Proposal full title:
Omics/Proteome-based donor-recipient stratification to allocate for kidney transplantation

Proposal acronym:
PROTEOTRANS

Type of funding scheme:
Research and Innovation Action

Work programme topics addressed:
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Name of the co-ordinating person:
Univ.-Prof. Dr. rer. nat. Joachim Jankowski
Director of the Institute for Cardiovascular Research, University Hospital of Aachen
Pauwelsstraße 30, D-52074 Aachen
Germany
Tel.: +49 (0) 241 80-82716
Email: jjankowski@ukaachen.de; www.imcar.rwthaachen.de

CC:
Prof. Dr. med. Martin Tepel
Senior Consultant and Clinical Professor in Nephrology with Special Assignments in Renal Medicine Research
Odense University Hospital, Department of Nephrology, and University of Southern Denmark
Institute for Molecular Medicine / Cardiovascular and Renal Research
Winsløwparken 21-3, DK-5000 Odense C
Denmark
Phone: +45-6550-3755, Fax: +45-6613-3479
Email: mtepel@health.sdu.dk
- List of participants:

<table>
<thead>
<tr>
<th>No.</th>
<th>Participant</th>
<th>Organization name</th>
<th>Country</th>
<th>Coordinator</th>
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<tr>
<td>1</td>
<td>University</td>
<td>University Hospital</td>
<td>Germany</td>
<td>Joachim Jankowski (M)</td>
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<td>University</td>
<td>Denmark</td>
<td>Martin Tepel (M)</td>
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<td>Hospital</td>
<td>University</td>
<td>Spain</td>
<td>Rafael Selgas (M)</td>
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<td>4</td>
<td>Hospital</td>
<td>University</td>
<td>France</td>
<td>Olivier Thaunat (M)</td>
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<td>Belgium</td>
<td>Maarten Naesens</td>
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<td>Romania</td>
<td>Ionel Sinescu (M)</td>
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<td>University</td>
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<td>Denmark</td>
<td>Hans Christian Beck (M), Lars Melholt Rasmussen (M)</td>
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<td>Diagnostic</td>
<td>Germany</td>
<td>Jochen Metzger (M), Harald Mischak (M)</td>
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<td>9</td>
<td>Nordic</td>
<td>Science A/S (NB)</td>
<td>Denmark</td>
<td>Federica Genovese (F), Morten Karsdal (M)</td>
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<td>10</td>
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<td>University</td>
<td>Austria</td>
<td>Daniela Dunker (F), Georg Heinze (M)</td>
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<td>Red Cross Blood</td>
<td>Finland</td>
<td>Jukka Partanen (M), Jouni Lauronen (M)</td>
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<td>12</td>
<td>Immundiagnostik</td>
<td>IMM</td>
<td>Germany</td>
<td>Susanne Dunker (F), Franz Paul Armbruster (M)</td>
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<td>Netherlands</td>
<td>Undine Samuel (F), Serge Vogelaar (M)</td>
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<td>Deutsche</td>
<td>StiftungOrgantransplantation</td>
<td>Germany</td>
<td>Axel Rahmel (M), Marie Lingemann (F)</td>
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<td>ttopstart BV</td>
<td>DTOP</td>
<td>Netherlands</td>
<td>Karin Bosch-Ebense (F)</td>
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WP2 Genomic analysis

- Objectives:
  …to study gene expression levels – “transcripts” - and genomic variation – “SNPs” - that forecast allograft function in kidney transplant recipients.

- Task 2.1. consists of full RNA sequencing (RNA-Seq) from blood and biopsy samples.
- Task 2.2. consists of determination of genomic variation, SNPs, in transplantation recipients and donors. Both GWAS and targeted gene analyses.

Samples from Helsinki, Finland

- All kidney tx’s are done in one single centre (Helsinki University Hospital) and all histocompatibility testings in one lab (FRC BS)

- The major study set, kidney tx done between 6/2015 - 7/2017:
  - expected number of tx = 300
  - HLA A, B, C, DRB1, DQB1 (intermediate resolution) typed; anti-HLA antibody status; x-match
  - Samples:
    - Donors: DNA & living spleen cells from all; serum/plasma only from coming tx
    - Patients: DNA, serum
  - Clinical follow-up and data available (during project period: acute, 1 y & 3 y outcome)
  - Excluded: all related donors and donors outside Finland

- Confirmatory, retro set, tx done between 1/2010 - 6/2015:
  - estimated number of tx: 800 tx
  - A,B, C, DRB1, DQB1 (low resolution) typed; anti-HLA antibody status; x-match
  - Samples:
    - Donors: DNA & living spleen cells (of most samples)
    - Patients: DNA, serum.
  - Clinical follow-up (during project period) 2 to over 5 years