MEDGENOME

MedGenome Labs Ltd
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Test Details

Test

HLA (Human Leukocyte Antigen) genes of the Major Histocompatibility Complex (MHC) encodes proteins that differentiates self from non self. It governs innate and adaptive immunity and plays critical role in disease and immune defenses [1]. HLA typing is useful for determining the best match donors for allogenic bone marrow and organ transplantation, disease studies and paternity testing [2, 3]. High resolution NGS based HLA typing is the gold standard for HLA typing [4]. Accurate HLA typing for upto 4-fields, with G group coding for identical nucleotide sequences is done for classical class I HLA genes A*, B*, C* and class II HLA genes DRB1*, DQB1* and DPB1*. This enables careful selection of donors thereby critically improving transplantation outcome [3, 5, 6, 7, 8].

Methodology

DNA extracted from buccal swab was used to amplify the HLA genes of interest by NGSgo kit from GenDx by long-range PCR, followed by fragmentation and library preparation to be sequenced on the Miseq/ NovaSeq Illumina platform. The libraries were sequenced to mean >80-100X coverage on Illumina sequencing platform. The raw sequence reads are aligned using a FASTA-like algorithm. Instead of aligning the reads to a single reference, however, the reads are aligned to all the alleles in the database. The IMGT/HLA database is used as the source of HLA alleles. To determine the SNP haplotypes, every position in the reference is evaluated to define homozygosity or heterozygosity. The heterozygous positions are evaluated to determine the cis-trans relationships (called phasing) between the bases at the individual heterozygous positions. All alleles in the library are compared against the possible haplotypes found in the previous steps. The number of nucleotide mismatches with each allele is determined, as well as the number of mismatches with the determined phasing data. Mismatches at exons and introns are treated separately. A list of alleles is selected with a limited number of mismatches. From these alleles, all possible genotypes are generated which will contain the most likely genotype(s) present in the original dataset. For each of these genotypes, the mismatch level of the two alleles with the phased data is determined. The genotype(s) with the lowest mismatch count is (are) reported [9].

Disclaimer:

- **HLA genotypes were determined based on the IMGT/HLA database release 3.52. The occurrence of HLA genotyping results and the number of different allele combinations by a NGS assay for an individual may change according to the version of the IMGT/HLA database release. Please contact MedGenome at a later date for any change.**
- **"This test was developed and its performance characteristics determined by MedGenome"**

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APPENDIX-I

G-group	NMDP Allele Code	Included Alleles
Satvik		
A*24:02:01G	A*24:EKZMC	24:02:01:01/24:02:01:02L/24:02:01:03/24:02:01:04/24:02:01:05/24:02:01:06/24:02:01:07/24:02:01:08/24:02:01:09/24:02:01:10/24:02:01:11/24:02:01:12/24:02:01:13/24:02:01:14/24:02:01:15/24:02:01:16/24:02:03Q/24:02:10/24:02:101/24:02:102/24:02:103/24:02:108/24:02:13/24:02:31/24:02:40/24:02:43/24:02:44/24:02:56/24:02:65/24:02:79/24:02:80/24:02:81/24:02:82/24:02:83/24:02:84/24:02:98/24:09N/24:11N/24:40N/24:76/24:79/24:83N/24:144/24:150/24:153/24:154/24:155N/24:163N/24:183N/24:231/24:249/24:250/24:251/24:263/24:264/24:265/24:266/24:267/24:268/24:269/24:270/24:271/24:352/24:353/24:354/24:383/24:385/24:388N/24:400/24:401/24:402
A*24:02:01G	A*24:EKZMC	24:02:01:01/24:02:01:02L/24:02:01:03/24:02:01:04/24:02:01:05/24:02:01:06/24:02:01:07/24:02:01:08/24:02:01:09/24:02:01:10/24:02:01:11/24:02:01:12/24:02:01:13/24:02:01:14/24:02:01:15/24:02:01:16/24:02:03Q/24:02:10/24:02:101/24:02:102/24:02:103/24:02:108/24:02:13/24:02:31/24:02:40/24:02:43/24:02:44/24:02:56/24:02:65/24:02:79/24:02:80/24:02:81/24:02:82/24:02:83/24:02:84/24:02:98/24:09N/24:11N/24:40N/24:76/24:79/24:83N/24:144/24:150/24:153/24:154/24:155N/24:163N/24:183N/24:231/24:249/24:250/24:251/24:263/24:264/24:265/24:266/24:267/24:268/24:269/24:270/24:271/24:352/24:353/24:354/24:383/24:385/24:388N/24:400/24:401/24:402
B*40:01:01G	B*40:EKZMU	40:01:01/40:01:02:01/40:01:02:02/40:01:02:03/40:01:02:04/40:01:02:05/40:01:02:06/40:01:02:07/40:01:25/40:01:36/40:01:37/40:01:42/40:01:45/40:01:48/40:01:52/40:55/40:141/40:150/40:151/40:179/40:221/40:236/40:241/40:247/40:264/40:272/40:278/40:299/40:301/40:329/40:338N/40:353
C*03:04:01G	C*03:EKZNF	03:04:01:01/03:04:01:02/03:04:01:03/03:04:01:04/03:04:01:05/03:04:01:06/03:04:01:07/03:04:01:08/03:04:03/03:04:20/03:04:36/03:04:43/03:04:44/03:04:55/03:04:58/03:100/03:101/03:105/03:106/03:211:01/03:211:02/03:212/03:213/03:218/03:219/03:236/03:252/03:294/03:303/03:354/03:358/03:359/03:366N/03:369/03:376/03:381/03:387
C*07:01:01G	C*07:EKZNK	07:01:01:01/07:01:01:02/07:01:01:03/07:01:01:04/07:01:01:05/07:01:01:06/07:01:01:07/07:01:01:08/07:01:01:09/07:01:01:10/07:01:01:11/07:01:01:12/07:01:01:13/07:01:01:14Q/07:01:01:15/07:01:01:16/07:01:01:17/07:01:01:18/07:01:01:19/07:01:01:20/07:01:01:21/07:01:01:22/07:01:01:23/07:01:01:24/07:01:02/07:01:09/07:01:19/07:01:39/07:01:61/07:06:01:01/07:06:01:02/07:18/07:52/07:153/07:166/07:337/07:343/07:419/07:458/07:588/07:591/07:607/07:610/07:615/07:617/07:618/07:619/07:621/07:623/07:624
DRB1*07:01:01G	DRB1*07:EKZPZ	07:01:01:01/07:01:01:02/07:01:01:03/07:01:18/07:01:21/07:34/07:72/07:79/07:81/07:85
DRB1*11:01:01G	DRB1*11:EJJTK	11:01:01:01/11:01:01:02/11:01:01:03/11:01:01:04/11:01:08/11:01:29/11:01:30/11:97
DQB1*02:01:01G	DQB1*02:EJJSN	02:01:01/02:01:08/02:01:26/02:01:27/02:02:01:01/02:02:01:02/02:02:01:03/02:02:01:04/02:02:02/02:02:03/02:02:05/02:04/02:06/02:09/02:10/02:48/02:59/02:64/02:79/02:80/02:81/02:82/02:89/02:96N/02:97/02:98/02:99/02:102/02:105/02:106
DQB1*03:01:01G	DQB1*03:EJJSR	03:01:01:01/03:01:01:02/03:01:01:03/03:01:01:04/03:01:01:05/03:01:01:06/03:01:01:07/03:01:01:08/03:01:01:09/03:01:01:10/03:01:01:11/03:01:01:12/03:01:01:14/03:01:01:15/03:01:01:16/03:01:01:17/03:01:01:18/03:01:01:19/03:01:01:20/03:01:04/03:01:05/03:01:09/03:01:10/03:01:11/03:01:12/03:01:20/03:01:26/03:01:31/03:01:35/03:01:36/03:01:39/03:01:40/03:01:41/03:09/03:19:01/03:21/03:22/03:24/03:29/03:35/03:42/03:49/03:50/03:51/03:84N/03:94/03:115/03:116/03:164/03:165/03:169/03:182/03:191/03:196/03:198/03:206/03:241/03:243/03:246/03:253/03:264/03:266/03:276N/03:281

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Deepika Arora
Lead Genome Analyst

Dr. Shruthi.P.S
MBBS, MD (Pathology)
Senior Hematopathologist
KMC Reg No. 78159

---------- End of Report ----------

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COLLEGE of AMERICAN PATHOLOGISTS

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HLA TYPING REPORT

HLA TYPING REPORT	
Sample information	
Name	**Satvik**
Order ID/Sample ID	**764973/8178923**
Gender	**Male**
Age / Relationship	**1 Year & 4 Months**
Sample type	**BUCCAL SWAB**
Collection date & time	**10-10-2023 17:19:00**
Receipt date & time	**11-10-2023 11:07:00**
Report date & time	**17-10-2023 15:47:21**
Clinical indication	**Juvenile myelomonocytic leukemia (JMML) with monosomy 7**
Test Requested	**MGM517 - HLA Typing High resolution (HLA A, B, C, DRB1, DQB1)**
Requested by	**Dr. Sangeeta Mudaliar, BJ Wadia, Haematology (Mumbai)**

TYPING RESULT

LOCUS	HLA-A*	HLA-B*	HLA-C*	HLA-DRB1*	HLA-DQB1*
Satvik					
HLA-CLASS I & II	**A*24:02:01G**	**B*40:01:01G**	**C*03:04:01G**	**DRB1*07:01:01G**	**DQB1*02:01:01G**
	A*24:02:13	**B*44:03:02G**	**C*07:06:01:01**	**DRB1*11:01:01G**	**DQB1*03:01:01G**

Comment

G code: G code is a group of alleles that have identical nucleotide sequences in the antigen recognition site. Allele Database Version used in the report is 3.52 & Software version is 2.30.1.29498 Refer Appendix-I for G-Groups and NMDP (National Marrow Donor Program) codes.

Interpretation

NA

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SEHGAL PATH LAB
PRECISION | INNOVATION | COMPASSION

43 YEARS OF CELEBRATING HEALTHCARE

DR. KUNAL SEHGAL
M.D. Pathology (PGI Chandigarh) Gold Medalist
Fellow (AUF) Hematopathology & Flowcytometry
(The Johns Hopkins Hospital, USA)

Master SATVIK BHAVESH KESHARI (CKID 89354)
Age: 1 Yrs 2 Mon Sex:Male B J WADIA Hospital
Lab No : 10235174
Permanent ID :

Registered On 11/09/2023 18:23:04
Collected On 11/09/2023 21:33:01
Authenticated On 14/09/2023 13:57:47
FLW/23-2961

Flow Cytometry for leukemias (Panel1)

Clinical history	? Acute leukemia
Instrument software	BD FACS LYRIC/BD FACS SUITE
Cell preparation method	Stain - Lyse - Wash
Gating strategy	10 colour FCM using CD 45 gating.

Descriptive Summary:- Flow cytometric immunophenotypic analyses of the sample was done.

The analysis shows a predominant population of myeloid cells along with lymphocytes and normal haematogones, erythroid precursors, prominent population of monocytes (~10%).

In addition ~4% myeloid blasts are seen. Myeloid blasts show normal expression patterns of CD33 , CD13, CD117, HLA DR , CD34 and CD38 . the CD34 bright CD38 dim population of these myeloid blasts express variable CD25 and CD11b. heterogeneous CD7 expression is also noted in blasts while other B cell and T cell markers are negative

In addition prominent population of myeloid and monocytic series cells showing normal pattern of maturation and differentiation.

IMPRESSION: Flow cytometry analysis shows ~4% normal myeloid blasts along with background prominent mylomonocytic maturation and differentiation.

Morphologically slides show leukocytosis, increased blasts with monocytosis and myeloid prominence. This along with the above flow cytometry findings favour an underlying Juvenile Myelo Monocytic Leukemia

Correlate with bone marrow aspirate and bone marrow biopsy along with detailed cytogenetic and molecular findings

Dr. VASUDHA KAUL, M.D. Pathology
Consultant, Sehgal Path Lab

Dr. KUNAL SEHGAL, M.D.
Director, Sehgal Path Lab

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MC-4055

To: Dept Of Hemato Oncology-Wadia Children Hospital
Acharya Donde Marg,
Parel,
Mumbai- 400012
Maharashtra
Report Of: Mast. SATVIK BHAVESH KESHARI

Sample ID	:	2300176507
Patient ID	:	1002380837
Collected on	:	11-09-2023
Received on	:	12-09-2023 13:35:00
Reported on	:	15-09-2023 19:22:32
Ref By	:	Dept Of Hemato Oncology-Wadia Children Hospital

MOLECULAR CYTOGENETICS (FISH) REPORT

Patient Name	: **Mast. SATVIK BHAVESH KESHARI**	**Age**	: **1 Year 2 Months**
		Gender	: **Male**
Physician Name	: **DR. SANGEETA MUDALIAR**	**Specimen**	: **Ok**
Provisional Diagnosis	: **Acute leukemia(AL)**	**Status**	
		Disease Status	: **N.A**
Specimen Type	: **Bone Marrow Aspirate (BMA)**		
Haematopathology Report	: **JMML**		
Test Requested	: **t(9;22) (*BCR-ABL1*) FISH, -7/del(7q) FISH**		

Test	: **-7/del(7q) FISH Analysis.**
Method	: Direct and 24 hr culture of Bone marrow aspirate followed by interphase cells preparation, Fluorescence in situ hybridization on interphase cells.
Probe	: Metasystem XL 7q22 / 7q36 TC probe. Limit of Detection: Locus specific deletion probe 5%, 5% (monosomy)
No. of Cells Analysed	: 200

Result:

-7/del(7q) FISH Analysis:

-7/del(7q)	7q22(CUX1) (Orange)	7q36(EZH2) (Green)	CEN7 (D7Z1) (Aqua)	No. Cells
Signal/s/Cells	1	1	1	36/200

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Phone: +91 22 41841438; Website: www.lilacinsights.com; For queries or complaints, please email: info@lilacinsights.com

Mast. SATVIK BHAVESH KESHARI

Sample ID: 2300176507

Interpretation: Fluorescence in situ hybridization (FISH) with above mentioned probe showed evidence of monosomy of chromosome 7 (Freq. 18%).

IMPRESSION: Present case revealed monosomy of chromosome 7.
Monosomy of chromosome 7 is recurrent abnormality in JMML as per lit reports Monosomy 7 is common 20-30% cases of JMML.
Monosomy 7 is most commonly associated with KRAS as a secondary mutation.

References:

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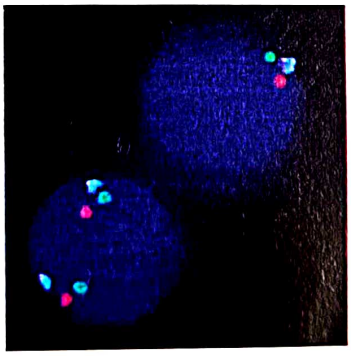

FISH on interphase cells showing monosomy of chromosome 7

Prepared By : **Mahima Patil**
Verified By : **Pranita Pawar**

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MC-4059

Mast. SATVIK BHAVESH KESHARI

Sample ID: 2300176507

Dr. P. S. Kadam Amare
Oncogeneticist
Chief & Lab Director "Cancer & Clinical Genetics"
Lilac Insights Pvt. Ltd.

Dr. Hrushikesh Lele
Sr. Scientific Officer
Oncocytogenetics Dept.
Lilac Insights Pvt. Ltd.

- End of Report -

Conditions of Reporting/Disclaimer:

- The report relates only to the specimen submitted to the lab which was verified and confirmed at the time of specimen collection. Also it is presumed that the specimen belongs to the patient named or identified, such verification being carried out at the point of generation of the said specimen.
- Although Conventional karyotyping is a gold standard method of cytogenetics which gives a global whole genomic view of multiple known, unknown chromosomal abnormalities, small cryptic, subtle aberrations below 7-8 Mb resolution can be missed.
- In spite of known sensitivity and efficiency of the genetic test, the test results have to be correlated with other clinical and pathological finding for conclusive diagnosis and disease management.
- A test request may be revised or generated by Lilac geneticist with an intimation to an Oncologist if: 1) Incomplete requisition 2) After haematopathology Update.
- In 1-2 % of APL cases, FISH may turn out to be negative due to PML/RARA probe design which unable to detect cryptic insertion of PML to RARA. In such rare cases, It is advisable to check PML-RARA by molecular methods.
- In case of Multiple Myeloma, flowcytometry report indicating abnormal plasma cell population is important for reference, as small abnormal clones may get deduced as per limit of detection policy in FISH analysis.
- In case of FFPE FISH, if H & E stained slides &/or histopathology report is not provided by customer , LILAC proceed with H & E staining followed by histopathology remarks along with marking of tumor area by our consultant pathologist.
- Assays are performed in accordance with standard procedure on receipt. The reported results are dependent on individual assay methods, equipment used, method specificity, sensitivity and quality of specimen(s) received.
- Lilac Insights Pvt. Ltd. has policy to return the FFPE blocks within one month after final reporting with proper documentation of the dispatch of the block to customer from accession dept, Lilac. After dispatch, if there is no intimation from customer within two weeks, Lilac will not be responsible for the Dispatched FFPE block.
- Soft copies of oncocytogenetics reports are sent to customer by office mail ID. Also, Hardcopies are sent to customer only on the address provided by client.

SRCC CHILDREN'S HOSPITAL
Managed by Narayana Health

Date: 12/10/2023

TO WHOM-SO-EVER ITMAY CONCERN

I wish to stat that **Satvik Keshari, 1.5 year / male, MRN 12520000163817,** has been diagnosed with **Juvenile Myelomonocytic leukemia. He is planned for Bone Marrow Transplant due to very high risk of leukemia. He does not have a fully matched sibling donor and hence planned for haplo-identical donor bone marrow transplant or matched unrelated donor.**

The **approximate cost of BMT would be 30 lakhs rupees** with an expected stay in the hospital for at least 42 days. This is an estimate only and is likely to change based on the actual expenditure.

BMT chemotherapy	Rs. 4,00,000/-
Supportive care (Antibiotics, other medicines, par-enteral mutation, professional charges)	Rs. 6,00,000/-
Blood bank and harvest charges	Rs. 2,00,000/-
Hospitalization (during BMT up to 42 days)	Rs. 5,00,000/-
Investigations	Rs. 3,00,000/-
Unrelated Donor Stem Cell cost or T cell depletion cost for haplo BMT	Rs. 10,00,000/-
Total cost estimate	Rs. 30,00,000/-

Dr. Chintan Vyas
Consultant Pediatric Hemato-Oncologist & Bone Marrow Transplant Physician
SRCC Children hospital, NH Group
Mumbai 400 034

Dr. Chintan Vyas
MMC: 2021107953

CONSULTATION SUMMARY

Patient MRN	:12520000163817	**Consultation Date**	:12/10/2023 02:29 PM
Patient Name	:Master Satvik Keshari	**Consultant**	:Dr. Chintan T Vyas (PAEDIATRIC ONCOLOGY, HAEMATO-ONCOLOGY & BMT)
Gender/Age/Dob	:Male , 1 Year 4 Months , 10/06 /22	**Consultation Type**	:OP , NEW VISIT
Patient Phone No	:9167945052		
Patient Address	:18,RAJDALARI BHAVAN WING B ,SHIVAJI NAGAR,Thane, Thane,Maharashtra,India, -400604		

DIAGNOSIS

- 445227008 | Juvenile myelomonocytic leukemia, Primary, Final, 12/10/2023

  Remarks: Monosomy 7, PTPN mutation.

CHIEF COMPLAINTS & HISTORY OF PRESENT ILLNESS

- nil :

VITALS

Blood Pressure : 100/70 mmHg

Heart Rate: 110 bpm
Temperature : 98 F

Respiratory Rate: 22 /min

Conscious level: Alert
Weight : 8.3 kg

MEWS Score: 3

PROCEDURE HISTORY

- No known surgical history

PAST MEDICAL HISTORY

- No significant past medical history

ALLERGY

- No known allergies

PLAN

- Advised for HLA reporting to search for MUD

  Also to look for haplo possibility, (T cell deplete)

  Parents explained about complications, cost, and success post BMT.

SOCIAL HISTORY

- No significant social history