

## News from Scandiatransplant office

### June 2020

Database update June 17<sup>th</sup>, 2020

### Introduction

### Headlines

- Test date uncertainty on Covid-19 infected patients post transplant
- Change in registration of selected medical values on deceased donors
- Include label in predefined extractions
- Fusion, transfer previous conclusions
- Next STEP match run
- Summer 2020

All previous newsletters can be found on the Scandiatransplant web page <u>http://www.scandiatransplant.org/news/newsletters</u>

#### Content

1	Introduction
2	Test date uncertainty on Vovid-
	19 infected patients post
	transplant
2	Change in registration of
	selected medical values on
	deceased donors
2	Include label in predefined
	extractions
3	Fusion, transfer previous
	conclusions
4	Next STEP match run
4	Summer 2020

### Purpose

By this information letter, we wish to communicate to you about status and progress related to the database, collaboration with groups related to Scandiatransplant and on-going working projects.

We hope that you will read it and share the information with whom it might concern.

Do not hesitate to contact us for further information, ideas, problems and help.

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## Test date uncertainty on Covid-19 infected patients post transplant

On patients that are Covid-19 positive post transplant the test date is obligatory to register in YASWA. However, we have experienced that in some cases the date is difficult to get hold of.

If this is the case, it is now possible to do the registration and at the same time tick of the new box 'Date uncertainty'.

Infection tests									
	Infection code	Result	Date of test/sample	Date uncertainty					
	CMV: Anti-CMV (Cytomegalovirus)	ND: Not done							
	CovAb: Anti-SARS-CoV-2 (Covid-19 antibody)	ND: Not done							
	Covid: SARS-CoV-2 RNA (Covid-19)	+: Positive	01-Jun-2020						
	EBV: Anti-EBV IgG (Epstein-Barr)	ND: Not done		(m)					
-				2000a					

# Change in registration of selected medical values on deceased donors

Entry of data has been changed in the 'medical info' tab on systolic blood pressure, diastolic blood pressure, MAP, pulse rate, diuresis and temperature.

Registration of these parameters have been moved to the bottom of the page and you are now able o register several results (date + time) and follow the development during hospitalization.

When you wish to add a new result, click on 'Add new':

Basic Infection Lab	oratory tests Medical info	Blood gas & vent	Medication HL/	Organ proc.	Organ offer O	rgan QC Paybace	Files
Proteinuria:	*		Prote	inuria comments:			
Hypotensive period:	Duration: from	to	min.	Cardiac arrest:	✓ Dura	ation: from to	min.
Hypertension:		~		Freated diabetes:		*	
Past/Pres Malign Neoplasia:		*					
Past/Present Drug Abuse:		~	Past/Pr	es Alcohol abuse:		*	
Smoker:	~			Pack year:			
Infection:		*		Cultures:	*		
Diseases/Abuses:							
Medical history:							
Current medical history:	hgjhjfhgh						
ECG:	*		EC	HO: 💙			
Coronary angiography:	*		Chest X-	ray: 💙			
Tracheal secretion:	*		Abdominal	CT: 💙			
Remarks:							
Add new						Graph-var.:	✓ Show
Date of measurement		Systolic blood pr	Diastolic blood pr	мар	Pulse rate	Diuresis	Temperature
⇒ 02-Jun-2020 10:00		123	45	3	65	120	37

### several select medical results

Possibility to add

### Include label in predefined extractions

In some of the predefined extractions only codes are included, you now have the option to add the label, this is done by ticking of the box in the report execute screen:

More reports		×
Choose report:	Recipient - Current waiting list, kidney	*
Center:	ST: Stockholm	~
Country:		~
	Labels instead of codes Cancel Execute	-

If you want to see the development graphical you select a parameter and click on show:



# Graphical illustration of development

Fusion, transfer previous conclusions

Before a STEP match run the tissue typing labs must import updated Fusion MFI data on their recipients and each time, they need manually to register conclusions that deviate from the default conclusion (everything above MFI of 2000 is positive and everything below negative).

Now a new button/functionality has been added, it will bring forward data from the previous sample where the conclusions are different from default setting 'M: MFI cut-off'. After bringing forward the previous conclusions the user will be able to modify and save the conclusions on the new sample.

Example...

Several Fusions results have been imported:



On the sample from 12-nov-2019 more antigens have manually been set as unacceptable (the AB list is longer and if you enter the sample you see values where status is different from 'M: MFI cut-off')

Help with transferring previous conclusions

	Scandianumber: 202877				Date of sample:	12-Nov-2	019 🖪	
ead data MFI	HLA	Status	MFI	HLA	Status	MFI	HLA	Status
7410	DRB1*04:01	M: MFI cut-off	102.68	DRB1*14:01	M: MFI cut-off	50.85	DPA1*02:01,DPB1*01:01	M: MFI cut-off
6554	DRB1*04:03	M: MFI cut-off	102.37	DPA1*01:04,DPB1*18:01	M: MFI cut-off	50.52	B*42:01	M: MFI cut-off
6304	DRB1*04:02	M: MFI cut-off	98.38	DRB4*01:03	M: MFI cut-off	49.13	B*40:02	M: MFI cut-off
5588	DRB1*04:04	M: MFI cut-off	90.14	B*15:02	M: MFI cut-off	48.68	B*15:10	M: MFI cut-off
5149	DRB1*04:05	M: MFI cut-off	89.90	DPA1*02:01,DPB1*15:01	M: MFI cut-off	47.24	B*15:03	M: MFI cut-off
2002	A*34:01	M: MFI cut-off	89.41	DRB1*11:01	M: MFI cut-off	46.51	DQA1*04:01,DQB1*04:02	M: MFI cut-off
1434	B*37:01	M: MFI cut-off	87.74	DRB1*11:04	M: MFI cut-off	45.89	B*78:01	M: MFI cut-off
975.55	DQA1*05:01,DQB1*02:01	U: Unacceptable	86.72	A*80:01	M: MFI cut-off	45.28	DPA1*02:01,DPB1*05:01	M: MFI cut-off
925.85	DRB1*09:02	M: MFI cut-off	85.05	DRB1*01:03	M: MFI cut-off	45.27	B*07:02	M: MFI cut-off
655.55	DRB1*07:01	M: MFI cut-off	84.68	DRB5*02:02	M: MFI cut-off	45.25	B*53:01	M: MFI cut-off
589.52	DRB1*09:01	M: MFI cut-off	83.21	DRB1*12:02	M: MFI cut-off	44.75	DRB1*15:02	M: MFI cut-off
579.62	DQA1*05:05,DQB1*03:01	U: Unacceptable	81.85	B*44:02	M: MFI cut-off	44.67	B*15:01	M: MFI cut-off
532.30	DQA1*03:02,DQB1*03:02	U: Unacceptable	77.70	B*27:05	M: MFI cut-off	44.28	B*27:08	M: MFI cut-off
515.76	DQA1*06:01,DQB1*03:01	U: Unacceptable	77.35	A*02:01	M: MFI cut-off	43.89	DRB1*14:02	M: MFI cut-off
512.97	DQA1*05:03,DQB1*03:01	U: Unacceptable	76.68	DRB1*15:01	M: MFI cut-off	43.14	DRB1*13:01	M: MFI cut-off
	DQA1*03:02,DQB1*03:03	M: MFI cut-off	75.59	DPA1*01:03,DPB1*01:01	M: MFI cut-off	42.57	C*07:02	M: MFI cut-off

To transfer these results to the newest/next sample you enter the newest/next sample and click on the new 'Add conclusions' button

A with mfi I	nfo					Back	Save Reset Add co	nclusions Filter; e.g. DRB1		
	candianumber: 202877				Date of sample:	06-Feb-2	020 🖪	Transfer previous conclusion		
Bead data										
MFI H	HLA	Status	MFI	HLA	Status	MFI	HLA	Status		
5854	ORB1*04:01	M: MFI cut-off	65.24	A*24:03	M: MFI cut-off	35.65	B*59:01	M: MFI cut-off		
4940 [	ORB1*04:03	M: MFI cut-off	64.48	B*47:01	M: MFI cut-off	34.92	B*53:01	M: MFI cut-off		
4803 0	DRB1*04:02	M: MFI cut-off	64.23	B*27:05	M: MFI cut-off	34.43	C*03:03	M: MFI cut-off		
4456 [	ORB1*04:04	M: MFI cut-off	63.74	B*44:03	M: MFI cut-off	33.68	DRB1*01:03	M: MFI cut-off		
3892	DRB1*04:05	M: MFI cut-off	62.98	DRB1*01:02	M: MFI cut-off	32.62	DRB1*14:02	M: MFI cut-off		
2817 /	A*34:01	M: MFI cut-off	62.97	DRB3*03:01	M: MFI cut-off	32.15	DRB1*15:01	M: MFI cut-off		
1294 E	3*37:01	M: MFI cut-off	62.67	B*41:01	M: MFI cut-off	31.37	B*81:01	M: MFI cut-off		
589.36	DRB1*09:02	M: MFI cut-off	60.99	DRB4*01:03	M: MFI cut-off	30.33	DPA1*01:05,DPB1*28:01	M: MFI cut-off		
511.05	A*66:01	M: MFI cut-off	59.88	B*18:01	M: MFI cut-off	30.21	A*02:06	M: MFI cut-off		
485.47	DQA1*05:01,DQB1*02:01	M: MFI cut-off	59.33	A*32:01	M: MFI cut-off	30.20	DRB1*15:03	M: MFI cut-off		
424.88	DRB1*07:01	M: MFI cut-off	59.11	A*68:01	M: MFI cut-off	28.14	A*24:02	M: MFI cut-off		
393.74 A	A*25:01	M: MFI cut-off	58.67	B*51:01	M: MFI cut-off	28.10	C*15:02	M: MFI cut-off		
368.12	ORB1*09:01	M: MFI cut-off	58.60	A*74:01	M: MFI cut-off	25.98	DPA1*03:01,DPB1*13:01	M: MFI cut-off		

You will now be able to modify and save data

### Next STEP match run

As previously announced the next STEP match run will take place September 1<sup>st</sup>, 2020.

Deadlines for the upcoming STEP match run:

- Deadline for data entry in YASWA (new pairs and updates) is August 27th, 2020, 10:00 CET
- Scandiatransplant office will do a quality check on data and send a list with pairs to be confirmed by each center August 27th, 2020
- Confirmation of pairs must be done to the Scandiatransplant office no later than August 31st, 2020, 12:00 CET
- STEP match run is made September 1<sup>st</sup>, 2020.

### **Summer 2020**

In July user support will be limited, due to summer vacation among the employees at the Scandiatransplant office.

We wish you all a very nice summer 🕅

Upcoming STEP deadlines

You are (almost) on your own 🕲