. However, this does not mean that MRD assessment has no merit, but may instead indicate that the current therapeutic options for MDS are limited. What would it mean if HMA therapy did not lead to a temporary suppression of *TP53* mutated clones? [84,92,94,96-99] The answer is that such a therapy would be less effective and bridge fewer patient with MDS/AML to HCT which is the only chance for cure. [84,94,100-102]

Pre-transplant Setting: Prognostication and Treatment Decision Making

Evidence has emerged indicating that MDS with 10% to 19% BM blasts shares important biological and clinical similarities with AML when entities are stratified by genetics. [5,6] Many studies that investigated the role of MRD in AML included a subgroup of MDS/AML, which allowed basic principles of MRD analysis to be applied to results of studies that enrolled AML patients as majority (**Table 1; supplementary Table 2**). [16,18,23,70,103] The creation of the new entity MDS/AML in the recently published International Consensus Classification (ICC) has introduced facts that affect the care of many MDS patients outside of clinical trials. [5] It is a reality that many academically affiliated transplant centers will use available MRD technologies, including less sensitive conventional techniques, in individual cases with the intent to improve the survival of their transplant-eligible MDS patients. Ideally, MRD measurements should be performed in special reference laboratories.

When non-intensive or intensive treatments are used as a bridge to HCT, pre-transplant MRD assessment can provide valuable prognostic information to influence the conditioning regimen and the post-transplantation plan. [26] Many retrospective studies have evaluated the prognostic impact of somatic mutations at the time of HCT on the outcome of MDS patients and, without implementing MRD assessment, proposed different genes associated with unfavorable prognosis. [104-110] Factoring in all consistent results and giving most weight to the largest study (Lindsley et al. [108]), which analyzed PB of 1514 MDS patients by NGS (reporting VAF threshold of 2%) before performing allogenic HCT, we can draw the following conclusions. First, mutations in *TP53* are consistently associated with the highest risk of relapse and decreased OS[28,104-107,109,110] that is not influenced by conditioning intensity. [108] Second, mutations in RAS pathway genes are associated with shorter OS due to increased risk of relapse, [107,109] specifically among patients 40 years of age or older who may not have received myeloablative conditioning. [108]

Post-hoc analyses of prospective studies in MDS/AML which incorporated MRD assessment after intensive treatment and/or before HCT consistently show a higher risk of relapse for patients with MRD positivity. [16,18,23,70,111] By performing 10-gene NGS-MRD in 48 CR samples from a randomized trial of transplant eligible younger patients up to 65 years of age, Dillon et al. demonstrated that myeloablative conditioning mitigated the relapse risk associated with MRD positivity of non-*DTA* mutations in MDS. [70] Since most MDS patients are older than 70 years or have other adverse factors beyond genetics, myeloablative conditioning is frequently not an option and other strategies to reduce relapse risk and improve OS must be explored. In a trial comparing reduced intensity regimens that included MDS patients (33% of 244), Craddock et al. showed that achieving a complete donor T-cell chimerism at 3 months – a potential surrogate marker for graft-versus-leukemia effect – but not the intensification of the conditioning regimen reversed the negative impact of pre-transplant MFC-MRD positivity on relapse incidence and OS. [23] Pretransplant MRD positivity is also not a contraindication to HCT because clinical trials like the VidazaAllo Study have demonstrated a better OS after HCT compared to continuation of HMA treatment. [101] In sum, these data suggest that MDS patients without MRD may avoid myeloablative conditioning and that MRD positivity is useful to steer high-risk patients into clinical trials. [94,101,102]

Post-transplant Setting: Avoiding Relapse

Since relapse of MDS after HCT is associated with a very poor prognosis, there is a great need for early detection and prevention through targeted intervention. [112] MFC, NGS, PCR and CD34+ sorted donor chimerism analyses have been successfully employed to detect MRD in the post-transplant setting (**Table 1; supplementary Table 2**). Duncavage et al. performed NGS-MRD in BM samples from 86 consecutive adult patients with MDS and secondary AML at 30 and 100 days after HCT to assess mutation clearance and related risk of relapse. [113] Before HCT, 96% (86/90) of analyzed patients had at least one detectable somatic mutation by whole exome sequencing and 79% (68/86) with the use of a generic myeloid NGS panel of 40

297 recurrently mutated genes. At day 30 posttransplant, 30% (26/86) of patients were MRD-positive
298 – only one patient had a sole DTA variant – defined by a VAF of ≥0.5% in the myeloid NGS
299 panel. After adjustment for conditioning regimen, MRD positivity ≥0.5% was associated with a
300 lower 1-year PFS compared to no detectable mutations at this threshold at 30 days
301 posttransplant (30.8% versus 57.1%; HR for progression or death, 2.09; 95% CI, 1.18 to 3.70; P
302 = 0.02). Importantly, patients with mutations detectable at VAF >0.1% at day 30 had a
303 statistically higher risk of progression (P <0.003 by Gray's test) and a shorter progression-free
304 survival (P = 0.021 by proportional hazards, chi-square test). However, only results of a more
305 elaborate NGS, which also detects patient specific non-myeloid related somatic mutations, were
306 reported for this threshold. Furthermore, MRD positivity at day 100 posttransplant which was
307 detected in 31% (18/58) of patients by incorporating patient-specific non-myeloid related somatic
308 mutations was also associated with a lower 1-year PFS (27.8% versus 77.5%; HR for
309 progression or death, 2.51; 95% CI, 1.26 to 5.01; P = 0.01). In multivariable analysis, age >60
310 years, secondary AML, *TP53* mutation and MRD positivity ≥0.5% at days 30 and 100 were
311 independently associated with disease progression or death.

312 Unfortunately, there are few prospective data on the treatment of MRD of MDS after
313 HCT, almost exclusively from AML studies that included a minority of high-risk MDS patients.
314 [103,114,115] In the RELAZA2 study, Platzbecker et al. used qPCR of leukemia-specific fusion genes
315 or mutant *NPM1* as well as donor chimerism analysis of sorted CD34+ cells from PB (threshold
316 mixed chimerism <80%) to detect MRD and initiate treatment with azacitidine. One-year relapse-
317 free survival was 46% (95% CI, 32% to 59%) in the 53 MRD-positive patients – 5 of whom had
318 MDS, who received the preemptive treatment. [103] Although efficacy of this preemptive approach
319 is also supported by a retrospective study, [116] randomized controlled trials between MRD-
320 positive and MRD-negative patients would be needed to give a definitive answer. Here, an NGS
321 panel-based MRD assay might be more informative than MFC, as posttransplant emerging
322 subclones with therapeutic targets could be better detected. [115]

Proposition for Future MRD Analysis in MDS

Tailor MRD to Goals of Therapy

MRD assessment, ideally a combination of NGS-MRD and MFC-MRD, should be incorporated in all clinical trials in MDS. Although CR is the ultimate goal of any MDS treatment because of the association with improved OS, we acknowledge that hematological improvement (HI) is also an important and meaningful clinical endpoint associated with improved quality of life that should be explored in clinical trials. [9] Genetic and morphologic responses do not perfectly correlate as shown by complete cytogenetic response (CCyR) which is associated with longer survival in high-risk MDS patients under HMA treatment but does not always lead to CR. [117] For that reason, in contrast to AML, we propose that the complete MRD response (MRD_{CR}) category should always include CCyR and be distinct from morphological responses such as CR or HI. Furthermore, variants in DTA genes should be documented ($DTA^{+/-}$) but generally not considered as MRD positivity (MRD^{+}).

Two clinical scenarios – 1) treatment with palliative intent, 2) treatment with curative intent – should be distinguished when applying MRD response criteria. In the former scenario, the application of MRD measurement is currently only reserved for clinical trials; in the latter, MRD assessment may already be offered in individual cases. This would have two advantages. In the palliative setting, where the focus is on PFS and HI, the interaction of morphology and residual subclones would be easier to describe and to investigate (e.g. HI with MRD^{+}-DTA^{+}). In the curative setting, where the main goal is to predict and to prevent relapse, the morphological response might be of lesser importance after induction treatment because of HCT (e.g. marrow CR with MRD_{CR}-DTA^{+}). The proposed provisional MRD criteria (**Table 2**) serve as a basis for discussion and will certainly need to be adjusted by suggestions from the stakeholders' community[9] and results of further studies.

An optimal gene panel for NGS-MRD has not yet been defined for MDS. The calculation of the IPSS-M requires analysis of 31 genes for risk stratification at diagnosis. [32] This panel can be used as a starting point for further refinements of NGS-MRD diagnostics in MDS (**supplementary Table 3**). As a minimum, we consider the 10-gene panel, which has been described as prognostic in patients with MDS and AML before conditioning for HCT (**supplementary Table 4**). [70] All detected mutations should be considered potential MRD markers (**supplementary Table 1**).

Timepoints of MRD Assessment

The optimal MRD measurement timepoints are not known and will always reflect the design of published clinical trials that demonstrate outcome differences between MRD-positive and MRD-negative patients. No evidence-based recommendation can be given for the setting of palliative treatment. Outside of clinical trials, a pragmatic suggestion would be to perform MRD testing in patients who have a long-lasting remission with HMAs and wish to reduce therapy, or who have indeterminate cytopenia despite achieving CCyR. For patients treated with the intention of cure, we pragmatically suggest performing MRD testing in BM for remission assessment before HCT as well as on days +30 and +100 after HCT. These timepoints would allow conditioning regimen (myeloablative versus reduced intensity) and immunosuppression (faster vs normal tapering of immunosuppressive agents) to be adjusted as well as optional donor lymphocyte infusion to be planned. If a molecular marker is present, further NGS-MRD assessments could be performed every 4-8 weeks in PB. Any MRD^{+} results should be confirmed by further testing to estimate clone kinetics.

Potential Role of New Methodologies

A major drawback of NGS-MRD is that the reported VAF represents the average frequency within a bulk cell population, making it impossible to provide information on the co-occurrence of multiple variants within a single subclone of that cell population. [79] Especially in

MDS, where CH is an integral part of its pathogenesis, the inability to distinguish residual CH from LSCs is still an obstacle to clearly establishing the presence of MRD in some cases. Single-cell analysis has great potential to revolutionize MRD assessment in this regard because it is able to resolve clonal architecture. For example, sequencing of single cells from enriched LSCs at diagnosis and during remission could explain which combinations of mutations are found in the same cell and steer more sensitive NGS-MRD detection. Recently, Dillon et al. have shown in a proof-of-principle in three AML patients that a tailored single-cell analysis integrating patient-specific mutations and structural variants from whole-genome sequencing as well as cell surface markers is able to determine which genetic alterations exactly are present in a single cell. [80] Single cell MRD analysis is in the early stages of development. Further studies, ideally in the context of prospective clinical trials, are necessary to demonstrate feasibility on a large scale.

Another promising approach to detect MRD is to perform NGS in CD34+ (or alternatively CD117+) selected cells from PB after magnetic cell separation or flow cytometric sorting. [75] In an analysis of 40 MDS/AML patients in CR after HCT, Stasik et al. demonstrated an impressively high sensitivity of 100% and specificity of 91% for detecting molecular relapse. [75] The lower limit of MRD detection was 10^{-6}, about 10-fold more sensitive than the measurement of donor chimerism as performed in the RELAZA2 study, and PB was superior to BM as a source of CD34+ cells.

Regarding minimally invasive MRD assessment, serial analysis of circulating cell-free tumor DNA for leukemia-specific mutations in serum may be the optimal approach for cytopenic MDS/AML patients. Previous studies in the post-HCT setting in patients with MDS/AML have demonstrated the principal feasibility of this methodology that must be standardized and prospectively investigated in different clinical scenarios. [47,48]

Standardization Efforts

The standardization of MRD methods is the key to accomplish reproducibility and comparability. The MRD working group of the ELN has published a blueprint on how to successfully carry out such an endeavor in AML. Reproducibility has to be demonstrated in clinical trials using a published standardized methodology. This means that, in addition to technological advancement, considerable standardization efforts will also be necessary in MDS in the future. A first step should be the definition of uniform MRD criteria.

Open Questions

Because the extent of discordance between MRD measured by MFC and NGS is currently unknown in MDS, we recommend that both methods be prospectively studied in parallel to determine clinically meaningful detection thresholds. Additionally, when NGS-MRD testing is used at specific timepoints in clinical trials, comparison of BM and PB source materials is recommended. The potential role of LSC based detection of MRD is unknown for MDS and should be explored. If patients are randomized between intensive versus non-intensive therapy, MRD assessment should be used to answer the question whether MRD negativity has the same value after both treatment types and what specific mutations are affected by either strategy. Copy number abnormalities and allelic imbalances including copy-neutral loss of heterozygosity are important in the pathogenesis of MDS but have rarely been discussed in the context of MRD. Furthermore, the significance of uncommon mutations from agnostic NGS approaches should be explored in more granularity to answer the question whether all non-DTA mutations or combinations thereof are predictive for relapse or progression. Single-cell sequencing is providing increasing insight into the role of subclones in treatment resistance and relapse. This technology could be used to determine the stage – diagnosis or relapse – at which escape clones emerge and thus possibly predict their occurrence.

Summary

A negative MRD test result indicates that there is no evidence of disease present, above a predefined test threshold. However, although MRD measurements give an important prognostic estimate, this estimate is not absolute because relapse is also observed in MRD-negative patients and MRD assessment is potentially hampered by source material processing, technique used, benign CH and timepoint of investigation. The landscape of MRD in MDS continues to evolve, with the introduction of new methods such as single-cell sequencing, however, a formal working MRD definition is needed now. We propose MRD response criteria built on currently available evidence. Since there remains no curative therapy for most MDS patients, implementation of MRD testing is an important part of clinical trial design and should be a secondary endpoint to achieve inter-trial comparability and efficacy quantification, and to improve our understanding of the relationship between residual CH and relapse. Clinically useful evidence to establish MRD as a biomarker will require both high quality randomized controlled trials and large collaborations.

Acknowledgments

This work was supported by funding from the Intramural Research Program, National Institutes of Health, National Cancer Institute, Center for Cancer Research.

Author contributions

Conception of the work: E.S., S.Z.P; Interpretation of Data: E.S., S.F., P.D.A., S.Z.P; Drafted the manuscript: E.S., S.F., P.D.A., S.Z.P. All authors have seen and approved the manuscript being submitted.

Conflict of interest

E.S.: Amgen (Honoraria).

P.D.A.: No conflict of interest.

S.F.: No conflict of interest

S.Z.P.: No conflict of interest.

Disclaimer

The views expressed in this work do not represent the official views of the National Institutes of Health or the United States Government.

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Figure and Table Legends.

Figure 1. Measurable Residual Disease Monitoring of MDS by Flow Cytometry: Potential Approaches.

Figure 2. Schematic depiction of the polyclonal evolution and trackable somatic mutations from clonal hematopoiesis, through CHIP and CCUS to MDS/AML. Each colored dot within the cell represents a distinct mutation, with two different transformed clones (dark circles) developing over time and one outcompeting the other (so called clone sweeping[40]). NGS of the bulk population can only detect genetic alterations with a frequency above the detection limit (LOD) which depends on the error-corrected sequencing methodology used. The variant allele frequency (VAF) represents the variant frequency within the bulk population without information on the co-occurrence of variants within a single subclone of that population that is under constant intrinsic competition and extrinsic pressure (treatment). Depending on the bulk composition, the same VAF can represent different mutational states on a single-cell level (demonstrated by chromosomes in the right lower corner of the figure) such as biallelic versus monoallelic mutation, homozygous versus hemizygous or heterozygous mutations. Importantly, such allelic imbalances, e.g. biallelic *TP53* mutation, are not limited to MDS/AML but can also be found in CH, CHIP and CCUS. CR, complete remission; CTx, chemotherapy; HMA, hypomethylating agent; LOD, limit of detection. The figure was adapted and modified from Stauber et al. [56]

Table 1. Summary of important studies with MDS patients and reported MRD results including allogeneic HCT. A more extensive version of this table can be found in the supplementary data (**supplementary Table 2**).

Table 2. Proposition for MRD response criteria in MDS.

790 **Table 1.**

Study	Population	Study design	Intervention	MRD methodology	Results
Mixed populations including palliative therapy					
Welch et al., 2016[97]	MDS (N=26), AML (de novo, N=54; relapsed, N=36)	Prospective, uncontrolled trial (N=84) and extension cohort (N=32)	10-day or 5-day decitabine	WES, NGS gene panel (LOD not specified)	Rate of any mutation clearance associated with morphological response
Hunter et al., 2021[94]	MDS (N=210), MDS/MPN (N=16), AML (N=102), t-MN (N=60)	Retrospective	HMA therapy (7% additional agents)	NGS gene panel (VAF ≥5%)	*TP53* mutation clearance associated with longer median survival (15.6 [negative] versus 7.7 [positive] months; P=0.001)
Sallman et al., 2021[96]	MDS (N=40), AML (N=11), MDS/MPN (N=4)	Phase 1b/2	Eprenetapopt plus azacitidine	NGS (PB; LOD 0.1%)	*TP53* mutation clearance associated with CR
Steensma et al., 2021[82]	ESA relapsed/ refractory lower-risk MDS (N=57)	Phase 2	Imetelstat	NGS (BM, PB)	*SF3B1* VAF reduction correlated with duration of transfusion independence
Yun et al., 2021[83]	MDS (N=95), secondary AML (N=52), MDS/MPN (N=10)	Retrospective	HMA (74%), intensive chemotherapy (45%), HCT (24%)	NGS gene-panel (BM, PB; MRD VAF ≥5%)	MRD negativity (median OS not reached versus 18.5 months; P=0.002) and *TP53* mutation clearance <5% were associated with better OS
Sallman et al., 2023[99]	MDS (N=95)	Phase 1b	Magrolimab plus azacitidine	MFC (LOD 0.02%)	- Small, heterogeneous high-risk cohort with 26% *TP53* mutant MDS - CR rate 33%, MRD negativity rate 23% - Trend for improved OS in patients who became MRD-negative
Nannya et al. 2023[84]	MDS (N=384)	Retrospective	Azacitidine	NGS gene panel (≥1%; LOD not specified)	Except for *DDX41*, post-treatment (≥ 4 cycles) clone size correlated with response

Pretransplant					
Festuccia et al., 2016[26]	MDS (N=285; 23% had advanced to AML before HCT) CMML (N=4)	Retrospective	HCT	MFC-MRD (LOD 0.001%-0.1%) plus cytogenetics/FISH	MRD status associated with CIR
Dillon et al., 2020[70]	MDS (N=48)	Subgroup analysis of a prospective phase 3 trial	RIC (N=23) versus MAC (N=25)	NGS 10-gene panel (PB)	- MRD status associated with OS (55% versus 79%; P=0.045) and CIR (40% versus 11%; P=0.022) at 3 years - Higher relapse rate in MRD-positive patients randomly assigned to RIC versus MAC: 60% versus 8% (P=0.010)
Craddock et al., 2021[23,111]	AML (N=164), MDS (N=80)	Phase 2 randomized trial	Standard RIC (N=108) versus intensified FLAMSA-Bu RIC (N=108)`	MFC (BM; LOD 0.02%-0.05%)	Pretransplant MRD positivity associated with 2-year CIR in MDS: 50.0% versus 21.1% (P=0.020)
Ma et al., 2023[118]	MDS-EB (N=103)	Retrospective	HCT	MFC (BM; LOD <0.01%-0.05%)	MRD status associated with DFS and OS
Posttransplant					
Bernal et al., 2014[25]	AML (N=49), MDS (N=38)	Retrospective	MAC (16%), RIC (84%)	MFC (BM; >0.01%)	- Positive pre-transplant MRD associated with positive MRD at day +100 - Positive MRD at day +100 associated with relapse (OR 6.55)
Duncavage et al., 2018[113]	MDS (N=90)	Retrospective	RIC (42%), MAC (58%)	NGS (BM; VAF ≥0.5%)	- 37% of patients were MRD positive at day +30, 31% at day +100 - MRD-positivity at days +30 and +100 associated with higher risk of disease progression or death

Nakamura et al. 2019[47]	AML (N=37), MDS (N=14)	Retrospective	HCT (MAC 100%; 92% cord blood)	Personalized droplet digital PCR assay (circulating tumor DNA from serum or DNA from matched BM; median LOD 0.04%)	- MRD positivity (either BM or serum) at 1 and 3 months associated with higher 3-year CIR and risk of death - ≥1.5-fold increase in ctDNA between 1 and 3 months post HCT associated with highest risk of relapse (HR=28.5; P=0.0001) and death (HR=17.4; P=0.0009)

AML, acute myeloid leukemia; BM, bone marrow; CIR, cumulative incidence of relapse; CIR, cumulative incidence of relapse; CMML, chronic myelomonocytic leukemia; CR, complete remission; DFS, disease-free survival; *DTA*, DNMT3A, TET2, ASXL1; ESA, erythropoiesis-stimulating agent; FISH, fluorescence in situ hybridization; FLAMSA-Bu, fludarabine, cytarabine, amsacrine, busulfan; HCT, allogeneic hematopoietic cell transplantation; HMA, hypomethylating agent; HR, hazard ratio; LOD, limit of detection; MAC, myeloablative conditioning; MDS, myelodysplastic syndrome; MDS-EB, MDS with excess blasts; MFC, multiparameter flow cytometry; MPN, myeloproliferative neoplasm; NGS, next generation sequencing; OR, odds ratio; OS, overall survival; PB, peripheral blood; RIC, reduced intensity conditioning; t-MN, therapy-related myeloid neoplasms; WES, whole exome sequencing.

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792 **Table 2.**

Category	Defining criteria
MRD_{CR}	1. Complete cytogenetic response* or normal karyotype, **and** 2. Complete MRD response: Negative results (lower limit of detection at least 0.1%) in all MRD tests (NGS, MFC, PCR) that were used
MRD_{LL}	1. Complete cytogenetic response* or normal karyotype, **and** 2. Any MRD above the detection limit of the assay but below the level of 0.1%
MRD^{+}	1. Complete cytogenetic response* or normal karyotype, **and** 2. Any MRD tests positive ≥0.1%
–$DTA^{+/-}$	Used as an additional MRD test qualifier: e.g. MRD_{CR}-DTA^{+}; MRD^{+}-DTA^{-}
MFC-MRD^{-}	1. MFC is used as a stand-alone test without other genetic or molecular tests 2. MFC-MRD negative: No detection of any leukemic clones by MFC (lower limit of detection 0.1%)
MFC-MRD^{+}	1. MFC is used as a stand-alone test without other genetic or molecular tests 2. MFC-MRD positive: Detection of leukemic clones by MFC with a frequency ≥0.1%
MRD relapse	1. Previous documentation of MRD_{CR}, MRD_{LL} or MFC-MRD^{-} after treatment, **and** 2. MRD relapse confirmed in a second consecutive samples, **and** 3. Newly detected MRD^{+}, **or** 4. Newly detected MFC-MRD^{+}, **or** 5. ≥1 $\log_{10}$ increase of VAF of previously detected DTA variants after day +100 of allogeneic HCT†

DTA, *DNMT3A*, *TET2*, *ASXL1*; LL, low level of detection (<0.1%); HCT, hematopoietic cell transplantation; HI, hematologic improvement; MFC, multiparameter flow cytometry; MRD, measurable residual disease; VAF, variant allele frequency.
*International Working Group 2023 response criteria (unchanged from IWG 2006). [9]
†Corroboration by sorted donor chimerism analyses recommended.

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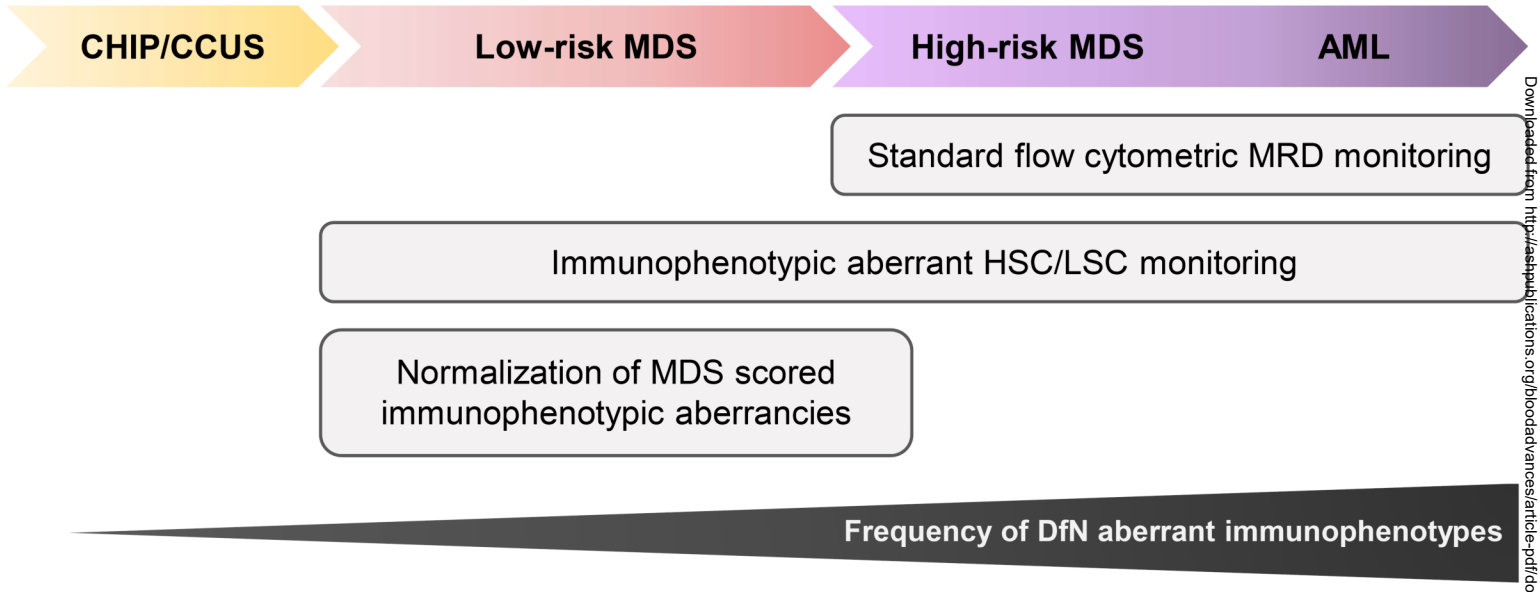
Figure 1



Approach	Targets	Potential Advantages
Standard flow cytometric MRD monitoring	Aberrant immunophenotype of baseline blasts (LAIP) and/or that is different from normal progenitors (DfN)	– Sensitive – Prognostically validated in combined AML/high-risk MDS cohorts
Immunophenotypic aberrant HSC/ LSC monitoring	Aberrant marker presence on $CD34^{+}CD38^{-}$ progenitors	– Sensitive – Potentially applicable to low- and high-risk MDS (~30% MDS patients have target)
Normalization of MDS scored immunophenotypic aberrancies	Overlap with DfN – Lymphoid marker presence: CD5, CD7, CD56 – Altered maturation pattern: • Neutrophils CD13 vs CD16 • Monocytes HLA-DR vs CD11b • Erythroid CD71 decrease	– Potentially applicable to low-risk MDS – MDS aberrancies/score validated for diagnosis – Assesses myeloid/erythroid differentiated subsets in addition to myeloid progenitors

Figure 1.

Figure 2

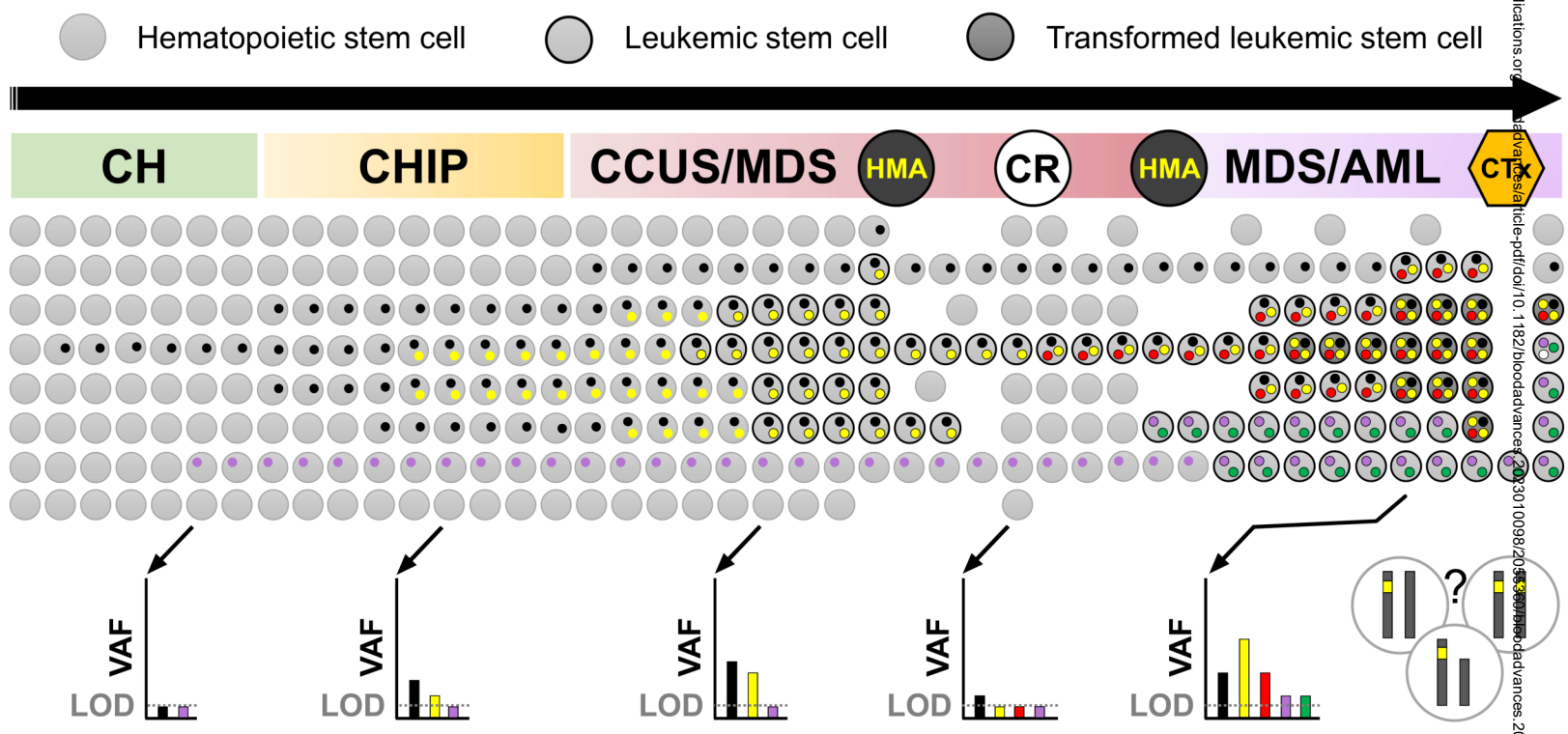


Figure 2.