

Agenda | Solve-RD Final Meeting 2023

24-26 April 2023 | Prague, CZ & online | all times CEST (Berlin time)

Meeting room: Congress Hall SUN1+2, Orea Hotel Pyramida Prague

Online: *tba*

Monday, 24 April 2023

13:00 Welcome & Introduction

Olaf Riess & Milan Macek

13:15 Session 1: Re-analysis of exomes & genomes

Chair: Alexander Hoischen & Nika Schuermans

SNV-InDel working group: Results and lessons learned from the analysis of 22,035 exomes and genomes from 6 European reference networks **(30)**

Leslie Matalonga, Barcelona

Systematic analysis and/or re-analysis of exome data from patients with early-onset developmental and epileptic encephalopathies **(61)**

Davide Mei, Florence

Solve-NMD in Paris: Project results **(33)**

Isabelle Nelson, Paris

🔍 Prevalence of mitochondrial disease genes in inherited peripheral neuropathies **(19)**
Tomas Ferreira, Cambridge

🔍 Heterozygous SPTAN1 frameshift mutations cause distal myopathy with neurogenic features **(15)**

Jonathan De Winter, Antwerp

🔍 Exome reanalysis and reverse phenotyping instrumental in solving a rare GOLGA2-associated neuromuscular disease with brain abnormalities **(34)**

Kiran Polavarapu, Ottawa

🔍 Re-analysis of whole exome data lead to diagnosis in unsolved patient with intellectual disability, spastic paraparesis, retinitis pigmentosa, hearing loss and dysmorphic facies **(37)**

Lukáš Ryba, Prague

🔍 Approach to Cohort-Wide Re-Analysis of Exome Data in 1000 Individuals with Neurodevelopmental Disorders **(02)**

Tobias Bartolomaeus, Leipzig

15 min discussion

14:35 Coffee Break | Free Poster Viewing

Foyer in front of Congress Hall SUN 1+2

15:20 Session 2: Re-analysis of exomes & genomes – continued –

Chair: Sergi Beltran & Iris te Paske

Customizing re-analysis for unsolved rare disease individual patients and integrating data from large-scale sequencing projects substantially improves diagnoses and leads to novel discoveries **(23)**

Adam Jackson, Manchester

Comprehensive reanalysis of copy number variant in exome sequencing data from 5,759 families results in 44 confirmed new diagnoses and 45 further candidate diagnostic variants for follow-up **(27)**

Steven Laurie, Barcelona

Full talks: 10 min + 5 min Q&A

🔍 Flash talks: 3 min w/o Q&A but joint discussion after a series of flash talks

Agenda | Solve-RD Final Meeting 2023

Structural variant calling in the Solve-RD whole exome sequencing cohort, data freezes one to three: added value to CNV analysis **(16)**

German Demidov, Tübingen

Combined loss of CDH1 and downstream regulatory sequences drive early-onset diffuse gastric cancer and increases penetrance of Hereditary Diffuse Gastric Cancer **(20)**

Carla Oliveira, Porto

🔍 Detection and characterization of a *de novo* Alu retrotransposition event causing NKX2-1-related disorder **(29)**

Francesca Magrinelli, London

🔍 Maternal mosaicism detected by trio-genome sequencing in an individual with RYR1-related congenital myopathy **(17)**

Berta Estévez Arias, Barcelona

🔍 Germline variants in PARP1 as potential cause of colonic polyposis in adults **(51)**

Laura Valle, Barcelona

🔍 2000 trio exome sequencing on research base: output and outlook **(01)**

Rami Abou Jamra, Leipzig

15 min discussion

The Solve-RD re-analysis approach – a summary

Sergi Beltran, Barcelona

17:00 Break

18:00 Welcome reception & poster session

Foyer in front of Congress Hall SUN 1+2

20:00 End of meeting day 1

Tuesday, 25 April 2023

9:00 Session 3: From deep phenotyping to functional analysis

Chair: Richarda de Voer & Kiran Polavarapu

The challenge of deep phenotyping in neonatal genetic epilepsies **(10)**

Evelina Carapancea, Brussels

In vivo functional characterization of novel FICD biallelic variants associated with Hereditary Spastic Paraplegia **(57)**

Grace Zhai, Miami

SRSF1 haploinsufficiency is responsible for a syndromic developmental disorder associated with intellectual disability **(59)**

Elke Bogaert, Ghent

🔍 The burden of titin variants on genetic counselling **(40)**

Marco Savarese, Helsinki

🔍 Deep phenotyping and genotyping in a childhood-onset Hereditary Spastic Paraplegia (HSP) cohort **(53)**

Ainara Salazar Villacorta, London

🔍 Altered nucleo-cytoplasmic distribution of PTBP1 is associated with rhizomelic osteochondrodysplasia and variable neurodevelopmental anomalies in humans and a mouse model **(43)**

Julien Paccaud, Dijon

🔍 A new gene, DCAF15, involved in Cornelia de Lange syndrome: Expanding the genetic spectrum **(54)**

Sahar I. Da'as, Doha

Full talks: 10 min + 5 min Q&A

🔍 Flash talks: 3 min w/o Q&A but joint discussion after a series of flash talks

15 min discussion

10:15 Coffee Break | Free Poster Viewing

Foyer in front of Congress Hall SUN 1+2

10:45 Session 4: New disorders & new phenotypic patterns

Chair: Ana Topf & Liedewei Van de Vondel

Recurrent variants in subunits of the Human Mediator complex affect brain development and lead to severe neurodegenerative diseases **(09)**

Elisa Cali, London

Modeling Pitt-Hopkins syndrome and new pathogenetic variants of TCF4: a step forward toward precision medicine **(58)**

Julien Paccaud, Dijon

🔍 C-terminal frameshift variant of TDP-43 with pronounced aggregation-propensity causes rimmed vacuole myopathy but not ALS/FTD **(60)**

Bart Dermaut, Ghent

🔍 Loss of phospholipase PLAAT3 causes a mixed lipodystrophic and neurological syndrome due to impaired PPAR γ signalling **(63)**

Nika Schuermans, Ghent

🔍 Novel biallelic variants expand the phenotypic spectrum of FAR1-related disorder **(47)**

Hatice Tasan, London

🔍 The influence of MECP2 mutation type and the polygenic risk scores in the clinical variability of Rett syndrome **(56)**

Kristina Zguro, Siena

15 min discussion

11:45 Lunch

Nebula restaurant (same as breakfast area)

13:30 Session 5: Bioinformatics and infrastructure

Chair: Gisèle Bonne & Steven Laurie

Phenotypic similarity-based approach for variant prioritization for unsolved rare disease embedding a data visualization of phenotypic similarity networks: a proposal of an analysis pipeline **(11)**

Maroua Chadil, Paris

Expanding the utility of MitoPhen: A study of diagnosed patients **(35)**

Thiloka Ratnaike, Cambridge

Treatabolome DB: linking gene and variants with treatments for rare diseases **(13)**

Sergi Beltran, Barcelona

A unified data infrastructure in support of large-scale rare disease research **(24)**

Lennart Johansson, Groningen

🔍 A new genomic analysis interface in RD-Connect GPAP in collaboration with Solve-RD, EJP-RD and ELIXIR to facilitate case solving and to boost cohort analysis for rare diseases **(12)**

Alberto Corvò, Barcelona

🔍 A centralized platform for the management and integration of genomic and phenotypic data for the study of rare disease **(62)**

Marta Rusmini, Genova

🔍 Solve-RD as a leading use-case at EGA **(49)**

Coline Thomas, EBI-EMBL

🔍 Using functional gene embeddings to prioritize novel candidate genes in rare disease **(06)**

Felix Brechtman, Munich

15 min discussion

Full talks: 10 min + 5 min Q&A

🔍 Flash talks: 3 min w/o Q&A but joint discussion after a series of flash talks

15:00 Coffee Break | Free Poster Viewing

Foyer in front of Congress Hall SUN 1+2

15:45 Session 6: Novel (molecular) strategies

Chair: Lisenka Vissers & Leslie Matalonga

Integration of RNA-seq with genotypic and phenotypic data across multiple rare diseases leads to increase diagnostics within Solve-RD **(55)**

Vicente A. Yepez, Munich

RNA-seq based outlier analysis allows identification of causal *NOP56* repeat expansions (SCA36) in patients negative by routine WES analysis **(05)**

Danique Beijer, Tübingen

Long-read sequencing in 65 genetically undiagnosed rare disease families **(46)**

Wouter Steyaert, Nijmegen

Molecular profiling of colorectal tumors from individuals suspected to have an adenomatous colorectal genetic tumor risk syndrome **(48)**

Iris te Paske, Nijmegen

Comprehensive molecular profiling of serrated polyps from individuals with serrated polyposis syndrome by whole-exome sequencing **(45)**

Anna Sommer, Bonn

Spanish Undiagnosed Rare Diseases Program (SpainUDP): A review after 8 years of experience **(28)**

Estrella Lopez-Martin, Madrid

🔍 Disease genes discovery in the Telethon Undiagnosed Diseases Program **(31)**

Manuela Morleo, Naples

🔍 Large inversion in the DMD gene identified using long read-whole genome sequencing: A case report from UNIFE **(64)**

Rita Selvatici, Ferrara

🔍 Detection of a large structural rearrangement in the DMD gene with Optical Genome Mapping and Long-read whole genome sequencing **(38)**

Anna Sarkozy, London

🔍 Trio genome analysis in 45 unsolved children with neuromuscular diseases **(32)**

Daniel Natera, Barcelona

🔍 WG Epigenomics: DNA methylation analysis strategies for RRBS **(42)**

Julia Schulze-Hentrich, Tübingen

Wrap-up & acknowledgements

Holm Graessner, University of Tübingen

18:00 Break

19:00 Guided walk to the Strahov Monastery Brewery

Meet the team from Prague Eventery at the hotel lobby for a guided walk to the restaurant

19:30 Joint dinner at Strahov Monastery Brewery

Strahovské nádvoří 301, 118 00 Prague 1; [Link to resraurant](#)

Wednesday, 26 April 2023

8:30 Towards the future of Rare Disease Diagnostics

Chair: Ana Rath & Gulcin Gumus

Towards a personalised systems biomedical approach for the diagnosis of inherited metabolic diseases

Ines Thiele, University of Galway

Hyperpersonalized therapies for the long tail of genetic disease

Timothy Yu, Boston Childrens Hospital and Harvard Medical School

Looking further: Patient organizations and advancing RD research on diagnosis

Gulcin Gumus, Eurordis

Solve-RD 2.0

Olaf Riess, University of Tübingen

10:15 Break

10:45 Impact of Solve-RD on research and care of RD patients

Chair: Han Brunner & Holm Graessner

Key Solve-RD achievements

Holm Graessner, University of Tübingen

Genomic Reanalysis of a Pan-European Rare Disease Resource Yields >500 New Diagnoses

Sergi Beltran, Barcelona & Alexander Hoischen, Nijmegen

Round table: The Future of Rare Disease diagnostics in Europe

- *Simona Bellagambi, EURORDIS Board of Directors and Uniamo*
- *Daria Julkowska, EJP-RD coordinator, INSERM*
- *Christina Kyriakopoulou, European Commission, DG Research & Innovation*
- *Milan Macek, Charles University Prague*
- *Olaf Riess, Solve-RD coordinator, University of Tübingen*
- *Lisenka Vissers, ERN ITHACA, Radboud UMC Nijmegen*
- *Timothy Yu, Boston Childrens Hospital and Harvard Medical School*

Closing remarks

12:30 End of meeting

13:30-15:00 Solve-RD review meeting – invitation only –

Chair: Holm Graessner

Agenda may be subject to change.