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TITLE: Meta-Analytical Online Repository of Gene Expression Profiles of MDS Stem Cells

PRINCIPAL INVESTIGATOR: Dr. Amit Verma, M.D.

CONTRACTING ORGANIZATION: Albert Einstein College of Medicine
Bronx, NY 10461-1602

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We propose to create an online searchable repository of gene expression profiles of CD34+ stem cells from patients with myelodysplastic syndromes (MDS) and healthy controls. We have devised a novel meta-analytical approach to integrate and normalize gene expression studies generated in different labs on different platforms and have shown it to be feasible and biologically valid in numerous publications. We have now successfully integrated data from 183 MDS samples in the database. This dataset has been used to screen for expression of all TGF-β related genes and has led to the discovery that negative regulator, SMAD7, was significantly underexpressed in MDS stem cells. This discovery elucidated the mechanism of activation of TGF-β signaling in MDS, even in the absence of high extracellular levels of TGF-β. After demonstrating the utility of this database in this study, we now propose to add information about MDS subtypes, blood counts, IPSS scores, patient demographics to this database. Investigators will be allowed to access this database online. This resource will continually be updated with newer data on an ongoing basis.
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Introduction:

MDS is a heterogeneous group of diseases characterized by bone marrow failure that leads to cytopenias. Newer therapeutic developments are impeded by limited insights into disease pathophysiology. Lack of cell lines and valid mouse models underscore the importance of research based on primary patient samples. These samples are hard to obtain in sufficient numbers. Our proposal will create a gene expression database that will include large numbers of all MDS subtypes. Moreover, this database will be generated by compiling gene expression profiles from CD34+ purified stem cells, thus ensuring that these profiles are not diluted due to heterogeneity of whole bone marrow samples. In addition to allowing researchers to study the expression patterns of selected genes, this database will also allow researchers to identify subtypes of MDS patients that will potentially benefit from novel therapies that target specific genes or genetic pathways.

Body:

We had previously shown that meta-analysis of microarray studies demonstrates feasibility of inter-platform data integration and reveals novel hematopoietic stem cell signatures. We tested the feasibility of conducting a meta-analysis of GE studies by using publically available data from studies that used normal bone marrow-derived hematopoietic progenitors. Data was integrated using both RefSeq and UniGene identifiers and normalized. We observed that in spite of variability introduced by experimental conditions and different microarray platforms, our meta-analytical approach can distinguish biologically distinct normal tissues by clustering them based on their cell of origin(1).

After demonstrating the feasibility of our meta-analytical approach, we wanted to construct a database of MDS stem cells and normal controls. We have now integrated data from 183 MDS CD34+ samples and 17 healthy controls. The data was integrated using unigene IDs, normalized and shown to be valid for further analysis (2). We have subsequently used this database in 4 studies that have led to important insights into the pathophysiology of MDS (2-5). In the first study, we showed that the SMAD2 protein is overexpressed in MDS. This protein is an effector of the TGF-β signaling pathway and is activated by the TGF-β receptor I kinase. In the next two studies, we wanted to determine the reasons for activation of TGF-β signaling pathway in MDS stem cells. Therefore, we used the MDS gene expression database to screen for expression of all TGF-β related genes and discovered that the negative regulator, SMAD7, was significantly underexpressed in MDS stem cells (3, 5). SMAD7 protein is an endogenous inhibitor of the TGF-β receptor I kinase. Functional studies revealed that reduction in SMAD7 (observed in the meta-analysis) leads to overactivation of the TGF-β receptor kinase even in the absence of high extracellular levels of the cytokine. These studies thus established SMAD7 reduction as a key intracellular event that leads to myelosuppressive TGF-β signaling and ineffective hematopoiesis in MDS (3, 5).
In another study, we determined that DOCK4, a GTPase exchange factor is underexpressed in MDS (Fig 2). This study also utilized the database we created to show DOCK4 underexpression in a large number of MDS samples (Fig 2)(Shown at Fig5 from ref 4).

After demonstrating the utility of this database in this study, we now propose to add information about MDS subtypes, blood counts, IPSS scores, patient demographics to this database. Investigators will be allowed to access this database online. This resource will continually be updated with newer data on an ongoing basis.


**Key Research Accomplishments:**

We have shown the feasibility of constructing a meta-analytical database of MDS stem cell samples and controls, and have shown that this database can be used in basic as well as translation studies in MDS.

**Reportable Outcomes:**

**Manuscript:**


**Conclusion:**

We have shown the feasibility of constructing a meta-analytical database of MDS stem cell samples and controls, and have shown that this database can be used in basic as well as translation studies in MDS. We will now incorporate clinical information to this database in the new phase of the funding period.

**References:**


**Appendices:**

None