

Mismatch Data Aggregator

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A. Introduction

The Mismatch Data Aggregator (MDA) is used to identify DSA to transplant mismatches (MM). The MDA is able to identify peak MFI and DSA over time to both serological and molecular mismatches.

The MDA is intended to be used in combination with 'Patient_SAB_combiner_0_9_december_2020', which combines Luminex single antigen bead (SAB) data output files from One Lambda's HLA Fusion software into a single document.

B. Instructions for Use

- 1) Create a folder for patient combiner files containing MFI data.
 - The patient combiner files must have the TX_ID in the file name and within it, the combiner output sheets must be included - ending in '_I' for class I data and '_II' for class II data.
- 2) Add the MDA to the same folder.
- 3) Within the MDA, input HLA type data into the DATA sheet. Non-essential columns are hidden. Columns to populate for each sample are:
 - J = TX_ID: Patient ID
 - K = TX_DATE: 1/1/2000 (dummy date used to capture all Luminex data)

- AN = tx_date2: Today's date
- Split columns: Serological HLA type*
- HR_Split columns: High resolution molecular HLA type*

** If donor data is missing/incomplete, the MDA will still function and process the data that is available. A full recipient serological or molecular HLA type is required for ideal function (see Section B.3. for further details).*

**DPB1 is not identified by the MDA.*

4) Add the number of rows to be processed (i.e. number of patients to be analysed) from the Data sheet in cell B3 of the CALC sheet.

- *Do not process >200 patients at any one time (more will cause Excel to crash).*

5) Click Calculate.

6) 3 Data sheets will be produced after the results tab.

- **Data 1:** Peak MFI per mismatch. Scroll to far right of sheet to see mismatches (row for each patient), and if DSA is present, the peak MFI and corresponding date of this sample is listed.
Columns FS – HB: Molecular DSA
Columns HD – IM: Serological DSA
- **Data 2:** Molecular mismatches with MFI data for all dates where DSA is detected.
- **Data 3:** Serological mismatches with MFI data for all dates where DSA is detected.

i) Mismatches displayed are from the donor HLA type.

- *Mismatches may be present in the molecular output (Data 1 & 2) that are not present in the serological output (Data 3).*

ii) xxx = No mismatch or no MFI data present for a mismatch.

iii) ND will be displayed where donor HLA type information is missing, except for DRB3/4/5 where the output will be 'xxx'.

iv) Homozygous donor MM are listed in Data 2 & 3 as follows:

- *If there is SAB data present, a single mismatch will be displayed.*
⇒ *Eg. The A locus will display only MM_A1.*
- *If there is no SAB data (no bead, or the recipient is non-sensitised) or the donor is matched, the mismatch will be displayed twice.*
⇒ *Eg. The A locus will display MM_A1 and MM_A2.*

C. Additional notes & troubleshooting

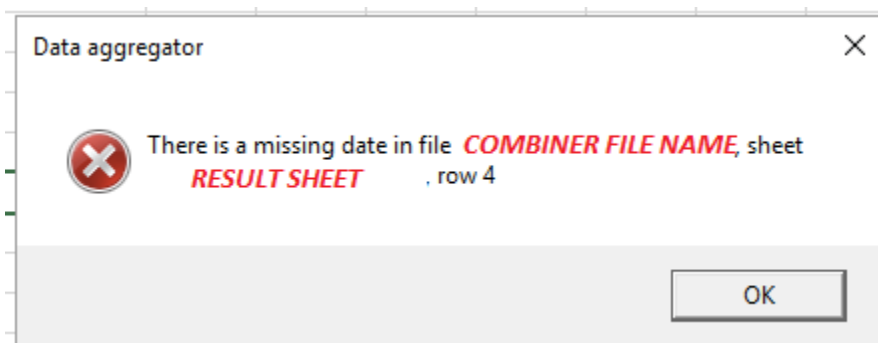
C.1. Combiner Formatting

Ensure combiners are correctly formatted before running the MDA to provide clear data and avoid error messages.

- Ensure all SAB samples in combiner have a date.
- Order SAB samples in combiner by date.
 - o If there are multiple samples for a DSA with the same peak MFI, the date of the sample identified in Data 1 is the date of the sample that appears first in the samples listed in the combiner (which isn't necessarily the most recent date – the combiner orders samples by Luminex session ID). This is most likely to occur if there is a MM but no specific DSA for a sensitised patient – MFI at that MM will be 0 on multiple occasions.
- Format MFIs to nearest whole number for ease of viewing.
- Remove repeat and diluted repeat samples from combiners to avoid duplicated repeated dates in aggregator.

C.2. Missing Date Error

If a sample in a combiner doesn't have a date, the MDA will display an error message:



Note down the combiner file name, data sheet and row of the sheet where data is missing. Click 'OK' on the error message.

Rerun the MDA after correcting to ensure all data is captured.

C.3. 'Stop on no allele?' Function (CALC page, cell B8, hidden)

This function indicates where HLA typing data is missing.

- If blank or 'n' input in B8, the output will be:
 - o ND for all loci, except DRB3/4/5 which will be 'xxx'.

- If anything else input in B8, a window will pop up which needs acknowledging every time there is a space. Data output for these gaps will then be 'xxx'.

Missing donor and recipient data are treated differently by the MDA.

- If recipient HLA type has data missing -> MDA cannot distinguish donor MM at that particular locus for either allele. ND will be present in output for MM_1 and MM_2.
- If donor HLA type has data missing -> MDA can distinguish MM at a locus. ND will be present for whichever MM is missing and the other MM will be identified.
- Molecular or serological recipient HLA type only may be present, and MDA still functions:
 - o If only molecular type, data will be present in Data 1 & 2.
 - o If only serological type, data will be present in Data 1 & 3.
 - o This is subject to above conditions for donor/recipient type completeness.

C.4. Date Override Function

If date data is missing from tx_date2, the date override function will operate when the MDA is run. The date override function works in order of preference: tx_date2 > End date (B7 CALC sheet, hidden) > 20/06/2016.

- Samples in combiner files are processed if:
 - o The sample date is between the TX_DATE (column J) and the tx_date2 (column AN).
 - o If tx_date2 (column AN) is blank, then the sample will be processed if the sample date is between the TX_DATE (column J) and the End Date in B7 on the CALC sheet. There is no requirement to populate B7 if tx_date2 is populated.
 - o If both B7 on the CALC sheet is empty then the sample is only processed if the sample date is between the TX_DATE (column J) and 20/06/2016.

We recommend placing today's date into tx_date2 (column AN) for each sample to ensure that all MFI data is processed by the aggregator.

C.5. Pre and post-transplant DSA identification

The MDA is validated for identifying DSA data both pre and post-transplant. Manipulation of date columns in DATA tab may allow identification of pre or post-transplant data only, but this function has not been validated.

For pre-transplant data only:

- TX_DATE: 1/1/2000.
- tx_date2: Date of transplant.

For post-transplant data only

- TX_DATE: Date of transplant.
- tx_date2: Today's date (or desired end date for data capture)