COMBIMS Newsletter

A novel drug discovery method based on systems biology: combination therapy and biomarkers for Multiple Sclerosis

Issue no. 2, June 2014

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The recruitment of MS patients and the collection of samples is complete

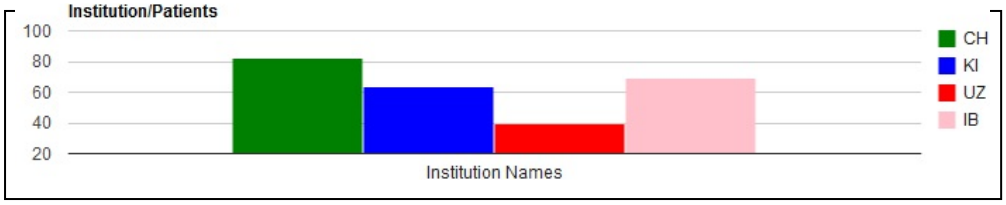
More information:
http://www.combims.eu

CombiMS update

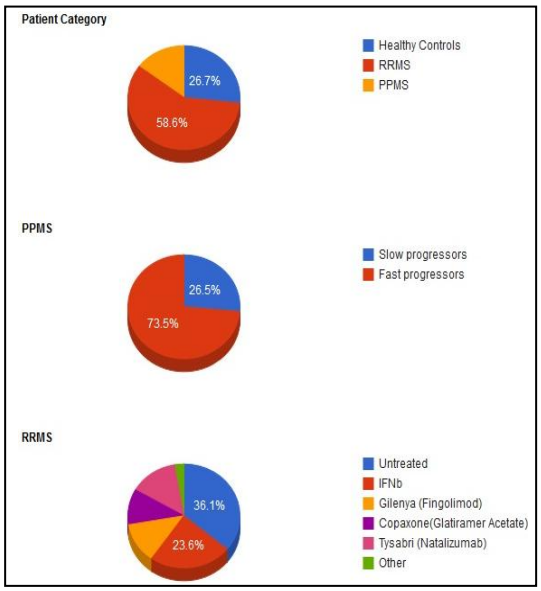
The CombiMS project has now completed the first half of its second year. The consortium has already completed the collection of samples from MS patients and healthy controls that was carried out over a 4-month period. The secure database containing clinical information from these patients is now closed, and phosphoproteomic, cytokine and genotyping data is currently being obtained from these samples. This data should be completed in the first weeks of July. A first version of the modelling pipeline will be ready by then, based on the fitting of the logic model developed earlier to the experimental data from the first set of patients. This will be updated with the full dataset when it becomes available.

Recruitment of MS patients and collection of samples

The clinical centres have recruited the MS patients and healthy controls for the study being carried out by the CombiMS consortium. A total of 255 individuals, MS patients and healthy controls, have been recruited by the clinical groups involved in the consortium (University of Zurich -UZ, Karolinska Institute -KI, Charité -CH and IDIBAPS -IB).



Of these 255 individuals, 26.7 % are healthy controls, 58.6 % are patients with relapsing-remitting MS (RRMS), including both slow and fast progressors, and 14.7 % are patients with primary progressive MS (PPMS) either untreated or treated with different drugs.

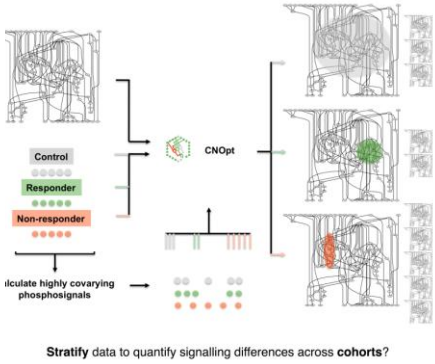


Dissemination activities and Publications

The article titled **"Signalling networks in MS: A systems-based approach to developing new pharmacological therapies"** is currently in press in the ***Multiple Sclerosis Journal***. The article summarizes the collected knowledge about pathways implicated into MS pathogenesis and describes the pipeline for the identification of new therapies based on the modeling of signaling pathways associated with MS and MS drugs.

The work of the CombiMS Consortium was presented by ProtATonce at the ***International Conference on Systems Biology of Human Disease*** in Boston (June 17-19, 2014). The abstract of the poster, titled **"Construction of a drug-induced phosphoprotein/cytokine dataset in clinical samples for Multiple Sclerosis"** was among the 12 selected, out of a total of 112, to be presented as a 5' talk on the main stage, where Theodore Sakellaropoulo from ProtATonce had the chance to deliver the oral presentation to an expert audience.

The mathematical modelling work of the CombiMS Consortium was presented by EMBL-EBI at the ***2nd EMBO Conference on Visualizing Biological Data (VIZBI 2014)*** *in Heidelberg (March 5-7, 2014).* The abstract and image of the poster, titled **"Visualize signalling to maximize understanding of multiple sclerosis"** can be found at the following link: *http://vizbi.org/Posters/2014/C14*



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4th Consortium meeting

The Fourth Meeting of the CombiMS Consortium was held at EMBL-EBI in Hinxton on the 27th of May, 2014. The members of the Consortium took stock of the work carried out during the first half of 2014 and discussed the activities to be undertaken in the last stage of the project. An overview was given on the cytokine and phosphoprotein data analysis, and of the quality control checks that have been carried out to ensure the quality of data. Special attention was paid to the strategy for normalizing and stratifying the data, as well as to the approach to be followed to integrate the different models developed. During the meeting, a Keynote lecture on Signalling in T cells was presented by Dr Balbino Alarcon from the Centro de Biologia Molecular Severo Ochoa (CBMSO) and a member of the project's Scientific Advisory Board, who also provided the CombiMS consortium with his recommendations on the progress and future activities of the consortium.

Forthcoming tasks

- Fit the models to the experimental data obtained from the healthy controls and MS patients in order to identify potential drug combinations to treat MS.
- Validate in vitro and in animal models the mechanism of pathogenesis of MS and drug combinations proposed from the models.
- Draft a publication describing the approach to develop large datasets reflecting the uniqueness of the CombiMS project.

SEVENTH FRAMEWORK PROGRAMME

The CombiMS project has received funding from the European Union Seventh Framework Programme (FP7/2007-2013) under grant agreement n° 305397.

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