Agenda | Solve-RD Annual Meeting 2022

25-26 April 2022 | online, Berlin time (CEST)

Monday, 25 April 2022

13:00 **Welcome & Introduction** (Olaf Riess, Tübingen)

13:15 **Session 1: Re-analysis of exomes & genomes**
(*Chair: Richarda de Voer, Nijmegen & Nika Schuermans, Ghent*)

Identification of disease-causing variants in rare disease patients through the programmatic reanalysis of Solve-RD exome and genome datasets (*Ida Paramonov, Barcelona*)

Findings of the Solve-RD Copy Number Variation Working Group following reanalysis of 11,000 exome datasets (*Steve Laurie, Barcelona*)

Mobile element insertions are the cause of genetic disease in a small fraction of patients (*Robin Wijngaard, Nijmegen*)

Flash talks (5 minutes each):

- Re-analysis of WES data from patients with multiple mitochondrial respiratory chain complex deficiencies reveals molecular diagnosis in half of the cohort (*Catarina Olimpio, Cambridge*)
- Cold Case (Season II): TTN deletion described after CNV analyses (*Isabelle Nelson, Paris*)
- Solved the unsolved: re-analysis of WES data identified the first structural variant associated to Kleefstra Syndrome (*Annalaura Torella, Naples*)
- A 2-year experience of data sharing through GPAP: a powerful tool to increase diagnostic yield (*Anne-Sophie Denommé-Pichon, Dijon*)

15 minutes discussion

14:35 **Break**

15:05 **Session 2: From deep phenotyping to new disorders and new phenotypic patterns**
(Chair: *Ana Rath, Paris & Elke de Boer, Nijmegen*)

Improvement of phenotypic similarity algorithms by the use of automated HPO annotations curation (*Oscar Hongnat, Paris*)

MitoPhen: A human phenotype ontology-based tool to identify mitochondrial DNA disease (*Thiloka Ratnaike, Cambridge*)

Flash talks (5 minutes each):

- Identification of a possible founder intronic DES mutation associated with variable CMS-MFM phenotype by re-analysis of exomes and reverse pheno-pathotyping (*Kiran Polavarapu, Ottawa*)
- Visualisation of networks obtained with phenotypic similarity calculation methodology through Cytoscape JS (*Maroua Chahdil, Paris*)
- Highlighting the Golgi Apparatus in CMT pathophysiology by the addition of a novel and recurrent GBF1 mutation (*Jonathan De Winter, Antwerp*)
- Expanding the phenotypic spectrum of WARS2-associated disorders: Additional cases within Solve-RD (*Martje Pauly, Lübeck*)

15 minutes discussion

16:10 **Keynote lecture**
(*Chair: Olaf Riess, Tübingen*)

Eric Minikel & Sonia Vallabh, Broad Institute, Cambridge, MA, USA
A genetically informed paradigm for primary prevention of prion disease.

16:55 **Break**

17:25 **Session 3: From re-analysis to novel molecular strategies**
(*Chair: Steven Laurie, Barcelona & Anna Sommer, Bonn*)

DeNovoCNN: A deep learning-approach to *de novo* variant calling in next generation sequencing data (*Gelana Khazeeva, Nijmegen*)

Identification of clinically relevant variants in homologous regions in 41,755 exomes (*Wouter Steyaert, Nijmegen*)

Germline genetic variants that affect Wnt signaling as potential cause of colonic polyposis (*Laura Valle, Barcelona*)

Chromatin profiling uncovers the gene-regulatory landscape underlying diverse monogenic antibody deficiencies (*Fangwen Zhao, Vienna*)

Flash talks (5 minutes each):

- Twist Enrichment Kits Have Lower Minimum Average Coverage Requirements in Clinical Diagnostics (*Burcu Yaldiz, Nijmegen*)
- Re-analysis of WES data of patients with intellectual disability and complex phenotypes (*Erika de Sensi, Parma*)
- The importance of the bibliographic surveillance in unsolved intellectual disability cases: 3 solved exome cases by Solve-RD (*Mathieu Georget, Paris*)
- Germline Pathogenic Variant Analysis of Colorectal Cancer Predisposing Genes by Targeted Long-Read Sequencing (*Iris te Paske, Nijmegen*)

15 minutes discussion

19:00 **End of meeting day 1**

Tuesday, 26 April 2022

13:00 **Session 4: Diagnostic & clinical utility**
(*Chair: Gulcin Gumus, Eurordis & Kiran Polavarapu, Ottawa*)

Genetic landscape of non-5q-SMAs and lower motor neuron diseases (*Mert Karakaya, Cologne*)

RFC1 Caller: Reliable detection of RFC1 expansions in WGS data (*Roisin Sullivan, London*)

Medical costs of children admitted to the Neonatal Intensive Care Unit: the role and possible economic impact of exome sequencing in early diagnosis (*Richelle Olde Keizer, Nijmegen*)

Treatabolome database: current state and new developments towards enhancing rare disease treatment visibility (*Carles Hernandez Ferrer, Barcelona*)

Flash talks (5 minutes each):

- New RD-Connect GPAP features implemented in collaboration with Solve-RD, EJP-RD and ELIXIR enable the diagnosis of rare disease patients with previously negative WES/WGS (*Alberto Corvo, Barcelona*)

- NGS findings in girl with onychodystrophia, chylotorax and behavioural disorder (*Marek Turnovec, Prague*)
- Whole-exome sequencing re-analysis of families with suspected Gastric Cancer tumour risk syndromes strengthens the role of PALB2 in diffuse gastric cancer and lobular breast cancer predisposition (*José Garcia Pelaez, Porto*)

10 minutes discussion

14:25 **Bio-Break**

14:30 **Future of Solve-RD workshop**
(*Chair: Holm Graessner, Tübingen*)

Introduction to workshop concept (*Holm Graessner, Tübingen*)

– change of meeting rooms –

Brainstorming & discussion in break-out rooms (participants select a workshop topic they'd like to join; further information will follow!)

15:00 **Break**

15:30 **Future of Solve-RD workshop *cont.***
(*Chair: Holm Graessner, Tübingen*)

Summary of break-out sessions (*topic leads*)

Joint discussion

Solve-RD in Rare Disease partnership (*speaker tbc*)

16:25 **Logistics & management**
(*Chair: Holm Graessner, Tübingen*)

Update on Solve-RD logistics & management (*Kornelia Ellwanger & Birte Zurek, Tübingen*)

16:55 **Break**

17:25 **Session 5: Functional & novel omics analysis**
(*Chair: Ana Topf, Newcastle upon Tyne & Iris te Paske, Nijmegen*)

Biallelic loss of FICD causes ER stress and synaptic disfunction in a Drosophila model of Hereditary Spastic Paraplegia (*Grace R. Zhai, Miami*)

SRSF1 haploinsufficiency is responsible for a new syndromic form of developmental delay including marfanoid habitus with intellectual disability (*Elke Bogaert, Ghent*)

Gene prioritization for rare diseases integrating genotype, RNA-seq and phenotype - lessons from a CAGI 6 challenger team (*Vicente Yépez, Munich*)

Flash talks (5 minutes each):

- Missense variants in ANKRD11 cause KBG syndrome by impairment of stability or transcriptional activity of the encoded protein (*Elke de Boer, Nijmegen*)
- De novo DCAF15 variant in three patients with features consistent with Cornelia de Lange syndrome phenotype (*Sahar Da'as, Qatar*)
- Modeling of human SMPX disease mutations using zebrafish (*Mridul Johari, Helsinki*)
- Functional analyses of PTPRT germline missense variants identified in patients with serrated polyposis syndrome (*Anna Sommer, Bonn*)

15 minutes discussion

18:45 **Wrap-up** (Han Brunner, Nijmegen)

19:00 **End of meeting**

Agenda may be subject to change.