# 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

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$\gamma\gamma$ 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 Brechtmann, 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*

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

## 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.

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