Date: August 28th, 2011

Place: Radisson Blu Atlantic Hotel, Stavanger, Norway

Present: Per Madsen (DK), Soren Borchersen (DK), Larry Schaeffer (CAN), Gerben de Jong (NL), Juan Pena (SP), Rachel Woods (NZ), Anne Winkelman (NZ), Bevin Harris (NZ), Filippo Miglior (CAN), Brian Wickham (IRL), Peter Amer (NZ), Andrew Cromie (IRL), Marcin Pszczola (POL), Jérémie Vandenplas (B)

Roel Veerkamp (NL), Eileen Wall (UK), Donagh Berry (IRL), Nicolas Gengler (B), Mario Calus (NL), Mike Coffey (UK), Sinéad McParland (IRL), Catherine Bastin (B), Erling Strandberg (SWE), Henk Bovenhuis (NL), Yvette de Haas (NL)

Discussion what to do with outcome of RobustMilk?

Interesting result (MIR-profiles, genomic predictions) have come out of RobustMilk. The project members are looking for the best way to utilise the results around Europe and elsewhere. Also we are looking for further collaboration after the projects finishes in eight month time. The RobustMilk partners are happy to share results with other partners, and are also happy to offer the infrastructure (in terms of methods and database) for further utilisation. It depends obviously on the interest of others and what they are willing to contribute to the grant scheme of things. The purpose of today is to start the discussion.

What has RobustMilk on offer (see eight presentation at Interbull): a database structure with new phenotypes on feed intake, progesterone, liveweight, energy balance etc. and genotypes from research herds. Procedures for for data handling, protection and combining. Genomic predictions for a set of new trait. MIR prediction equations for milk quality (fatty acids), feed intake and energy balance.

The outcome of the discussion is that there is a general interest to contribute to an international effort to enlarge the dataset and develop prediction equations further, so that the estimates for the genomic and MIR prediction equations will become more reliable.

Possible projects that can add substantial data to the existing database are in:

- Denmark (Peter Lovendahl): methane, feed intake on experimental farm (150 cows)
- New Zealand/Australia (Bevin Harris): feed intake and genotypes on heifers (2000 animals)
- USA (Mike VandeHaar): feed intake and genotypes of probably 8000 cows
- Netherlands – MilkGenomics (Wageningen University, CRV): MIR-profiles of 2000 cows
- Italy (Parco Tecnologico Padano – PTP (Alessandra Stella / John Williams)): huge number of cows with GC and progesterone
- Canada (Filippo Miglior): large project will start with collection of MIR and Fatty acids
- OptiMIR (through Nicolas Gengler): new EU-project
- …

Most interest is in combining data on Dry matter intake, including DMI-related traits like energy balance and predicted methane emissions, and on MIR-profiles. A lot of effort is already put on fatty acids in for example Optimir project and other initiatives. It is not the main priority, unless genotypes of sires with breeding values for fatty acid compositions would like to be contributed.

It is mentioned that in the end it might be good to set up an "Interbull structure" for the international collaboration and combination of data. However, for the start we need a few parties that have the energy to set it all up, with Interbull in the back of their heads. A nice goal would be to publish international DGVs for feed efficiency and dry matter intake in 1.5 years.

Brian Wickham indicated that from a cattle breeders perspective it is important that research herds (and research project on practical farms) will play a major role in collecting phenotypes for new traits that are not measured in practice. It is definitely worthwhile to put energy on combining info of all experimental herds 'in the world' and to join forces.

For this Peter Amer suggests to set up a rough protocol on the standards that the data need to meet, before it is accepted as additional info in the database. This is especially important when an organisation is willing to invest in collecting more data to contribute!

When more data is added in the database, Andrew Cromie states that it might be wise to get a list of genomic breeding values for these new traits, and use that in the conversations with the stakeholders. To show them that there is potential in it, but that more phenotypes are needed to increase reliabilities and for this money is needed!

Gerben de Jong says that this meeting was good to get a clear idea of what the project group wants, and that every partner should re-think it a bit and translate it to what is possible. Then bilateral discussions can get started with Roel (as contact person), because each case is an individual case.

It is agreed that Roel Veerkamp will take the initiative to summarise the data requirements and send this around. If other partners are interested they can contact Roel.Veerkamp@wur.nl to be included in the mailing list.