



World Congress on Genetics Applied to Livestock Production



Rotterdam | The Netherlands
3 - 8 July 2022



WCGALP 2022

PROGRAMME BOOK

www.wcgalp.com



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Welcome reception



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Welcome

On behalf of the Organising Committee, we are very delighted to welcome you in Rotterdam for the 12th World Congress on Genetics Applied to Livestock Production (WCGALP), the premier international conference for livestock genetics. We have had eleven successful congresses since the '70s; in Madrid (Spain, 1974 and 1982), Lincoln (USA, 1986), Edinburgh (UK, 1990), Guelph (Canada, 1994), Armidale (Australia, 1998), Montpellier (France, 2002), Belo Horizonte (Brazil, 2006), Leipzig (Germany, 2010), Vancouver (Canada, 2014), and Auckland (New Zealand, 2018), and we are especially proud that despite the many uncertainties, we (as a worldwide community without a formal organisation structure) managed to put together such an interesting program and meet again in Rotterdam.

The conference will cover all aspects of genetics applied to livestock production in 65 sessions. Next to the exciting plenary speakers and the recurrent technical and species orientated sessions, there are sessions focusing on specific challenges for animal breeding, like large-scale phenotyping of individual animals, use of whole genome sequence data and improving genomic prediction, and sessions on the contribution that genetics can make to societal challenges, like animal welfare, climate change, biodiversity or control of infectious diseases.

It is the first time that WCGALP will be fully hybrid with 20% of the registrations participating online throughout the world. This will create challenges for the organisation, but certainly opened up the participation for people that were otherwise not being able to attend. The other novel aspect of this WCGALP is that we introduce pitches instead of the classical poster session. With the pitches we aim to give every contribution the attention it deserves in a hybrid setting, and therefore every session starts with short pitches on the podium.

Finally, we thank the numerous sponsors, committees, and chairs that are so tremendously important for organising this conference. Without their solidarity and financial support, this event would not have been possible. On behalf of the Organising Committee, we wish you all a good stay in Rotterdam.

Yvette de Haas and Roel Veerkamp

Committees

(<https://wcgalp.com/committees>)

Local organising committee

Roel Veerkamp (Wageningen University & Research, chair)
Yvette de Haas (Wageningen University & Research, chair)
Johan van Arendonk (Hendrix Genetics)
Erik Mullaart (CRV)
Peter Loenen (Topigs Norsvin)
Randy Borg (Cobb-Vantress)
Mike Jacobs (Wageningen Academic Publishers)
Congress by design

Sponsor committee

Yvette de Haas (Wageningen University & Research, chair)
Kor Oldenbroek (Wageningen University & Research)
Peter Loenen (Topigs Norsvin)
Marco Bink (Hendrix Genetics)
Randy Borg (Cobb-Vantress)

Scientific advisory committee

Roel Veerkamp (chair)
Johan van Arendonk

Wageningen University & Research

Martien Groenen
Henk Bovenhuis
Mario Calus
Hans Komen
Han Mulder

ESR members

Biaty Raymond
Michael Aldridge

International with a Dutch touch

Julius van der Werf (Australia)
Peter Visscher (Australia)
Michael George (Belgium)
Theo Meeuwissen (Norway)
Dirk Jan de Koning (Sweden)
Jack Dekkers (United States)

International

Jennie Pryce (Australia)
Simone Guimares (Brazil)
Christine Baes (Canada)
Tadelle Dessie (Ethiopia)
Andres Legarra (France)
Henner Simianer (Germany)
Alessandro Bagnato (Italy)
Donagh Berry (Ireland)
Felipe de J. Ruiz (Mexico)
Beatriz Villanueva (Spain)
Uthairat Na-Nakorn (Thailand)
Andrea Wilson (United Kingdom)
Eileen Wall (United Kingdom)
Alison van Eenennaam (United States)

Communication team

Michael Aldridge (Wageningen University & Research)
Pascal Duenk (Wageningen University & Research)
Harmen Doekes (Wageningen University & Research)

Advisory board

Martin Scholten (Wageningen University & Research, chair)
Angus Haslett (on behalf of Breed4Food partners)
Gijs Scholman (Lely Holding)
Pierre Berntsen (ABN-AMRO bank)
Erling Strandberg (on behalf of EAAP Genetics commission)
Susanne Hermes (president WCGALP permanent committee)
Filippo Miglior (secretariat WCGALP permanent committee)
Brian Wickham (organiser WCGALP2018)

Permanent WCGALP committee

Susanne Hermes (President, Australia)
Filippo Miglior (Secretary, Canada)
Maria Wurzing (Austria)
Fernando Cardoso (Brazil)
Lusheng Huang (China)
Hélène Gilbert (France)
Jörn Bennewitz (Germany)
Gopal Gowane (India)
Donagh Berry (Ireland)
Alessandra Stella (Italy)
Yutaka Masuda (Japan)
Alexander Kahi (Kenya)
Richard Spelman (New Zealand)
Björg Heringstad (Norway)
Ewa Sell-Kubiak (Poland)
Frikkie Naser (South Africa)
Luis Varona (Spain)
Mario Calus (The Netherlands)
Georgios Banos (United Kingdom)
Heather Huson (United States)
Ron Lewis (United States)

Conference venue

Host City

Rotterdam is a young and dynamic city with an energetic and creative mindset. A city with world class architecture, an open and cosmopolitan atmosphere and a hip & happening art, festival and culinary scene. There's always something to see or do in Rotterdam, making it the perfect city to organize a top class congress.

Venue

De Doelen International Conference Center Rotterdam
Schouwburgplein 50
Rotterdam, The Netherlands

Accessibility

The conference is held in De Doelen, a city-center, state-of-the-art venue for conferences and concerts. De Doelen, Rotterdam, is located within 2 minutes walking distance from Rotterdam Central Station. De Doelen is not only the cultural focal point of Rotterdam, but it also features state of the art convention facilities and services, with the needs of the organiser and the delegate in mind.

Highlights of De Doelen

The exceptional appeal of De Doelen lies in its dual function as concert hall and conference centre. This is highlighted by the design of the building: remarkable 1960's functionalist architecture of the original concert hall beautifully contrasting with the dynamic and modern design of the conference centre.



Floor plans

Ground Floor

- Main entrance hall
- Registration Desk
- Cloakroom
- Rotterdam Tours desk (Excursions)
- Parallel session room (Van Cappellen Zaal)
- Speaker Service Centre

First Floor

- Plenary room (Grote Zaal)
- Parallel session rooms (Jurriaanse Zaal, Eduard Flipse Zaal)
- Exhibition (Grote Zaal Foyer)
- Breed4Food Café (Arcadis Zaal/Feestzaal) – Cobb, CRV, Hendrix Genetics, Topigs Norsvin)

Second Floor

- Smaller meetings rooms (Zeelenberg Zaal)
- Parallel session rooms (Jurriaanse Zaal, Eduard Flipse Zaal)

Third Floor

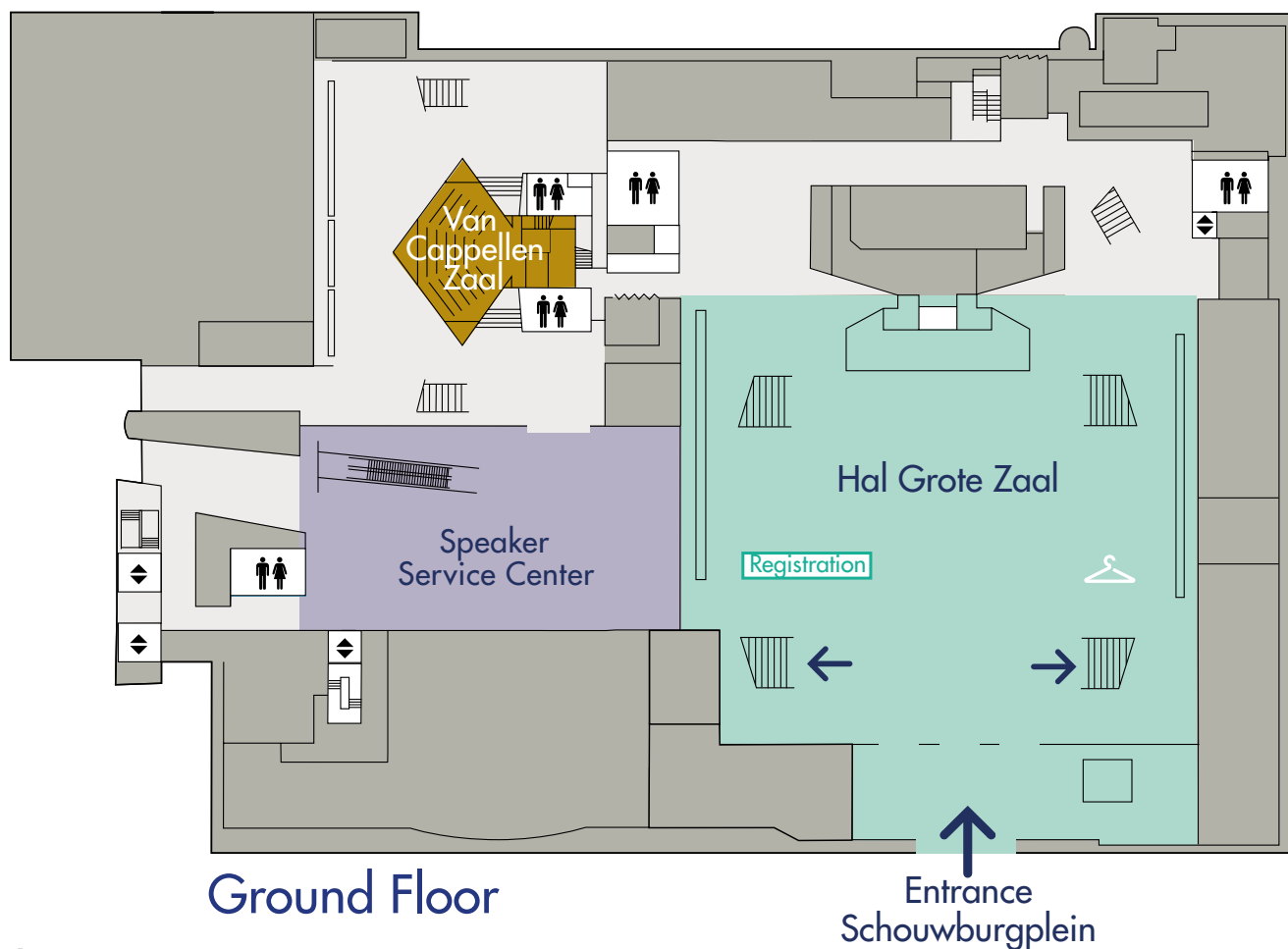
- Parallel session room (Willem Burger Zaal)
- Smaller meeting rooms (Hudig Zaal, Schadee Zaal, Van Beuningen Zaal)

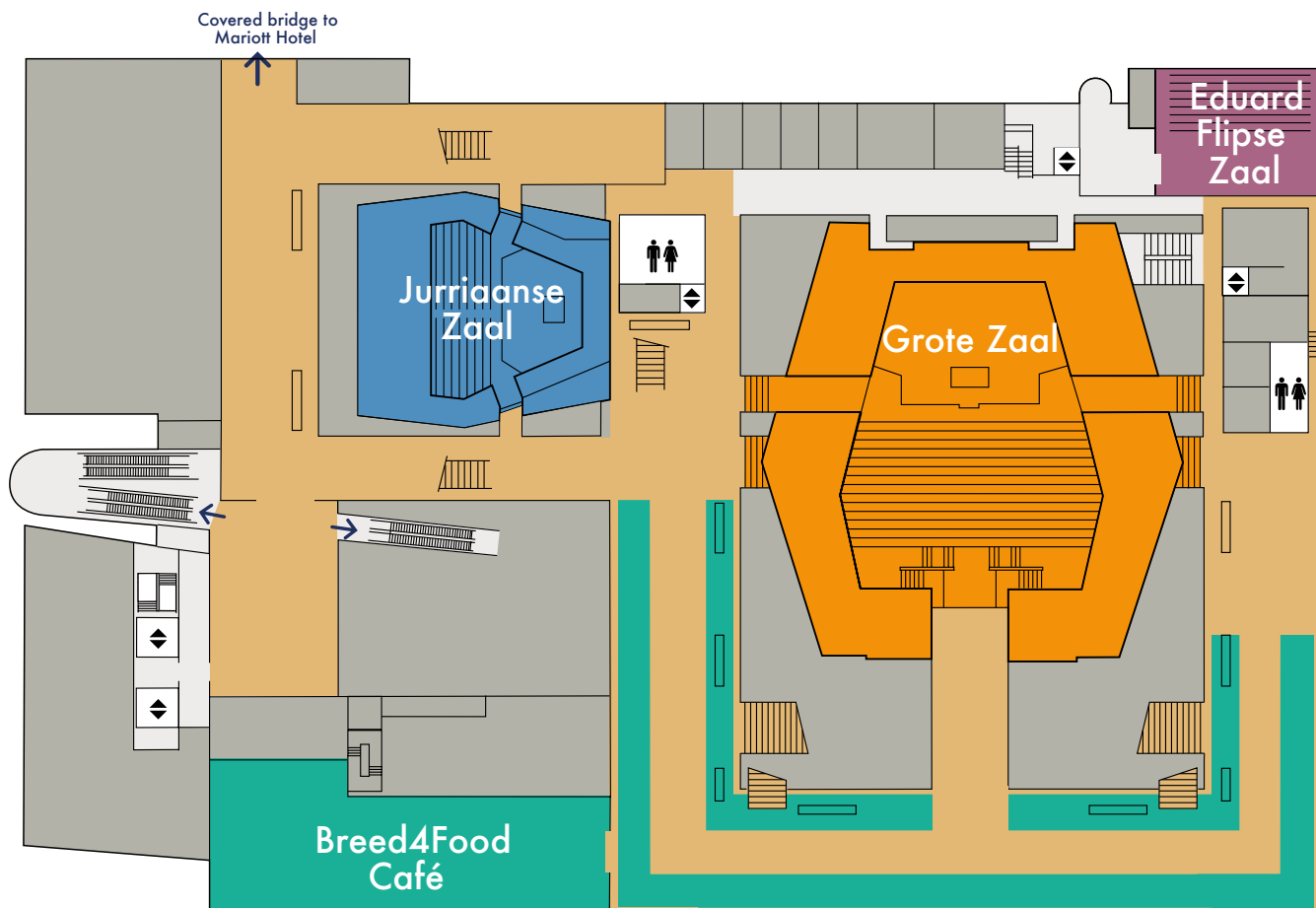
Fourth Floor

- Lunch Symposium room (Van Weelde Zaal)
- Smaller meetings rooms (Van der Vorm Zaal, Plate Zaal, Van Rijkevorsel Zaal, Ruys Zaal)

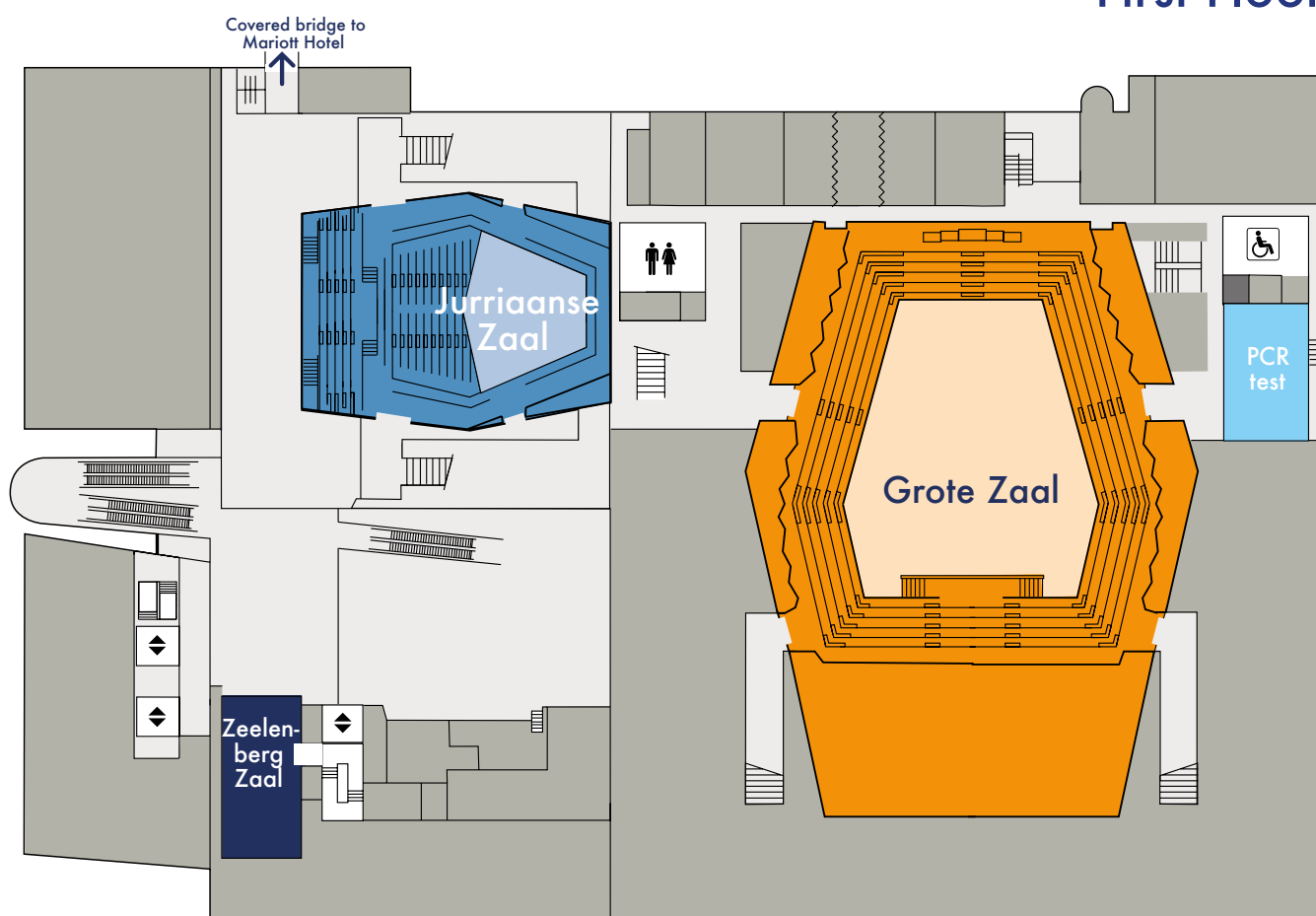
Plenary and Session Rooms:

	Grote Zaal
	Van Cappellen Zaal
	Eduard Flipse Zaal
	Jurriaanse Zaal
	Willem Burger Zaal
	Entrance/registration/cloakroom
	Exhibition
	Lunch Symposia
	Speaker Service Centre
	Meeting rooms
	Catering

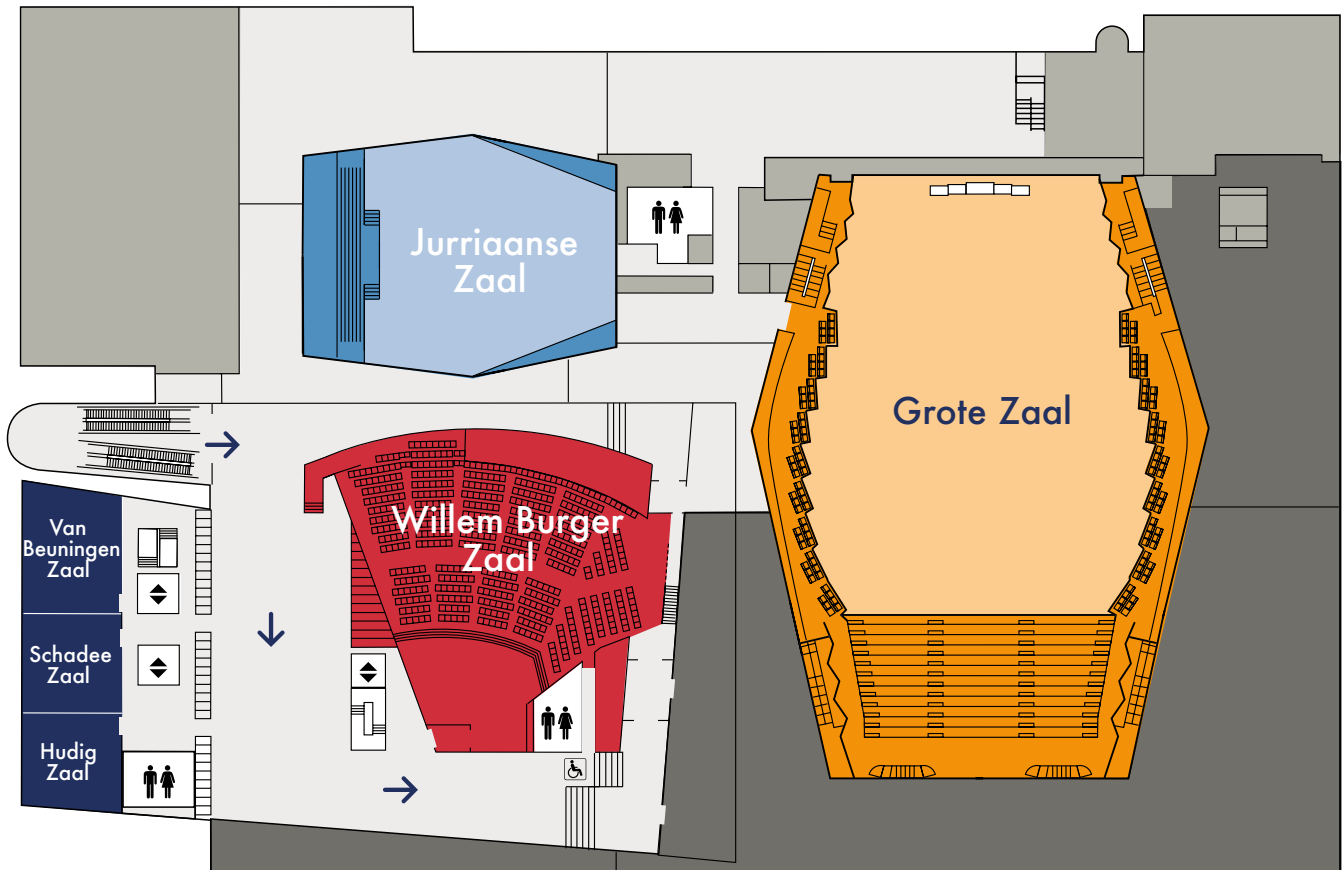




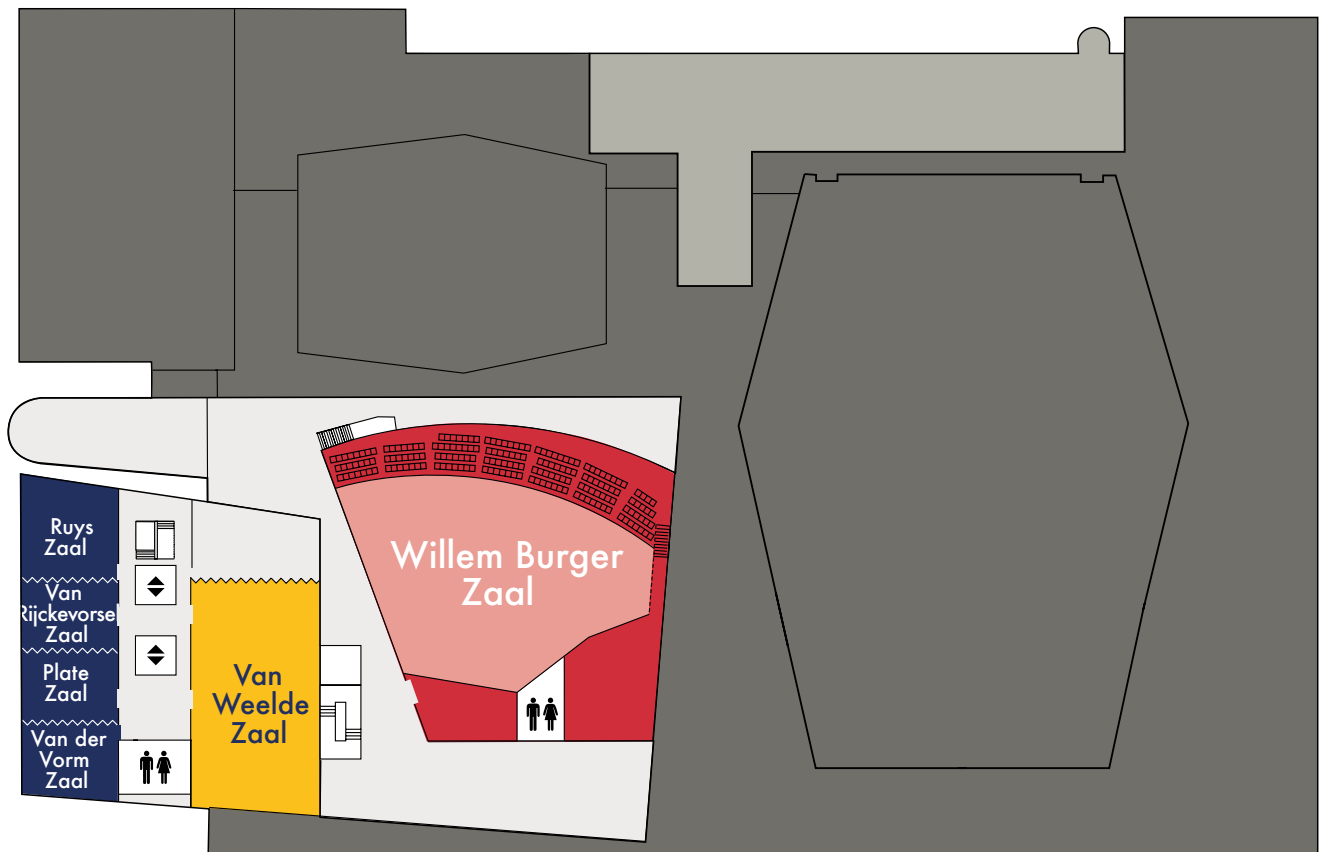
First Floor



Second Floor



Third Floor



Fourth Floor

Information for participants

Conference website: www.wcgalp.com
Conference e-mail: wcgalp@congressbydesign.com
Local organizer: Wageningen University & Research – www.wur.nl

Venue

De Doelen International Conference Center Rotterdam
Schouwburgplein 50
Rotterdam

Opening hours for participants

Official entrance of conference for participants on:

Sunday 3 July	15:00 – 21:00
Monday 4 July	07:30 – 18:30
Tuesday 5 July	07:30 – 20:00
Wednesday 6 July	07:30 – 14:00
Thursday 7 July	07:30 – 18:30
Friday 8 July	07:30 – 18:30

Registration desk

The registration desk is open for participants on the following days and times:

Sunday 3 July	15:00 – 21:00
Monday 4 July	07:30 – 18:30
Tuesday 5 July	07:30 – 18:30
Wednesday 6 July	07:30 – 14:00
Thursday 7 July	07:30 – 18:30
Friday 8 July	07:30 – 18:30

Badges and identification

Upon registration, each participant will receive a name badge to be worn at all times during the conference and social events. Lost name badges can be replaced for a fee of € 25.

Wifi

Strong, reliable Wifi is available at the venue.

Name: WCGALP 2022

Password: Rotterdam

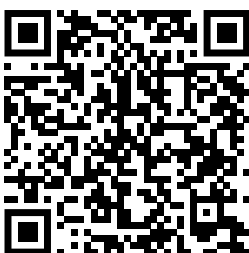
Congress App

The WCGALP2022 will be hosted in-person in Rotterdam, The Netherlands, as well as online. In order to engage with the online participants, we encourage to use of the WCGALP App. Through this app you will not only be able to find information on the programme and sponsors, you will also be able to connect with online participants. The App is available on Google Play and in the App Store.

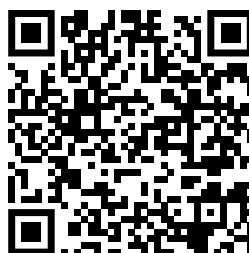
NB: When you download the App, you will be directed to the generic Events Air App. Please enter the Event code to be enter the customized WCGALP App.

Event Code: WCGALP2022

iOS App



Android App



If you do not have a QR reader, search for the name of the App: **The Event App by EventsAir**

Speaker Service Centre

All speakers are required to visit the Speaker Service Centre to check their (uploaded) slides prior to their session.

If you have not already uploaded your slides, it is highly recommended to still do so. Please follow the upload instructions you received by email.

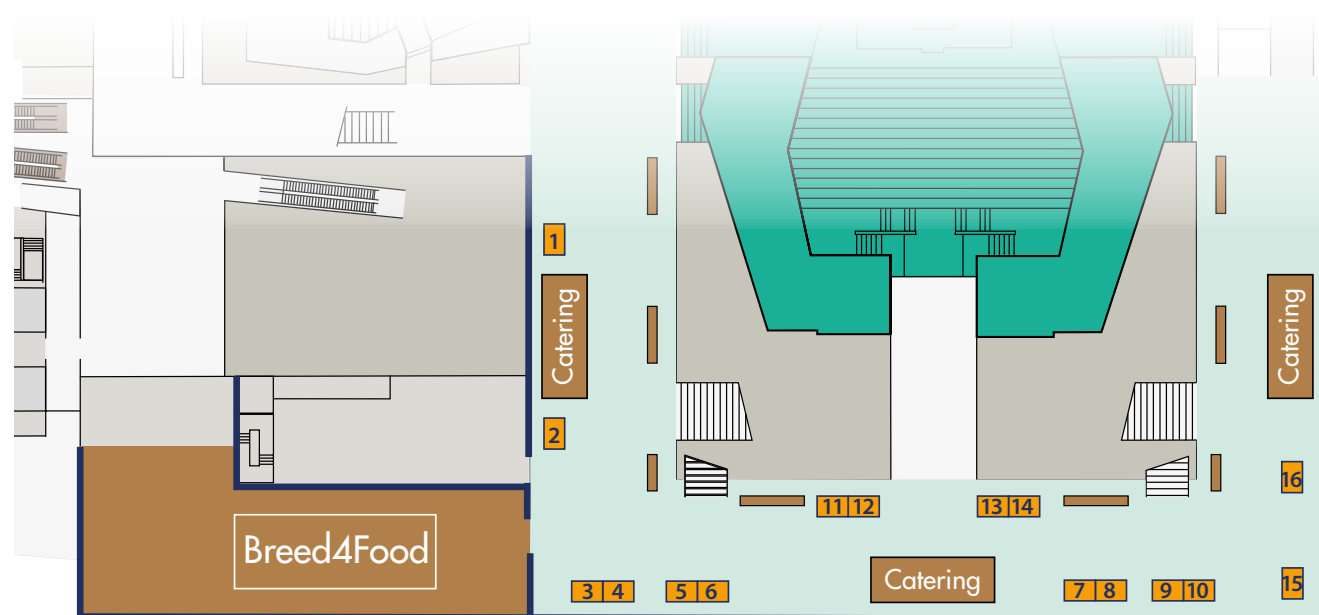
For those who have uploaded their slides, please visit the Speaker Service Centre at least 1 hour before the start of your session to check your slides.

For those who did not upload their slides, please visit the Speaker Service Centre at least 2 hours before the start of your session.

Opening hours of the Speaker Service Centre

Sunday 3 July	15:00 – 21:00
Monday 4 July	07:30 – 18:30
Tuesday 5 July	07:30 – 18:30
Wednesday 6 July	07:30 – 14:00
Thursday 7 July	07:30 – 18:30
Friday 8 July	07:30 – 16:00

Exhibition



Exhibition hours:

Sunday July 3	18:00 – 21:00
Monday July 4	08:00 – 18:00
Tuesday July 5	08:00 – 18:00
Wednesday July 6	08:00 – 13:30
Thursday, July 7	08:00 – 18:00
Friday July 8	08:00 – 18:00

Booth no.	Exhibitor name
1	Hokofarm Group
2	Wageningen Academic Publishers / OMIA
3	3 CR Bioscience Ltd
4	Gencove
5	NEOGEN
6	NEOGEN
7	Aviagen
8	Lohmann / Hy-Line
9	LABOGENA DNA

Booth no.	Exhibitor name
10	Fluidigm B.V.
11	LGC Biosearch Technologies
12	Irish Cattle Breeding Federation (ICBF)
13	Zoetis
14	Illumina Inc.
15	Caisley International GmbH
16	Eurofins Genomics
Breed4Food (Feestzaal)	Cobb, CRV, Hendrix Genetics, Topigs Norsvin

Covid information

Although in the Netherlands all Covid-related restrictions for incoming travellers are lifted, we are fully aware that we organise a World congress. Your health is our utmost concern.

Using the red, yellow or green sticker on your name badge, you can indicate the contact distance where you are comfortable. Feel free to wear facemasks.

For the latest information on COVID you should follow the conference information., but our general advice is:

- to be fully vaccinated;
- or recovered from a covid infection in the past 180 days;
- or have recently been tested using PCR.

Furthermore, we advise preventive self-testing during the week and therefore we provide delegates with two tests in their conference bag for screening. Additional tests are available at the front desk.

When you have Covid symptoms it is strongly advised you test before taking part in the conference activities. If you test positive, self-isolation is mandatory (<https://www.rivm.nl/en/coronavirus-covid-19/quarantine-and-isolation>). Also, we ask you to inform the conference organisation, so we can support you and can take precautionary measures when needed.

The most recent travel advice is on www.netherlandsworldwide.nl or www.wijsopreis.nl

For those who require a negative PCR or Antigen test for traveling home, we have arranged testing inside the venue on Thursday 7 July. Please come to the registration desk in advance to add your name to the list and to learn more. PCR tests should be taken in the morning. The cost is EUR 65 for a PCR test and EUR 45 for an Antigen test. Payment can be made in the testing room (Monchy, 2nd Floor).

Food and beverages

Coffee/tea breaks and lunches are served from Monday to Friday on the First Floor. For detailed menus, come by the Registration Desk.

Dietary restrictions indicated by you during online registration have been communicated to the caterer. For questions about specific ingredients, and special diets, please ask the catering staff.

Car-Parking

There are several secure car parks in the direct vicinity of the venue. For Parking Schouwburgplein 1 and 2. De Doelen sells tickets for a reduced price.

Time zone

The summer time zone in The Netherlands is GMT + 2 hours.

Electricity

Electric power is supplied at 220 volts AC (50 Hz). If you are bringing electrical or electronic devices, be sure to bring a two-pin continental adapter.

The power supply within the venue is as follows:

Single Phase: 220-240 V, 50 Hz

Every shell scheme construction is provided with power socket of 1KWatt. Please ensure you order a sufficient number of sockets to prevent overloading.

In the Netherlands, the power sockets used are of type C / F: Type F: This socket also works with plug C and E Type C: This socket also works with plug E and F.

Excursions

Day: Wednesday 6 July, 13:30

Visit the Registration desk for last-minute tickets

Fee: EUR 30

For detailed programme questions, please visit the Rotterdam Tours desk in the Main entrance.

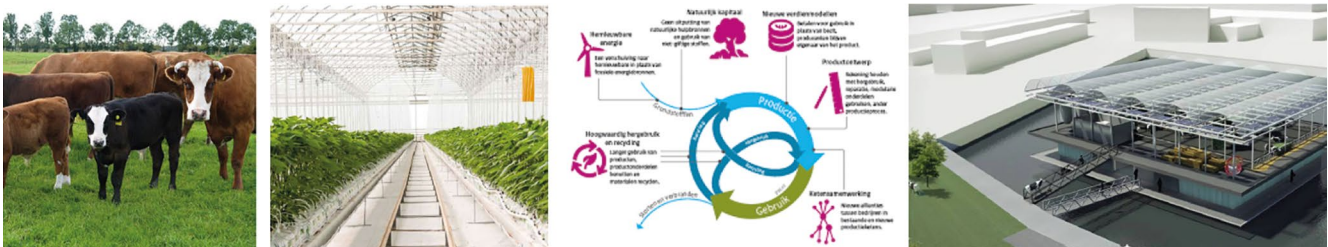
Excursion 1: Windmills Kinderdijk – World UNESCO Heritage Site

Hop on the Waterbus, a public ferry cruising the Maas River which will bring you right to Kinderdijk: the most famous windmills in the world and a UNESCO World Heritage site. Watch an introduction movie on the history of Kinderdijk and the Dutch expertise in water management, take a boat ride with miller-guide along the mills, visit a (working) mill and try on wooden shoes.



Excursion 2: Floating Farm

Floating Farm is a well-known feature as a stand-alone showcase of bringing awareness to food, its footprint and supply chains. It is located in the Maas River in the west side of Rotterdam's city centre. The authentic theme of Circularity in the region is related to the story of the double-purpose cow called Blaarkop. Here near Rotterdam, the cows are fed with a waste product of local Jenever production. The manure turned out to be a good match for growing vegetables in the greenhouses, etc. This historically imbedded and proven circularity is a profoundly inspiring topic. An expert on the Blaarkop / Circularity story will accompany you at the Floating Farm and provide you with some very relevant content within this professional sector.



Excursion 3: Factory visit Lely: Premium robotics for the future

Lely is one of the leading international robot developers. The Lely Campus, which houses the factory and HQ of Lely, is located just of Rotterdam in a town called Maassluis. Lely directs all its efforts towards creating a sustainable, profitable, and enjoyable future in farming. Focusing their work mainly on the cow, the company develops premium robotics and data systems that increase animal welfare, flexibility and the production on the dairy farm. Lely invites you for a tour around their production facility and to share your opinion, as they would like to conclude the visit with a lively discussion about current topics in the dairy sector.



Excursion 4: World Port Rotterdam

Climb on board and visit the spectacular seaport of Rotterdam. Experience a special cruise through one of the largest harbours in the world amid the hustle and bustle of various inland and sea-going vessels. The city's impressive skyline with imposing buildings will glide past, followed by unique views of wharfs, docks and ultra-modern trans-shipment operations involving thousands of containers. The tour finishes by sailing past the ss Rotterdam, the former flagship of the Holland America Line. A guided walking tour through city centre will get you to the quay and back.



Excursion 5: Rotterdam city of Architecture

Visit all the city's famous buildings in a single, compact tour. A guide will accompany you and take you to beautiful architectural gems in Rotterdam. You will hear the story of the built city from 13:00 until the present. You will visit the latest world-famous Depot, passing iconic public art. On the way to the Markthal, you will see historical City Hall, and we will pass a small innovative city park in front of the church of St Lawrence. In the Markthal, your guide will tell you all about the amazing design and colourful ceiling. This tour is packed with architectural goodies and a 'meet & taste' at one of the entrepreneurs in the Markthal, next to the famous yellow Cube Houses at Old Harbour. A super complete tour.



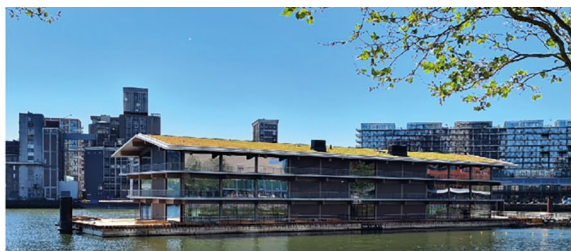
Excursion 6: Picturesque Delfshaven

Delfshaven is the Amsterdam of Rotterdam, a special heritage area with old Dutch facades lining the canal. Delfshaven was also the departure point of the Pilgrim fathers. From here, they set off for the new world on the other side of the ocean. Your guide will take you to Delfshaven by tram; and walk and talk you through this special neighbourhood with its layered stories, from its historical wealth to today's multicultural diversity. Discover the typical Dutch windmill and the various historic buildings that are now home to famous beer houses – a taste is included in the tour.



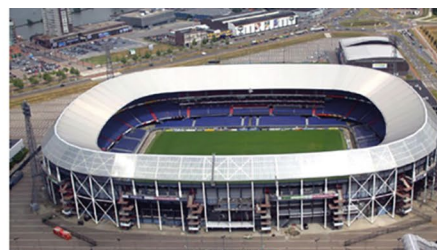
Excursion 7: Floating Office & Rotterdam Confiture

In the Rijnhaven, a harbour in the city center, a small number of tiny houses are floating. A keen and neat design of light materials. A year before, in the same Rijnhaven the Floating Office was opened. Discover these innovative and environmentally resilient concepts from the quays of the metropolitan Wilhelminapier. Afterwards, the guide will take you a little further up in multicultural Afrikaanderwijk to stop at Rotterdamsche Confiuur. Here you will hear the engaging story of this social resilience enterprise and have a bite or two to taste. A truly inspiring excursion.



Excursion 8: WCGALP Soccer

The WCGALP tradition! We're afraid we won't be able to arrange for you to play in the famous 'de Kuip', the home of Feyenoord. But we for sure can organize your traditional soccer tournament on fields at a great spot, either within Rotterdam's spectacular city sights or amidst a green park. What a great way to combine sporting and networking.



Social events

Opening Plenary and Welcome Reception

Opening Plenary: Sunday 3 July, 18:00 – 18:30, Grote Zaal, De Doelen

Welcome Reception: Sunday 3 July, 18:30 – 20:30, First Floor, Exhibition area

Dinner & Party: Blijdorp Zoo

Wednesday 6 July

Doors open at 18:30

Dinner and entertainment from 19:00 – 22:30.

Visit the Registration desk for last-minute tickets

Fee: EUR 40

This dinner & party at Blijdorp Zoo is meant to be an informal get-together: while visiting the zoo you can sample several dishes and drinks. At some of the animal locations, further information about the role of animal breeding will be given.



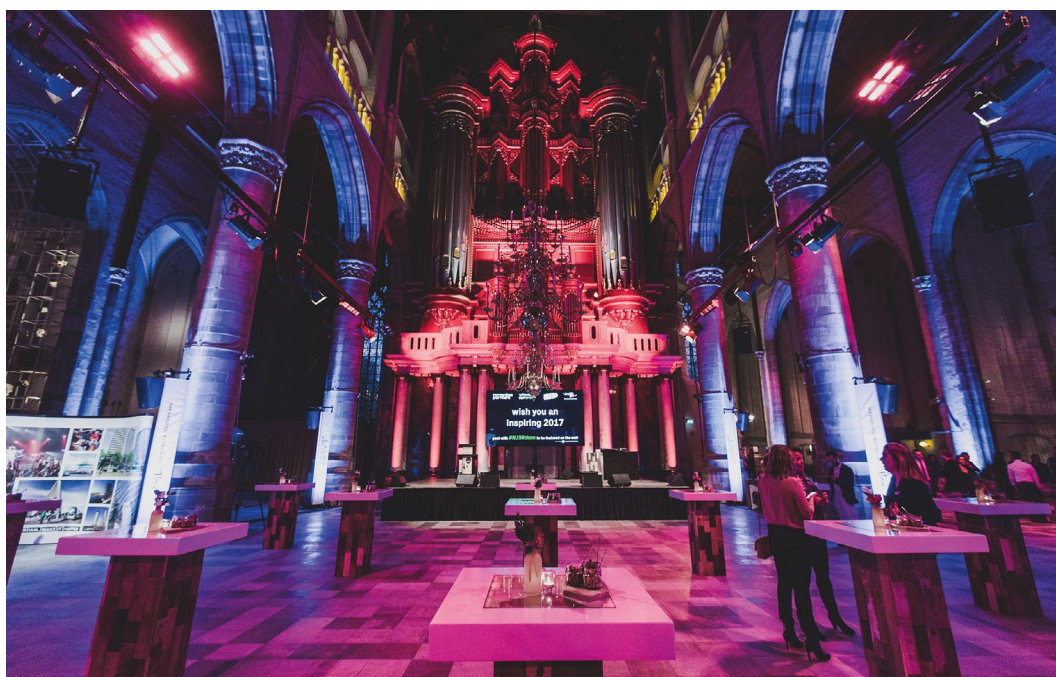
Farewell Dinner & Party: Laurenskerk

Friday 8 July, 19:30 – 01:00

Visit the Registration desk for last-minute tickets

Fee: EUR 120

The Laurenskerk is the perfect setting for our Farewell Dinner & Party. This church provides a very charming ambience. You will be welcomed by an aperitif, and after a varied menu is served, the DJs will start to play the music and invite people to come to the dance floor, or stay near the bar if that is preferred.



General programme

		Grote Zaal		Willem Burger Zaal
Mon 04 July 22 08:30 – 09:30	1	Plenary 1		
		Break		
Mon 04 July 22 10:00 – 12:00	2	Challenges – Improving genomic prediction (1)	3	Society – Contributions animal breeding to animal welfare
Mon 04 July 22 12:00 – 13:30		Lunch		
Mon 04 July 22 13:30 – 15:30	8	Challenges – Improving genomic prediction (2)	9	Challenges – Resource allocation and genetics of feed intake and efficiency (1)
		Break		
Mon 04 July 22 16:00 – 18:00	13	Methods and Tools: Genomic prediction (1)	14	Challenges – Resource allocation and genetics of feed intake and efficiency (2)
Tue 05 July 22 08:30 – 09:30	18	Plenary 2		
		Break		
Tue 05 July 22 10:00 – 12:00	19	Methods and Tools: Genomic prediction (2)	23	Caprine/Ovine (1)
Tue 05 July 22 12:00 – 13:30		Lunch		
Tue 05 July 22 13:30 – 15:30	25	Methods and Tools: Genomic prediction (3)	29	Caprine/Ovine (2)
		Break		
Tue 05 July 22 16:00 – 18:00	30	Methods and Tools: Software and Computing Strategies (1)	34	Caprine/Ovine (3)
Wed 06 July 22 08:30 – 09:30	35	Plenary 3: Discussion delivering genetic progress around the world		
		Break		
Wed 06 July 22 10:00 – 12:00	36	Methods and Tools: Software and Computing Strategies (2)	40	Bovine Beef (1)
Wed 06 July 22 12:00 – 13:30		Lunch		
		Excursions		
Thu 07 July 22 08:30 – 09:30	42	Plenary 4		
		Break		
Thu 07 July 22 10:00 – 12:00	44	Challenges – Genetic control of infectious disease transmission and impact (1)	46	Bovine Dairy - Genome informed breeding
Thu 07 July 22 12:00 – 13:30		Lunch		
Thu 07 July 22 13:30 – 15:30	50	Challenges – Genetic control of infectious disease transmission and impact (2)	52	Bovine Dairy - Genetic evaluation methods
		Break		
Thu 07 July 22 16:00 – 18:00	55	Developing countries	57	Bovine Dairy - Phenotype is king
Fri 08 July 22 08:30 – 09:30	59	Plenary 5		
		Break		
Fri 08 July 22 10:00 – 12:00	60	Statistical genetics: Machine learning, deep learning and artificial intelligence	63	Society – Genetic solutions to achieve net zero carbon emission in livestock systems
Fri 08 July 22 12:00 – 13:30		Lunch		
Fri 08 July 22 13:30 – 15:30	66	Statistical genetics: GWAS (1)	69	Novel traits: Environment and greenhouse gas (1)
		Break		
Fri 08 July 22 16:00 – 18:00	71	Statistical genetics: GWAS (2)	74	Novel traits: Environment and greenhouse gas (2)

		Jurriaanse Zaal		Van Cappellen Zaal		Eduard Flipse Zaal		Van Weelde Zaal
Mon 04 July 22 08:30 – 09:30								
Mon 04 July 22 10:00 – 12:00	4	Novel phenotyping tools: Sensor devices	6	Companion animals	5	Challenges – Use of multi-omics data		
Mon 04 July 22 12:00 – 13:30							7	Lunch seminar: Fluidigm
Mon 04 July 22 13:30 – 15:30	10	Novel phenotyping tools: Machine learning and computer vision (1)	12	Aquaculture (1)	11	Functional Annotation of Genomes: Causal variants & gene discovery (1)		
Mon 04 July 22 16:00 – 18:00	15	Novel phenotyping tools: Machine learning and computer vision (2)	17	Aquaculture (2)	16	Functional Annotation of Genomes: Causal variants & gene discovery (2)		
Tue 05 July 22 08:30 – 09:30								
Tue 05 July 22 10:00 – 12:00	20	Challenges – Understanding and utilizing genetic diversity (1)	22	Free communications	21	Society and gene editing and reproduction		
Tue 05 July 22 12:00 – 13:30							24	Lunch seminar: Genus
Tue 05 July 22 13:30 – 15:30	26	Challenges – Understanding and utilizing genetic diversity (2)	27	Novel traits: Health and well-being (1)	28	Epigenetics, structural variants and exploiting transcriptome (1)		
Tue 05 July 22 16:00 – 18:00	31	Young scientist career development (with drinks EFFAB/FABRE-TP till 19:00)	32	Novel traits: Health and well-being (2)	33	Epigenetics, structural variants and exploiting transcriptome (2)		
Wed 06 July 22 08:30 – 09:30								
Wed 06 July 22 10:00 – 12:00	38	Challenges – Delivering genetic progress in systems around the world	47	Bovine Beef (2)	37	Society – Genetics in the tropics		
Wed 06 July 22 12:00 – 13:30							41	Lunch seminar: Illumina
Thu 07 July 22 08:30 – 09:30								
Thu 07 July 22 10:00 – 12:00	43	Challenges – Across species and breed genomics genetics	53	Bees and other insects (1)	45	Design of breeding programs		
Thu 07 July 22 12:00 – 13:30							48	Lunch seminar: Bayer
Thu 07 July 22 13:30 – 15:30	49	Challenges – Use of whole genome sequence information (1)	58	Bees and other insects (2)	51	Breeding goals and selection strategies		
Thu 07 July 22 16:00 – 18:00	54	Challenges – Use of whole genome sequence information (2)	64	Equine	56	Operational breeding programs		
Fri 08 July 22 08:30 – 09:30								
Fri 08 July 22 10:00 – 12:00	61	Genetic diversity and inbreeding (1)	68	Porcine (1)	62	Methods and Tools: Breeding goals		
Fri 08 July 22 12:00 – 13:30							65	Lunch seminar: BIOSEARCH Technologies
Fri 08 July 22 13:30 – 15:30	67	Genetic diversity and inbreeding (2)	73	Porcine (2)	70	Avian (1)		
Fri 08 July 22 16:00 – 18:00	72	Genetic diversity and inbreeding: Genebanking	39	Education	75	Avian (2)		

Scientific programme

Monday 30 August

Session 01.

Plenary (1)

Room: Grote Zaal

Chair: Roel Veerkamp

- 08:30 [Measure, predict and act; a paradigm of genetics applied to livestock production now and into the future](#)
Calus, M.P.L.; Berry, D.P.; Pryce, J.E.

Session 02.

Challenges – Improving genomic prediction (1)

Room: Grote Zaal

Chair: Mario Calus, Andres Legarra, Gustavo de los Campos

- 10:00 [Accuracy of prediction for a genomic evaluation in rotational crossbreeding scheme: Montbéliarde x Holstein x Red Danish](#)
Croiseau, P.; Saintilan, R.; Baur, A.; Croué, I.; Ducrocq, V.; Thomasen, J.R.; Karaman, E.; Boichard, D.; Leclerc, H.; Cuyabano, B.C.D.
- 10:02 [Genomic evaluation for two-way crossbred performance in cattle](#)
Mei, Q.; Liu, H.; Xiang, T.; Christensen, O.
- 10:04 [Improving accuracy of genomic prediction in distant populations by collecting sequence data over generations](#)
Nawaz, M.Y.; Gondro, C.
- 10:06 [Comparison of genomic prediction methods for residual feed intake in broilers](#)
He, Z.; Li, S.; Li, W.; Ding, J.; Zheng, M.; Li, Q.; Fahey, A.G.; Wen, J.; Liu, R.; Zhao, G.
- 10:08 [Impact of foreign phenotype data on single-step genomic evaluation of test-day protein yields for German Holsteins](#)
Alkhoder, H.; Liu, Z.; Segelke, D.; Reents, R.
- 10:10 Discussion
- 10:15 [Extend mixed models to multi-layer neural networks for genomic prediction including intermediate omics data](#)
Zhao, T.; Zeng, J.; Cheng, H.
- 10:30 [The holobiont 'predictome' of immunocompetence in pigs](#)
Calle-García, J.; Ramayo-Caldas, Y.; Zingaretti, L.M.; Quintanilla, R.; Ballester, M.; Pérez-Enciso, M.
- 10:45 [The long and short of Nanopore genomic prediction: the effect of read length on prediction accuracy](#)
Lamb, H.; Nguyen, L.; Randhawa, I.; Hayes, B.; Ross, E.
- 11:00 [Accuracy of genomic prediction of dry matter intake in Dutch Holsteins using sequence variants from meta-analyses](#)
Gredler-Grandl, B.; Raymond, B.; Chitneedi, P.K.; Cai, Z.; Panzanilla-Pech, C.I.V.; Fischer, D.; Bolormaa, S.; Chud, T.S.; Wang, Y.; Li, C.; Villanueva, B.; Fernandez, A.; Kuehn, C.; Lidauer, M.H.; Pryce, J.E.; Plastow, G.; Baes, C.F.; Charfeddine, N.; Veerkamp, R.F.; Bouwman, A.C.
- 11:15 [Genomic prediction of bull fertility in Italian Brown Swiss cattle](#)
Pacheco, H.A.; Battagin, M.; Rossoni, A.; Cecchinato, A.; Peñagaricano, F.
- 11:30 [On the use of SNPs of large effect to improve prediction accuracy in pigs](#)
Lopes, M.S.; Derks, M.F.L.; Van Son, M.; Gjuvsland, A.B.; Sevilano, C.A.; Grindflek, E.; Knol, E.F.

- 11:45 [Including environmental variables in genomic models for carcass traits in Hanwoo beef cattle](#)
Makanjuola, B.O.; Rovere, G.; Cuyabano, B.C.D.; Lee, S.H.; Gondro, C.

Session 03.

Society – Contributions animal breeding to animal welfare

Room: Willem Burger Zaal

Chair: Bas Rodenburg, Susanne Hermes, Christine Nicol

- 10:00 [Genetic analysis of number of functional teats, piglet survival, and piglet weight in organic pigs](#)
Zaalberg, R.M.; Chu, T.T.; Jensen, J.; Villumsen, T.M.
- 10:02 [Genetic analysis of feeding behaviour and tail lesions](#)
Grindflek, E.; Nordbø, Ø.; Olsen, D.; Enger, E.G.; Martinsen, K.H.
- 10:04 [Response to selection for social dominance including both direct and indirect genetic effects](#)
Tuliozi, B.; Mancin, E.; Gomez Proto, G.; Mantovani, R.; Sartori, C.
- 10:06 [Empowerment of the Italian small ruminant sector: new traits and tools toward a sustainable management](#)
Negro, A.; Cortellari, M.; Bionda, A.; Grande, S.; Cesarani, A.; Carta, A.; Macciotta, N.; Biffani, S.; Crepaldi, P.
- 10:08 Discussion
- 10:15 [How can breeding for improved animal welfare meet societal expectations and challenges?](#)
Wallenbeck, A.
- 10:45 [Swine inflammation and necrosis syndrome \(SINS\) and its association with biting behavior after weaning](#)
Leite, N.G.; Knol, E.F.; Nuphaus, S.; Tsuruta, S.; Vogelzang, R.; Lourenco, D.
- 11:00 [Breeding for future social license for beef production](#)
Miller, S.P.; Retallick, K.J.
- 11:15 [Selection for piglet mortality and litter size in outdoor organic pig production systems](#)
Chu, T.T.; Zaalberg, R.M.; Jensen, J.; Villumsen, T.M.
- 11:30 [Heritability of daily activity over time in broilers](#)
Ellen, E.D.; Van Der Sluis, M.; De Klerk, B.; Henshall, J.; De Haas, Y.; Rodenburg, T.B.; Bijma, P.

Session 04.

Novel phenotyping tools: Sensor devices

Room: Jurriaanse Zaal

Chair: Ines Adriaens, Christine Baes, Sarita Guy

- 10:00 [Estimates of genetic parameters for milkability traits derived from automatic milking systems in North American Holstein](#)
Pedrosa, V.B.; Boerman, J.P.; Gloria, L.S.; Chen, S.Y.; Montes Gonzalez, M.E.; Doucette, J.S.; Brito, L.F.
- 10:02 [Classifying the likelihood of conception in dairy cow with milk mid-infrared spectra before the first insemination](#)
Lou, W.; Shi, R.; Ducro, B.; Van Der Linden, A.; Mulder, H.A.; Oosting, S.J.; Liu, L.; Wang, Y.
- 10:04 Discussion
- 10:15 [Use of tracking technology for phenotyping laying hens within cage-free housing](#)
Montalcini, C.M.; Petelle, M.B.; Gebhardt-Henrich, S.G.; Toscano, M.J.
- 10:30 [Learning behaviour of dairy cows in automated milking systems: genetic parameters and suggested candidate genes](#)
Schafberg, R.; Rosner, F.; Oelschlägel, D.; Swalve, H.H.

- 10:45 [Repeatability estimates of grazing and rumination activity of Merino sheep measured using wearable sensors](#)
Almasi, F.; Khansefid, M.; Nguyen, H.; Desai, A.; Pryce, J.E.; Stear, M.
- 11:00 [Deep data recording for developing resilience traits in Swiss cattle populations: a proof of concept and an application](#)
Bapst, B.; Von Rohr, P.; Seefried, F.R.
- 11:15 [Test-day genetic evaluations: a tool to measure herd resilience through monthly milk records](#)
Mattalia, S.; Rocland, M.; Aguerre, S.; Poppe, M.
- 11:30 [Genomic selection of postpartum anoestrus recorded with accelerometer collars to improve beef cattle fertility](#)
Fontanillas, E.; Prieur, V.; Michenet, A.; Auvray, G.; Mante, J.
- 11:45 [Developing precision livestock farming in practice: using sensor time series data for breeding decision support systems](#)
Statham, J.M.E.; Burton, K.L.; Adriaens, I.; Lora, I.; Cozzi, G.; De Haas, Y.; Kamphuis, C.; Vedder, L.; Loke, B.; Friggens, N.C.

Session 05.

Challenges – Use of multi-omics data

Room: Eduard Flipse Zaal

Chair: Martien Groenen, Angela Canovas, Christian Reimer, Elisabetta Giuffra

- 10:00 [Using allele-specific expression to uncover cis-regulation in bovine muscle](#)
Bruscadin, J.J.; Cardoso, T.F.; Diniz, W.J.S.; Afonso, J.; De Souza, M.M.; Petrini, J.; Da Silva, V.H.; Zerlotini, A.; Coutinho, L.L.; Regitano, L.C.A.
- 10:02 [Enrichment of causative variants in tissue-specific and shared ATAC-Seq peaks in cattle](#)
Yuan, C.; Tang, L.; Lopdell, T.; Oget-Ebrad, C.; Costa Monteiro Moreira, G.; Gualdron, J.L.; Cheng, Z.; Salavati, M.; Wathes, D.C.; Crowe, M.A.; Gplus E, C.; Coppieters, W.; Charlier, C.; Druet, T.; Georges, M.; Takeda, H.
- 10:04 [Preliminary investigation into the association of members of the rumen biome with production traits in Afrikaner cattle](#)
Cason, E.D.; Alom, J.; Barnard, J.; Fair, M.; Vermeulen, P.D.; Neser, F.W.C.
- 10:06 [Maternal effect on the metagenomic composition determining the intramuscular fat content in rabbits](#)
Zubiri-Gaitán, A.; Mora, M.; Casto-Rebollo, C.; Santacreu, M.A.; Blasco, A.; Hernández, P.; Ibáñez-Escriche, N.
- 10:08 [The gut microbiome profile varies among individuals of different longevity](#)
Biada, I.; Ibáñez-Escriche, N.; Blasco, A.; Santacreu, M.A.
- 10:10 [Comparing methods to summarize gut microbiota composition in estimating microbiability of host phenotypes in swine](#)
He, Y.; Maltecca, C.; Howard, J.; Huang, Y.; Gray, K.; Tiezzi, F.
- 10:12 Discussion
- 10:15 [Organoids as a research tool in animal breeding and nutrition](#)
Verschuren, L.M.G.; Schokker, D.; Verstringe, S.; Kruijt, L.; De Wit, A.A.C.; Van Der Valk, E.G.T.; Kar, S.K.; Ellen, E.D.
- 10:30 [Simulation of host-microbiome evolution throughout a divergent selection experiment](#)
Casto-Rebollo, C.; Pocrnic, I.; Gorjanc, G.; Ibáñez-Escriche, N.
- 10:45 [Rumen bacteria do not provide improved genetic evaluation of dairy traits in sheep](#)
Martinez Boggio, G.; Christensen, O.F.; Legarra, A.; Allain, C.; Meynadier, A.; Marie-Etancelin, C.
- 11:00 [Phenotypic characterization of organoids derived from pig intestine segments](#)
Blanc, F.; Mongellaz, M.; Pepke, F.; Bevilacqua, C.; Riviere, J.; Vilotte, M.; Giuffra, E.; Egidy, G.

- 11:15 [Can microbial data improve prediction of breeding values of efficiency traits in pigs fed conventional or fiber diets?](#)
Déru, V.; Tiezzi, F.; Carillier-Jacquín, C.; Blanchet, B.; Cauquil, L.; Zemb, O.; Bouquet, A.; Maltecca, C.; Gilbert, H.
- 11:30 [Investigating new technologies for on-site real-time sequencing for any animal scientist](#)
Ostrovski, H.; Savegnago, R.P.; Huang, W.; Gondro, C.
- 11:45 [Impact of the bovine reference genome \(ARS-UCD1.2\) on functional annotation at genome, transcriptome and methylome level](#)
Cánovas, A.; Fonseca, P.A.S.; McKay, S.; Medrano, J.F.

Session 06.

Companion animals

Room: Van Cappellen Zaal

Chair: Jack Windig, Erling Strandberg, Jeff Schoenebeck

- 10:00 [Diversity status and future breeding strategy for Tatra hound in Slovakia](#)
Kasarda, R.; Moravčíková, N.
- 10:02 [Genome-wide association study for ectopic ureter in three dog breeds](#)
Stella, A.; Cassani, V.; Majolino, G.; Cozzi, P.; Biffani, S.; Biscarini, F.; Minozzi, G.
- 10:04 [Linkage disequilibrium variability in the Czechoslovakian wolfdog genome as a result of long-term artificial selection](#)
Moravčíková, N.; Kasarda, R.; Vostrý, L.; Vostrá-Vydrová, H.; Vašek, J.; Čílová, D.
- 10:06 [Applications of single-molecule real-time isoform sequencing \(Iso-Seq\) for unravelling complexity of dog transcriptomes](#)
Zhang, W.; Eory, L.; Salavati, M.; Clark, E.; Smith, J.; Archibald, A.L.; Schoenebeck, J.J.
- 10:08 Discussion
- 10:15 [Genome-wide signals of positive selection identified in livestock guardian dogs](#)
Shihabi, M.; Glavaš, V.; Cubric-Curik, V.; Zorc, M.; Dovč, P.; Curik, I.
- 10:30 [Implementation of single-step GBLUP for complex behaviour traits in Labrador Retrievers used as service dogs](#)
Riser, M.M.; Leighton, E.; Russenberger, J.; Moser, C.; Fragomeni, B.
- 10:45 [Longevity and major causes of death are heritable in Irish Wolfhound](#)
Van Gemert, C.J.A.; Windig, J.J.; Berg, P.
- 11:00 [The Vaika project: a multidisciplinary study of canine aging and the genetic mechanisms influencing the aging process](#)
Huson, H.J.; Andrianova, E.L.; Fleyshman, D.I.; Brodsky, L.; Loftus, J.P.; Wakshlag, J.J.; Gudkov, A.V.
- 11:15 [Genomic diversity in selected Austrian dog populations](#)
Mészáros, G.; Mészárosová, M.; Geretschlager, A.
- 11:30 [Breed differences in the management of dog breeding](#)
Janes, M.; Lewis, T.W.; Ilška, J.J.; Gorjanc, G.; Woolliams, J.A.
- 11:45 [Inbreeding and litter size in Dutch pedigreed dogs](#)
Windig, J.J.; Margarita, M.L.; Doekes, H.P.

Session 07.

Lunch seminar: Fluidigm

Room: Van Weelde Zaal

Chair:

- 12:00 Lunchtime Satellite Symposium: Design and validation of high-throughput real-time PCR systems for detection of porcine and bovine respiratory and enteric pathogens using the BioMark platform

Session 08.

Challenges – Improving genomic prediction (2)

Room: Grote Zaal

Chair: Mario Calus, Andres Legarra, Gustavo de los Campos

- 13:30 [Considering chromosomal trait correlations improves accuracy of genomic prediction](#)
Schmidtman, C.; Segelke, D.; Bennewitz, J.; Tetens, J.; Thaller, G.
- 13:32 [Effects of truncation and false positives in selection of markers for genomic prediction](#)
Loh, Z.; Van Der Werf, J.H.J.; Clark, S.
- 13:34 [Genomic selection for breeding values under identity disequilibrium](#)
Cantet, R.J.C.; Angarita-Barajas, B.K.; Forneris, N.S.; Munilla, S.
- 13:36 [Effect of informative polymorphism on accuracy of genomic prediction and heritability](#)
Tahir, M.S.
- 13:38 Discussion
- 13:45 [Long distance associations generate erosion of genomic breeding values of candidates for selection](#)
Boichard, D.; Fritz, S.; Croiseau, P.; Ducrocq, V.; Cuyabano, B.; Tribout, T.
- 14:00 [Definition of reliabilities for models with metafounders](#)
Bermann, M.; Misztal, I.; Lourenco, D.; Aguilar, I.; Legarra, A.
- 14:15 [A new metric to assess reference populations for genomic selection in Australian beef breeds](#)
Moore, K.L.; Ferdosi, M.H.; Girard, C.G.; Walkom, S.F.; Johnston, D.J.
- 14:30 [Decreasing computing cost of categorical data analysis](#)
Hidalgo, J.; Misztal, I.; Tsuruta, S.; Bermann, M.; Garcia, A.; Retallick, K.; Lourenco, D.
- 14:45 [Within and Across breed Single Step genomic prediction for somatic cell count including foreign information](#)
Mrode, R.; Winters, M.W.; Coffey, M.
- 15:00 [Using convolutional neural networks for image-based genomic prediction in mice](#)
Perez, B.C.; Savchuk, A.; Duenk, P.; Calus, M.P.L.; Bink, M.C.A.M.
- 15:15 [Selection for robustness: exploring the value of genomic prediction, reaction norm models and phenotyping strategies](#)
Ghaderi-Zefreh, M.; Doeschl-Wilson, A.; Riggio, V.; Matika, O.; Pong-Wong, R.

Session 09. Challenges – Resource allocation and genetics of feed intake and efficiency (1)

Room: Willem Burger Zaal

Chair: Birgit Gredler-Grandl, Helene Gilbert, Wendy Rauw

- 13:30 [Modelling multiplicativity in feed efficiency by regression on expected feed intake](#)
Lidauer, M.H.; Negussie, E.; Mehtiö, T.; Mäntysaari, P.; Kokkonen, T.; Mäntysaari, E.A.
- 13:32 [Alternative models to predict residual feed intake in Hereford breed and effects on their breeding values accuracy](#)
Pravia, M.I.; Navajas, E.A.; Aguilar, I.; Ravagnolo, O.

- 13:34 [Feed intake can be predicted as quantitative or qualitative traits](#)
Tortereau, F.; Marie-Etancelin, C.; Marcon, D.; Weisbecker, J.-L.
- 13:36 [Prediction of breeding values for feed intake in pigs using individual versus group records along with correlated traits](#)
Zhang, C.; Kemp, R.A.; Dekkers, J.C.M.; Plastow, G.S.; Gao, H.
- 13:38 [Phenotypic and genetic associations between feed efficiency and FTIR milk-spectra](#)
Toledo-Alvarado, H.O.; Tempelman, R.J.; Lopez-Cruz, M.; Vandehaar, M.J.; Santos, J.E.P.; Peñagaricano, F.; Khanal, P.; De Los Campos, G.
- 13:40 [Genetic relationships between weight loss in early lactation and daily milk production until 305 days in Holstein cows](#)
Tribout, T.; Minéry, S.; Vallée, R.; Saille, S.; Saunier, D.; Ducrocq, V.; Faverdin, P.; Boichard, D.
- 13:42 [Influence of body condition score genomic index on performance trajectories over the lactation period in Holstein cows](#)
Lefebvre, R.; Faverdin, P.; Barbey, S.; Jurquet, J.; Tribout, T.; Boichard, D.; Martin, P.
- 13:44 Discussion
- 13:45 [Feed efficiency and resource allocation trade-offs: theory, evidence and prospects](#)
Douhard, F.; Rupp, R.; Gilbert, H.
- 14:15 [Mechanistic-based prediction of selection response on resilience and feed efficiency traits in dairy cattle](#)
Bouquet, A.; Slagboom, M.; Thomasen, J.; Friggens, N.C.; Kargo, M.; Puillet, L.
- 14:30 [Towards the characterisation of animal robustness by dynamic energy allocation indicators in fattening pigs](#)
Lenoir, G.; Muñoz-Tamayo, R.; Flatres-Grall, L.; David, I.; Friggens, N.C.
- 14:45 [Milk metabolite profiles in goats selected for longevity support link between resource allocation and resilience](#)
Ithurbide, M.; Wang, H.; Huau, C.; Palhière, I.; Fassier, T.; Pires, J.; Larsen, T.; Cao, J.; Friggens, N.C.; Rupp, R.
- 15:00 [Lifetime feed efficiency and deep phenotypes from scarce feed intake records using the mechanistic LiGAPS-dairy model](#)
Van Der Linden, A.; Schopen, G.C.B.; Gredler-Grandl, B.; De Jong, G.; Sol, M.; Van Der Beek, S.; Veerkamp, R.F.
- 15:15 [Genetic analysis of feed efficiency in Atlantic salmon](#)
Sonesson, A.K.; Hatlen, B.; Gjerde, B.; Difford, G.F.; Brunsvik, P.; Meuwissen, T.H.E.; Norris, A.

Session 10. **Novel phenotyping tools: Machine learning and computer vision (1)**

Room: Jurriaanse Zaal

Chair: Claudia Kamphuis, Jan Lassen, Guilherme Rosa, Pascal Duenk

- 13:30 [Automated individual walking distance of group-housed broilers: a comparison between ground-truth, RFID, and video](#)
Doornweerd, J.E.; Fodor, I.; Kootstra, G.; Veerkamp, R.F.; De Klerk, B.; Van Der Sluis, M.; Bouwman, A.C.; Ellen, E.D.
- 13:32 [Automated processing and phenotype extraction of ovine medical images using deep learning and computer vision](#)
Robson, J.F.; Denholm, S.J.; Coffey, M.
- 13:34 [VTag: automatic pipeline to annotate video data for pig phenomics studies](#)
Chen, C.J.; Morota, G.; Cheng, H.
- 13:36 [Milk spectra selection for equations development to predict milk technological traits](#)
Frizzarin, M.; Gormley, I.C.; Casa, A.; McParland, S.
- 13:38 [Using supervised machine learning for honey harvest prediction](#)
Ramirez Diaz, J.; Manunza, A.; A. De Oliveira, T.; Bobbo, T.; Silva, V.; Cozzi, P.; Biffani, S.; Stella, A.; Minozzi, G.

13:40 Discussion

13:45 [Validation of computer vision algorithms for classifying video segments applied to behavioural phenotyping of pigs](#)

Steibel, J.P.; Han, J.; Chen, C.; Siegford, J.; Norton, T.; Colbry, D.

14:15 [Automated estimation of pose features in broilers using computer vision](#)

Fodor, I.; Doornweerd, J.E.; De Klerk, B.; Bouwman, A.C.

14:30 [Predicting carcass cut yields in cattle from digital images using artificial intelligence](#)

Matthews, D.; Pabiou, T.; Evans, R.D.; Beder, C.; Daly, A.

14:45 [Digital phenotyping to improve Atlantic salmon feed efficiency and welfare](#)

Difford, G.F.; Lindberg, S.K.; Heia, K.; Hatlen, B.; Durland, E.; Gjerde, B.; Alvestad, R.; Mota, V.; Noble, C.; Norris, A.; Boison, S.; Afseth, N.K.; Wold, J.P.; Sonesson, A.K.

15:00 [Prediction of roughage intake of dairy cows combining milk mid-infrared spectra and cow variables by deep learning](#)

Gebregiwerigis, G.T.; Afseth, N.K.; Kidane, A.; Prestøkken, E.; Meuwissen, T.H.E.

15:15 [CFIT – a 3D camera based system to measure individual feed intake and predict body weight in commercial farms](#)

Lassen, J.; Thomasen, J.R.; Borchersen, S.

Session 11. Functional Annotation of Genomes: Causal variants & gene discovery (1)

Room: Eduard Flipse Zaal

Chair: Martijn Derks, Antonio Reverter Gomez, Amanda Chamberlain, Mathew Littlejohn

13:30 [Detection of genes influenced by environmentally responsive cis-regulatory variation in porcine immune cells](#)

Murani, E.; Hadlich, F.; Ponsuksili, S.; Wimmers, K.

13:32 [Insight into the most significant quantitative trait locus for calving traits on BTA18 in Holstein dairy cattle](#)

Dachß, N.; Upadhyay, M.; Hannemann, E.; Hauser, A.; Krebs, S.; Blum, H.; Seichter, D.; Russ, I.; Gehrke, L.J.; Thaller, G.; Medugorac, I.

13:34 [Finding potentially causal genetic factors for meat tenderness using eQTL study in Hanwoo cattle](#)

Chung, Y.; Chung, K.; Dinh, P.; Choi, I.; Lee, S.

13:36 [The application of mixed linear models for the estimation of functional effects on bovine stature based on SNP summary](#)

Kotlarz, K.; Kosinska-Selbi, B.; Cai, Z.; Sahana, G.; Szyda, J.

13:38 [Predicted isoforms of a Brahman cow revealed by full-length transcript sequencing](#)

Nguyen, L.T.; Cheng, Y.; Kuo, R.I.; Hayes, B.J.; Ross, E.M.

13:40 [Meta-analysis of genome-wide association studies for litter size in pigs indicates new causal variants](#)

Sell-Kubiak, E.; Derks, M.F.L.; Lopes, M.S.; Dobrzanski, J.; Szwaczkowski, T.

13:42 [Selection signatures analyses revealed genes associated with adaptation in selected goat breeds in Kenya](#)

Waineina, R.W.

13:44 [Investigation of host genetic role in PCV2 infections](#)

Wijesena, H.R.; Kachman, S.K.; Ciobanu, D.C.

13:46 [Olfaction: a critical force driving adaptive evolution in Yaks](#)

Kour, A.; Niranjana, S.K.; Jayakumar, S.; Pukhrambam, M.; Sarkar, M.

13:48 [Functional analysis of selective sweeps to identify phenotypic traits in South African Nguni cattle](#)

Zwane, A.A.; Nxumalo, K.S.; Makgahlela, M.L.; Van Marle-Koster, E.; Maiwashe, N.

- 13:50 [Fine-mapping of candidate causal genes for tail length in the Merinolandschaf breed](#)
Lagler, D.K.; Kunz, E.; Eck, K.; Seichter, D.; Russ, I.; Mendel, C.; Lühken, G.; Upadhyay, M.; Medugorac, I.
- 13:52 Discussion
- 14:00 [Massive detection of cryptic recessive genetic defects in livestock mining millions of life trajectories](#)
Guintard, A.; Besnard, F.; Cano, E.-M.; Hozé, C.; Leclerc, H.; Boussaha, M.; Grohs, C.; Barbat, A.; Fritz, S.; Escoufflaire, C.; Rivièr, J.; Péchoux, C.; Danchin-Burge, C.; Foucras, G.; Relun, A.; Plassard, V.; Arcangioli, M.-A.; Mattalia, S.; Boichard, D.; Capitan, A.
- 14:15 [A de novo missense mutation of COL1A1 causes Osteogenesis Imperfecta type 2 and premature delivery in Normande Cattle](#)
Grohs, C.; Corbeau, J.; Jourdain, J.; Boussaha, M.; Plassard, V.; Barbat, A.; Hamelin, C.; Mortier, J.; Boichard, D.; Guatteo, R.; Capitan, A.
- 14:30 [CRISPR-Cas9 gene editing enables functional evaluation of a host Synaptogyrin-2 missense variant in PCV2b infection](#)
Walker, L.R.; Vu, H.; Ciobanu, D.C.
- 14:45 [Sequence-based GWAS meta-analyses for beef production traits](#)
Sanchez, M.P.; Tribout, T.; Kadri, N.; Chitneedi, P.K.; Maak, S.; Hozé, C.; Boussaha, M.; Croiseau, P.; Philippe, R.; Spengeler, M.; Kühn, C.; Wang, Y.; Pausch, H.; Boichard, D.
- 15:00 [Deciphering genetic variants from whole genome affecting duodenum, liver and muscle transcriptomes in pigs](#)
Crespo-Piazuelo, D.; González-Rodríguez, O.; Mongellaz, M.; Acloque, H.; Mercat, M.-J.; Bink, M.C.A.M.; Huisman, A.E.; Ramayo-Caldas, Y.; Sánchez, J.P.; Ballester, M.
- 15:15 [Analysis of mortality rates in the female progeny of Holstein bulls allows discovery of new dominant genetics defects](#)
Besnard, F.; Leclerc, H.; Cesbron, N.; Boussaha, M.; Grohs, C.; Jewell, N.; Piton, A.; Barasc, H.; Femenia, M.; Dorso, L.; Strugnell, B.

Session 12.

Aquaculture (1)

Room: Van Cappellen Zaal

Chair: Hans Komen, Ross Houston, Diogo Hashimoto, Mark Camara

- 13:30 [Conserved QTL and chromosomal inversions affect resistance to columnaris disease in two rainbow trout populations](#)
Calboli, F.C.F.; Koskinen, H.; Nousianen, A.; Fraslin, C.; Houston, R.D.; Kause, A.
- 13:32 [Multi-trait genome wide association study in correlated traits: fillet colour and body weight in Atlantic salmon](#)
Sae-Lim, P.; Boison, S.; Baranski, M.
- 13:34 [Implementation of genomic selection on production and quality traits and linkage disequilibrium in *Crassostrea gigas*](#)
Jourdan, A.; Boudry, P.; Enez, F.; Haffray, P.; Chenier, F.; Vetois, E.; Allal, F.; Leroy, P.; Phocas, F.; Bugeon, J.; Degremont, L.; Morvezen, R.
- 13:36 Discussion
- 13:45 [Genetic correlation between IP and cohabitation challenge test model for *Piscirickettsia salmonis* in Atlantic salmon](#)
Manosalva, C.; Pavez, M.L.; Sae-Lim, P.; Norris, A.; Baranski, M.; Boison, S.A.
- 14:00 [Using 'population-specific haplotypes' to select for resistance to SRS in an admixed population of coho salmon](#)
Moen, T.; Ødegård, J.; Grammes, F.; Knutsen, T.; Deerenberg, R.; Cichero, D.
- 14:15 [Genetic architecture of resistance to infectious hematopoietic necrosis virus in three aquaculture rainbow trout strains](#)
Vallejo, R.L.; Gao, G.; Fragomeni, B.O.; Cheng, H.; Shewbridge, K.L.; Long, R.L.; Martin, K.E.; Naish, K.A.; Palti, Y.

- 14:30 [Potential of imputation for cost-efficient genomic selection for resistance to *Flavobacterium columnare* in rainbow trout](#)
Fraslin, C.; Nousiainen, A.; Koskinen, H.; Kause, A.; Houston, R.D.
- 14:45 [Genomic prediction of complex traits in European sea bass: random cross-validation and leave-one-family-out validation](#)
Faggion, S.; Bertotto, D.; Bonfatti, V.; Freguglia, M.; Bargelloni, L.; Carnier, P.
- 15:00 [Genetics of parasite attraction in Atlantic salmon: potential for group-level protection against sea lice](#)
Ødegård, J.; Kjøglum, S.; Medina, M.; Torgersen, J.S.; Korsvoll, S.A.; Deerenberg, R.; Yáñez, J.M.; Cichero, D.; Lopez, P.; Moen, T.
- 15:15 [A major QTL affects resistance to viral nervous necrosis in farmed European seabass](#)
Mukiibi, R.; Robledo, D.; Peñaloza, C.; Ferraresso, S.; Franch, R.; Bertotto, D.; Freguglia, M.; Laureau, S.; Pascoli, F.; Toffan, A.; Tsigenopolous, C.; Bargelloni, L.; Houston, R.

Session 13.

Methods and Tools: Genomic prediction (1)

Room: Grote Zaal

Chair: Mario Calus, Vincent Boerner, Gregor Gorjanc

- 16:00 [Benchmark SNPs selection strategies to achieve optimum prediction in small population](#)
Mancin, E.; Sartori, C.; Tulliozi, B.; Proto, G.G.; Mantovani, R.
- 16:02 [Genetic correlations among longevity, fertility, udder health and type traits including or not genomic information](#)
Rostellato, R.; Maugan, L.-H.; Ducrocq, V.
- 16:04 [Alternative SNP weighting for genomic prediction methods in the presence of causative variants](#)
Santana, B.; Riser, M.M.; Fragomeni, B.
- 16:06 [Including selected sequence variants in genomic predictions for age at first calving in Nellore cattle](#)
Campos, G.S.; Silva, D.A.; Neves, H.H.R.; Lourenco, D.; Júnior, G.A.F.; Fonseca, L.F.S.; Albuquerque, L.G.; Carneiro, R.
- 16:08 [Increasing accuracy of single-step evaluations of functional longevity including information from correlated traits](#)
Maugan, L.-H.; Tribout, T.; Rostellato, R.; Mattalia, S.; Ducrocq, V.
- 16:10 [Multi-trait genomic estimation of genetic parameters for growth and carcass traits of Duroc pigs](#)
Akanno, E.C.; Thekkoot, D.M.; Zhang, C.; Bierman, C.; Plastow, G.; Kemp, R.A.
- 16:12 [Accounting for nuclear- and mito-genome in genetic evaluation and breeding of dairy cattle](#)
Mafra Fortuna, G.; Zumbach, B.J.; Johnsson, M.; Pocrnic, I.; Gorjanc, G.
- 16:14 Discussion
- 16:15 [Using residual regressions to quantify and map signal leakage in genomic prediction](#)
Valente, B.D.; De Los Campos, G.; Grueneberg, A.; Chen, C.Y.; Ros-Freixedes, R.; Herring, W.O.
- 16:30 [Capitalizing on complex annotations in Bayesian genomic prediction for a backcross population of growing pigs](#)
Mollandin, F.; Gilbert, H.; Croiseau, P.; Rau, A.
- 16:45 [Predictive ability of genomic prediction in layers when including CADD scores as genome function information](#)
Bink, M.C.A.M.; Calus, M.P.L.; Derks, M.F.L.; Visscher, J.; Perez, B.C.
- 17:00 [Across-sex genomic prediction using pre-selected SNP sets in cattle](#)
Olasege, B.S.; Tahir, M.S.; Porto-Neto, L.R.; Hayes, B.J.; Fortes, M.R.S.
- 17:15 [Genomic prediction with incomplete omics data](#)
Karaman, E.; Milkeviych, V.; Cai, Z.; Janss, L.; Sahana, G.; Lund, M.S.

- 17:30 [A Bayesian hierarchical model to integrate a mechanistic growth model in genomic prediction](#)
Yu, H.; Van Milgen, J.; Knol, E.; Fernando, R.; Dekkers, J.
- 17:45 [Mega-scale mixed models for genome-wide prediction with thousands of high-throughput phenotyping traits](#)
Qu, J.; Runcie, D.E.; Cheng, H.

Session 14. Challenges – Resource allocation and genetics of feed intake and efficiency (2)

Room: Willem Burger Zaal

Chair: Birgit Gredler-Grandl, Helene Gilbert, Wendy Rauw

- 16:00 [Validation and genetic analysis of a feed efficiency criterion in French Lacaune ewes](#)
Machefert, C.; Robert-Granie, C.; Hassoun, P.; Parisot, S.; Allain, C.; Portes, D.; Lagriffoul, G.; Astruc, J.M.; Larroque, H.
- 16:02 [Gene co-expression networks contributing to variation in residual feed intake in bovine hepatic tissue](#)
Keogh, K.; McGee, M.; Kenny, D.A.
- 16:04 [Genetics parameters of feed efficiency in dairy goats, under commercial conditions](#)
Chassier, M.; Mosnier, F.; Rupp, R.; Bluet, B.; Bailly-Salins, A.; Palhière, I.
- 16:06 [Genetic analysis of predicted dry matter intake and gross feed efficiency in South African Holstein cows](#)
Madilindi, M.A.; Zishiri, O.T.; Dube, B.; Banga, C.B.
- 16:08 [Single-step genomic prediction for metabolic body weight of Nordic Red dairy cattle](#)
Kempe, R.M.; Mehtiö, T.; Leino, A.-M.; Koivula, M.; Pitkänen, T.J.; Stephansen, R.B.; Mäntysaari, E.A.; Negussie, E.; Pösö, J.; Nielsen, U.S.; Fikse, W.F.; Aamand, G.P.; Lidauer, M.H.
- 16:10 [Application of imputed data and single-step GBLUP in the study of residual feed intake trait of Nellore cattle](#)
Silva, J.A.I.I.V.; Oliveira, M.H.V.; Castilhos, A.M.; Toro-Ospina, A.M.; Srihi, H.; Varona, L.
- 16:12 [Relationship between proxies of energy states and nitrogen use efficiency for Holstein cows in early lactation](#)
Chen, Y.; Grelet, C.; Vanderick, S.; Hu, H.; Gengler, N.
- 16:14 [genetic variation exists in nitrogen use efficiency for lactating cows in grass-grazed dairy systems](#)
Tavernier, E.; Gormley, I.C.; Delaby, L.; McParland, S.; O'Donovan, M.; Berry, D.P.
- 16:16 [Study of the causal relationship between the rabbit cecal microbiota and host's growth and feed efficiency](#)
Piles, M.; Mora, M.; Sánchez, J.P.; Ramayo-Caldas, Y.; González-Rodríguez, O.; Velasco-Galilea, M.
- 16:18 [Part of the functional rumen core microbiome is influenced by the bovine host genome and associated with feed efficiency](#)
Martinez-Alvaro, M.; Mattock, J.; Weng, Z.; Dewhurst, R.J.; Cleveland, M.A.; Watson, M.; Roehe, R.
- 16:20 [Identifying diversity in cattle performance using Bayesian inference and a model](#)
Ramirez, J.F.; Puillet, L.; Friggens, N.C.
- 16:22 [Feed efficiency of crossbreds of Montbéliarde, Viking Red, and Holstein with Holstein cows fed two alternative diets](#)
Heins, B.J.; Pereira, G.M.; Hansen, L.B.
- 16:24 Discussion
- 16:30 [Genetic and phenotypic associations among production, feed efficiency and immune traits in indigenous chicken of Kenya](#)
Miyumo, S.A.; Wasike, C.B.; Ilatsia, E.D.; Bennewitz, J.; Chagunda, M.G.G.
- 16:45 [Novel genetic parameters to improve gRFI in dairy cattle using big data from multiple lactations and countries](#)
Stephansen, R.B.; Martin, P.; Gredler-Grandl, B.; Manzanilla Pech, C.I.V.; Sahana, G.; Ducrocq, V.; Baes, C.; Schenkel, F.; Veerkamp, R.F.; Lassen, J.

- 17:00 [Genetic parameters of feeding behaviour traits in parental lines of a mule duck](#)
Chapuis, H.; Lagüe, M.; Gilbert, H.
- 17:15 [Estimates of genetic parameters for feeding behavior traits and its association with feed efficiency in Holstein cows](#)
Cavani, L.; Brown, W.E.; Parker Gaddis, K.L.; Tempelman, R.J.; Vandehaar, M.J.; White, H.M.; Peñagaricano, F.; Weigel, K.A.
- 17:30 [Protein efficiency is heritable but not genetically correlated with meat quality in pigs](#)
EwaoluwaGbemiga, E.O.; Bee, G.; Kasper, C.
- 17:45 [Genetic analysis of digestibility traits in pigs measured by near-infrared spectroscopy](#)
Martinsen, K.H.; Enger, E.G.; Grindflek, E.; Afseth, N.K.; Mydland, L.T.; Wallen, S.; Meuwissen, T.H.E.

Session 15. **Novel phenotyping tools: Machine learning and computer vision (2)**

Room: Jurriaanse Zaal

Chair: Claudia Kamphuis, Jan Lassen, Guilherme Rosa, Pascal Duenk

- 16:00 [Video-based analysis of dairy cow behaviour: detection of lying down and standing up](#)
Adriaens, I.; Ouweltjes, W.; Hulsegge, I.; Kamphuis, C.
- 16:02 [Image-based cattle conformation prediction using deep learning methods](#)
Segelke, D.; Alkhoder, H.; Wabbersen, J.
- 16:04 [Prediction of fat percentage and visceral weight from whole fish images with multi-input neural network](#)
Xue, Y.; Bastiaansen, J.W.M.; Komen, H.
- 16:06 [A case-control GWAS for the chicken plumage colour using a computer vision approach](#)
Heo, S.; Cho, S.; Park, J.; Kim, M.; Cho, E.; Jin, D.; Cha, J.; Koh, Y.J.; Lee, J.H.
- 16:08 [Machine learning to predict somatic cell count at the subsequent test-day record in the Italian Mediterranean Buffaloes](#)
Bobbo, T.; Matera, R.; Pedota, G.; Ramirez-Diaz, J.; Manunza, A.; Stella, A.; Cotticelli, A.; Neglia, G.; Biffani, S.
- 16:10 [Application of machine learning algorithms to develop behavioural and stress phenotypes for sheep](#)
Keshavarzi, H.; Campbell, D.L.M.; Lee, C.
- 16:12 Discussion
- 16:15 [Computer vision systems to advance high-throughput phenotyping in livestock](#)
Dorea, J.R.R.; Rosa, G.J.M.
- 16:45 [Tracking multiple cows simultaneously in barns using computer vision and deep learning](#)
Kamphuis, C.; Adriaens, I.; Ouweltjes, W.; Hulsegge, I.
- 17:00 [A computer vision system for individual tracking of group housed rabbits](#)
Sánchez, J.P.; Muñoz, I.; González, O.; Pascual, M.; Perucho, O.; Alsina, P.; Piles, M.
- 17:15 [Clustering of Meishan and Large White sows for activity defined from image analysis, and influence on piglet mortality](#)
Girardie, O.; Bonneau, M.; Billon, Y.; Bailly, J.; David, I.; Canario, L.
- 17:30 [Using machine learning to predict feed intakes of meat sheep from animal traits and ruminal microbiota](#)
Le Graverand, Q.; Marie-Etancelin, C.; Weisbecker, J.L.; Meynadier, A.; Marcon, D.; Tortereau, F.
- 17:45 [The magic of predicting shapes from DNA](#)
Pérez-Enciso, M.; Zingaretti, L.M.

Session 16. Functional Annotation of Genomes: Causal variants & gene discovery (2)

Room: Eduard Flipse Zaal

Chair: Martijn Derks, Antonio Reverter Gomez, Amanda Chamberlain, Mathew Littlejohn

- 16:00 [Candidate genes for milk, growth and immune system traits in Brazilian Iberian-derived Locally Adapted cattle breeds](#)
Verardo, L.L.; Machado, M.A.; Panetto, J.C.C.; Silva, M.V.G.B.
- 16:02 [Copy Number Variation analysis in Nguni and Bonsmara crossbred cattle](#)
Kooverjee, B.B.; Soma, P.; Naser, F.W.C.; Van Der Nest, M.A.; Scholtz, M.M.
- 16:04 [Resequencing of casein genes in Swedish Red Cattle with varying milk coagulation properties](#)
Vanhala, T.K.; Lewerentz, F.; Buhelt Johansen, L.; Sibersen, C.; Paulsson, M.; Glantz, M.; De Koning, D.J.
- 16:06 [Major histocompatibility complex \(MHC\) Class II DRB gene Exon-2 of Indian camel breeds show limited genetic diversity](#)
Prakash, V.; Jyotsana, B.; Suthar, S.
- 16:08 [Transcriptome profile of liver from pigs fed with two different levels of soybean oil revealed the NF- \$\kappa\$ B1 modulation](#)
Larissa Fanalli, S.; Pereira Martins Da Silva, B.; Nery Ciconello, F.; Reecy, J.; Koltes, J.; Koltes, D.; Correia Almeida Regitano, L.; Cesar Carvalho Balieiro, J.; Lehmann Coutinho, L.; Barreto Mourao, G.; Costa Monteiro Moreira, G.; Vezzoni De Almeida, V.; Luchiari Filho, A.; Silva Mello Cesar, A.
- 16:10 [SPP1 gene polymorphisms within Intron-IV and Exon-IV region and their association with milk traits in Gaolao cattle](#)
Kate, R.R.; Kale, D.S.; Singh, J.; Patil, D.V.
- 16:12 Discussion
- 16:15 [Building *in vitro* tools for livestock genomics: chromosomal variation within the PK15 cell line](#)
Johnsson, M.; Hickey, J.M.; Jungnickel, M.K.
- 16:30 [Conserved non-coding elements of the Bovine genome](#)
Kadri, N.K.; Pausch, H.
- 16:45 [A massively parallel reporter assay to screen bovine regulatory variants](#)
Littlejohn, M.D.; Lopdell, T.J.; Trevarton, A.; Moody, J.; Tiplady, K.M.; Burborough, K.A.; Prowse-Wilkins, C.P.; Chamberlain, A.J.; Goddard, M.E.; Snell, R.G.
- 17:00 [Detection of causative genes for resistance against cardiomyopathy syndrome in Atlantic salmon using omics data](#)
Aslam, M.L.; Gonen, S.; Boison, S.A.; Leder, E.; Baranski, M.; Norris, A.; Robinson, N.; Koga, S.; Østbye, T.-K.K.; Dagnachew, B.
- 17:15 [Genetic regulation of ear size in Slovenian and Greek sheep breeds](#)
Klawatsch, J.; Papachristou, D.; Koutsouli, P.; Seichter, D.; Russ, I.; Simčič, M.; Bizelis, I.; Medugorac, I.
- 17:30 [Large-scale 'omics fine-mapping identifies expression quantitative trait loci significantly affecting cattle phenotypes](#)
Xiang, R.; Goddard, M.E.; Prowse-Wilkins, C.P.; Reich, C.M.; Mason, B.A.; Garner, J.B.; Marett, L.C.; MacLeod, I.M.; Chamberlain, A.J.

Session 17.

Aquaculture (2)

Room: Van Cappellen Zaal

Chair: Hans Komen, Ross Houston, Diogo Hashimoto, Mark Camara

- 16:00 [The potential indicator for resilience of Sukamandi strain tilapia grown in brackish water ponds](#)
Aththar, M.H.F.; Setyawan, P.; Imron, I.; Gunadi, B.; Camara, M.; Komen, H.; Bastiaansen, J.W.M.

- 16:02 [Exploiting genomics to infer population structure and genetic variability in wild and farmed seabream and seabass](#)
 Villanueva, B.; Fernández, A.; Peiro-Pastor, R.; Peñaloza, C.; Houston, R.D.; Sonesson, A.K.; Tsigenopoulos, C.S.; Bargelloni, L.; Gamsiz, K.; Karahan, B.; Gökçek, E.Ö.; Fernández, J.; Saura, M.
- 16:04 [Comparison of tank and commercial sea-pen family evaluation of Chinook salmon \(*Oncorhynchus tshawytscha*\) in New Zealand](#)
 Scholtens, M.R.; Dodds, K.G.; Clarke, S.M.; Walker, S.P.; Tate, M.L.; Miller, R.; Slattery, T.; Symonds, J.E.
- 16:06 [Testing fat content or feeding behaviour as indirect selection criteria for feed efficiency using trout isogenic lines](#)
 Pouil, S.; Kernéis, T.; Quillet, E.; Lallias, D.; Labbé, L.; Phocas, F.; Dupont-Nivet, M.
- 16:08 Discussion
- 16:15 [The possibilities of using electronic sensors for aquaculture breeding](#)
 Abbink, W.; Palstra, A.; Agbeti, W.; Lembo, G.; Komen, J.
- 16:45 [Genetic parameters and genome-wide association study of resistance to acute hyperthermia in rainbow trout](#)
 Lagarde, H.; Lallias, D.; Patrice, P.; Prchal, M.; François, Y.; D'Ambrosio, J.; Acin-Perez, A.; Cachelou, F.; Haffray, P.; Dupont-Nivet, M.; Phocas, F.
- 17:00 [QTLs controlling swimming performance and their effect on growth in Nile tilapia \(*Oreochromis niloticus*\)](#)
 Yu, X.; Mengistu, S.B.; Mulder, H.A.; Palstra, A.P.; Benzie, J.A.H.; Trinh, T.Q.; Groenen, M.A.M.; Komen, H.; Megens, H.J.
- 17:15 [Optimizing genotyping effort in aquaculture breeding programs by pre-selection of candidates](#)
 Roozeboom, C.; Gulzari, B.; Komen, H.; Camara, M.; Bastiaansen, J.W.M.
- 17:30 [Prediction of production traits by using body features of gilthead seabream \(*Sparus aurata*\) obtained from digital images](#)
 Gulzari, B.; Mencarelli, A.; Roozeboom, C.; Komen, H.; Bastiaansen, J.W.M.
- 17:45 [Comparison of genomic selection barramundi breeding schemes for multiple environments with strong GxE](#)
 Lillehammer, M.; Robinson, N.A.; Jones, D.B.; Massault, C.; Loughnan, S.; Cate, H.S.; Harrison, P.J.; Strugnell, J.M.; Zenger, K.R.; Jerry, D.R.

Session 18.

Plenary 2

Room: Grote Zaal

Chair: Yvette de Haas

- 08:30 [Genetics of quantitative traits in natural populations: lessons from long term studies of wild animals](#)
 Pemberton, J.M.

Session 19.

Methods and Tools: Genomic prediction (2)

Room: Grote Zaal

Chair: Mario Calus, Vincent Boerner, Gregor Gorjanc

- 10:00 [Nordic Holstein single-step test day model using metafounders and blending of foreign information](#)
 Koivula, M.; Strandén, I.; Aamand, G.P.; Mäntysaari, E.A.
- 10:02 [Effects of missing or wrong pedigree records on Single-Step predictions](#)
 Pimentel, E.C.G.; Edel, C.; Emmerling, R.; Götz, K.-U.
- 10:04 [An alternative method to consider a reference population in single-step SNP BLUP model without separating genomic terms](#)
 Osawa, T.; Baba, T.; Masuda, Y.; Kawahara, T.; Goto, Y.

- 10:06 [Accuracy of pedigree and genomic predictions of meat quality in a multi-breed cattle using single and two step model](#)
Evans, R.D.; Naderi, S.; Berry, D.P.
- 10:08 [Single-step genomic prediction in small breeds: Finncattle case](#)
Kudinov, A.A.; Koivula, M.; Strandén, I.; Aamand, G.P.; Mäntysaari, E.A.
- 10:10 [Challenges to implement an interim genomic prediction for young animals in Wallonia, Belgium](#)
Wijnrocx, K.; Mota, R.R.; Dufrasne, M.; Gengler, N.
- 10:12 [New insights into the computation of the inverse of the numerator relationship matrix for genotyped animals](#)
Maiwashe, A.
- 10:14 [GAPLS – a novel method to genomically rank bulls for daughter reproductive performance](#)
Li, Y.; Lehnert, S.; Porto-Neto, L.R.; McCulloch, R.; McWilliam, S.; Alexandre, P.; McDonald, J.; Smith, C.; Reverter, A.
- 10:16 [Performance of identity-by-state and identity-by-descent genomic models for meat traits in a cross-pig F2 population](#)
Angarita, B.K.; Steibel, J.P.; Cantet, R.J.C.; Forneris, N.S.
- 10:18 [Modelling missing pedigree with metafounders and validating ssGBLUP evaluation for Uruguayan Holstein dairy cattle](#)
López-Correa, R.D.; Legarra, A.; Aguilar, I.
- 10:20 [Estimating metafounder relations for Finnish multibreed beef population](#)
Taskinen, M.; Leino, A.-M.; Pitkänen, T.J.; Mäntysaari, E.A.
- 10:22 [A deregression method for a single-step SNP BLUP model using all genotype data](#)
Liu, Z.; Masuda, Y.
- 10:24 [Variance component estimation for single-step genomic BLUP for Australian terminal sire sheep](#)
Gurman, P.M.; Li, L.; Swan, A.A.; Moghaddar, N.; Van Der Werf, J.H.J.
- 10:26 [Finetuning hyperparameters increases the prediction accuracy in single-step genetic evaluation](#)
Neshat, M.; Moksedul Momin, M.D.; Truong, B.; Van Der Werf, J.H.J.; Lee, S.; Lee, S.H.
- 10:28 Discussion
- 10:30 [Comparison of single-step and multi-step evaluations for U.S. milk, fat, and protein](#)
Mota, R.R.; Cesarani, A.; Vanraden, P.M.
- 10:45 [Large-scale multiple-trait single-step marker model implementation](#)
Harris, B.L.; Sherlock, R.G.; Nilforooshan, M.A.,
- 11:00 [An iterative method for deregressed proof in single-step genomic BLUP and its application to a dairy cattle population](#)
Masuda, Y.; Liu, Z.; Sullivan, P.
- 11:15 [Efficient approximation of reliability for genomic breeding values in large systems](#)
Eding, H.
- 11:30 [Evaluating the suitability of subjectively defined base populations](#)
Ten Napel, J.; Vandenplas, J.; Calus, M.P.L.; Strandén, I.; Lidauer, M.; Veerkamp, R.F.
- 11:45 [Maximum likelihood estimation of metafounder parameters for single and multiple breeds](#)
Christensen, O.F.; Legarra, A.

Session 20.

Challenges – Understanding and utilizing genetic diversity (1)

Room: Jurriaanse Zaal

Chair: Mirte Bosse, Beatriz Villanueva, Tom Druet

- 10:00 [Genetic variability in the individual inbreeding load: genomic prediction for artificial purging](#)
Varona, L.; López-Carbonell, D.; Srihi, H.; Ramirez, M.; Martínez, P.; Hermida, M.; Altarriba, J.; Casellas, J.
- 10:30 [Inbreeding depression in livestock: comparing trait groups and inbreeding measures](#)
Doekes, H.P.; Bijma, P.; Windig, J.J.
- 10:45 [Global and local genome ancestry reveals signal of Merinization in Noire de Thibar sheep](#)
Baazaoui, I.; Ciani, E.; Mastrangelo, S.; Bedhiaf-Romdhani, S.
- 11:00 [Common heterozygosity-rich regions \(HRR\) across the genomes of commercial and local goat breeds](#)
Biscarini, F.; Manunza, A.; Cozzi, P.; Stella, A.
- 11:15 [Markhor-derived introgression of PAPSS2 confers high-altitude adaptability in Tibetan goats](#)
Li, C.H.A.O.
- 11:30 [Patterns of inbreeding and selection using runs of homozygosity in North American dairy cattle](#)
Lozada-Soto, E.A.; Tiezzi, F.; Cole, J.B.; Vanraden, P.M.; Maltecca, C.
- 11:45 [Exploring genetic diversity and selection signatures in indigenous African cattle breeds](#)
Friedrich, J.; Bailey, R.; Talenti, A.; Marshall, K.; Prendergast, J.; Wiener, P.

Session 21.

Society and gene editing and reproduction

Room: Eduard Flipse Zaal

Chair: Karel de Greef, Imke Tammen, Mike McGrew, Alison Van Eenennaam, Julie Lamy, Trudee Fair, Jaana Peippo

- 10:00 [Effect of alternative synchronisation treatments on the vaginal microbiota of ewes and their impact on pregnancy rate](#)
Reinoso-Peláez, E.L.; González-Recio, O.; González, C.; Saura, M.; Fernández, A.; López-García, A.; Saborío-Montero, A.; Calvo, J.H.; Ramón, M.; Serrano, M.
- 10:15 [Modelling of direct-transfer vitrification of bovine embryos](#)
Lamy, J.; De Wit, A.; Fotinga-Meiring, F.; Mullaart, E.; Zak, L.; Knol, E.; Ellen, E.; Woelders, H.
- 10:30 [Fertility analysis in stallions: a 35-year retrospective genetic study in the Argentinean Thoroughbred](#)
Karlau, A.; Molina, A.; Antonini, A.; Demyda-Peyrás, S.
- 10:45 [Bull effects on *in vitro* embryo production quality traits are repeatable and heritable](#)
Gebreyesus, G.; Secher, J.B.; Lund, M.S.; Kupisiewicz, K.; Ivask, M.; Su, G.
- 10:47 [Five years of optimizing the assisted reproduction protocol for European eel: what worked and what didn't?](#)
Palstra, A.P.; Jéhannet, P.; Heinsbroek, L.T.N.; Swinkels, W.
- 10:49 [Random regressions for modelling semen production traits in HF purebred and crossbred bulls using Bayesian framework](#)
Ambike, V.B.; Venkataramanan, R.; Karthickeyan, S.M.K.; Tirumurugaan, K.G.; Bhavé, K.G.; Swaminathan, M.
- 11:09 [Removing the dopaminergic inhibition with CRISPR-Cas9 to study the progression of sexual maturation in zebrafish](#)
Jéhannet, P.; De Wit, A.C.C.; Brugman, S.; Zhang, Y.; Bogerd, J.; Palstra, A.P.
- 11:11 [Societal aspects of animal breeding: a bibliometric analysis](#)
Van Der Sluis, M.; De Greef, K.H.; Bonekamp, G.
- 11:13 [The need for harmonized, risk-based regulation of gene editing in livestock](#)
Van Eenennaam, A.L.; Mueller, M.L.

- 11:15 [Broadening the debate on breeding innovations: on public engagement and the role of the Democs game](#)
Meijboom, F.L.B.; Bruce, D.M.; Kramer, K.; Bruce, A.
- 11:30 [Perceptions of genome editing in farm animals by livestock stakeholders](#)
Duclos, R.; Delanoue, E.; Journaux, L.; Guemene, D.; Sourdioux, M.; Bidanel, J.P.
- 11:45 [Production of a germline ablated bull using CRISPR/Cas9 to target NANOS3 in bovine zygotes](#)
Mueller, M.L.; McNabb, B.R.; Owen, J.R.; Hennig, S.L.; Ross, P.J.; Van Eenennaam, A.L.

Session 22.

Free communications

Room: Van Cappellen Zaal

Chair: Henk Bovenhuis, Dirk Jan De Koning, Jörn Bennewitz

- 10:00 [A data-architecture to monitor and collect cow-individual methane emissions real-time from commercial dairy farms](#)
Hulsegge, I.; Schokker, D.; Klandermans, G.G.J.; Kamphuis, C.
- 10:02 [An ontology approach for the collection and management of genetic traits and milk protein data](#)
Franzoni Migliorati, C.; Van Kaam, J.B.C.H.M.; Finocchiato, R.; Lombardi, C.A.; Marusi, M.; Cassandro, M.
- 10:04 [Genotyping errors in SNP markers: types, consequences, and a novel detection method](#)
Rauw, W.M.; Gil, M.G.; Torres, O.; Gomez-Raya, L.
- 10:06 [LncRNAs variability in skeletal muscle of Polish Landrace boars](#)
Hofman, B.; Szyda, J.; Frąszczak, M.; Mielczarek, M.
- 10:08 [Inclusion of average rainfall in genetic evaluation of SA Holsteins to mitigate genotype by environment interaction](#)
Van Niekerk, M.; Neser, F.W.C.; Van Wyk, J.B.; Ducrocq, V.
- 10:10 [Development of an automatic method to estimate IMF for fattening pigs in breeding program](#)
Flatres-Grall, F.G.
- 10:12 [Assessing genomic prediction of economic trait in alpacas: a simulation study](#)
Mamani, G.C.; Santana, B.F.; Jarquín, D.
- 10:14 [Somatic cell count and its relationship with udder type traits in Italian Mediterranean Buffaloes \(*Bubalus bubalis*\)](#)
Gómez, M.M.; Cimmino, R.; Gombia, Y.; Zullo, G.; Biffani, S.
- 10:16 Discussion
- 10:30 [Estimating vertical path coefficients of transmission of non-genetic inherited effects from a similarity matrix](#)
David, I.; Larzul, C.; Ricard, A.
- 10:45 [Building on Falconer's work on environmental sensitivity and scale](#)
Waters, D.L.; Van Der Werf, J.H.J.; Clark, S.A.
- 11:00 [Impact of a non-Gaussian dependence structure on REML estimation of the bivariate genetic animal model](#)
Rohmer, T.; Ricard, A.; David, I.
- 11:15 [Impact of genotyping strategy on the accuracy of genomic prediction for survival in pigs](#)
Liu, T.; Nielsen, B.; Christensen, O.F.; Lund, M.S.; Su, G.
- 11:30 [Effect of a TLR1A polymorphism on natural antibodies in poultry](#)
Bovenhuis, H.; Berghof, T.V.L.; Visker, M.H.P.W.; Arts, J.A.J.; Visscher, J.; Van Der Poel, J.J.; Parmentier, H.K.
- 11:45 [Geometry meets Genomics](#)
Gomez Raya, L.; Rauw, W.M.; Hess, A.

Room: Willem Burger Zaal

Chair: Jan ten Napel, Joanne Conington, Daniel Brown, Nicolas Gengler

- 10:00 [Genetic and Genomic approaches to ewe's artificial insemination success in the Spanish Assaf and Manchega sheep breeds](#)
Serrano, M.; Jiménez, M.A.; Ramón, M.; González-Recio, O.
- 10:02 [The impact of sire on variation in methane production and dry matter intake in sheep](#)
O'Connor, E.; McGovern, F.M.; Dunne, E.; Morrison, S.J.; Boland, T.M.; McHugh, N.
- 10:04 [Milk transcriptome analysis to elucidate the impact of prepubertal nutrition in dairy ewes residual feed intake](#)
Suárez-Vega, A.; Gutiérrez-Gil, B.; Hervás, G.; Marina, H.; Pelayo, R.; Toral, P.G.; Esteban-Blanco, C.; Frutos, P.; Arranz, J.J.
- 10:06 [Inbreeding and effective population size of United States Katahdin sheep](#)
Becker, G.M.; Burke, J.M.; Lewis, R.M.; Miller, J.E.; Morgan, J.L.M.; Rosen, B.D.; Van Tassell, C.P.; Notter, D.R.; Murdoch, B.M.
- 10:08 [Genetic diversity and population structure of dairy goat populations in Kenya](#)
Muhonja, C.; Wainaina, R.W.; Wasike, C.B.; Ngeno, D.K.; Ilatsia, E.D.
- 10:10 [Resolving the genetic structure of 18 Greek and neighbouring sheep populations](#)
Kominakis, A.; Tarsani, E.; Hager, A.; Antonakos, G.; Mastranestasis, I.; Gkelia, D.; Hadjigeorgiou, I.
- 10:12 [Genetic determinism of quality of lamb leather in Lacaune dairy sheep breed](#)
Larroque, H.; Dugas, E.; Woloszyn, F.; Plisson-Petit, F.; Gayraud, J.; Duchêne, J.-C.; Frayssignes, J.; Gille, A.; Brenot, S.; Allain, D.; Drouilhet, L.
- 10:14 [Heritability and genomic analysis of coagulation event in sheep milk](#)
Gaspa, G.; Cesarani, A.; Correddu, F.; Congiu, M.; Dimauro, C.; Pauciullo, A.; Macciotta, N.P.P.
- 10:16 [Genetic parameters across European and North American Alpine goats for two milk production and one udder type traits](#)
Teissier, M.; Brito, L.F.; Schenkel, F.; Bapst, B.; Bruni, G.; Fresi, P.; Robert-Granié, C.; Larroque, H.
- 10:18 [Wool colour traits in Gotland sheep and association with a deletion in ASIP](#)
Johansson, A.M.
- 10:20 Discussion
- 10:30 [Breeding initiatives around reduction of methane emissions in meat sheep – an international review](#)
Lambe, N.R.
- 11:00 [Measuring methane in sheep production systems – phenotypic factors affecting output](#)
McGovern, F.M.; O'Connor, E.; Farrell, L.; Dunne, E.; Wall, E.; McHugh, N.
- 11:15 [Genetics of methane emissions in a multi-breed sheep population](#)
McHugh, N.; O'Connor, E.; Berry, D.P.; Dunne, E.; Farrell, L.; Rafter, P.; McDermott, K.; McGovern, F.M.
- 11:30 [Modelling of productivity, profitability, and greenhouse gas emissions of Irish sheep flocks divergent in genetic merit](#)
Farrell, L.J.; McHugh, N.; Pabiou, T.; Bohan, A.; McDermott, K.; Shalloo, L.; Herron, J.
- 11:45 [Using milk fatty acids as biomarkers to improve feed efficiency in dairy sheep](#)
Marina, H.; Hervás, G.; Pelayo, R.; Toral, P.G.; Suárez-Vega, A.; Gutiérrez-Gil, B.; Esteban-Blanco, C.; Frutos, P.; Arranz, J.J.

Room: Van Weelde Zaal

Chair:

12:00 Lunchtime Satellite Symposium: A more sustainable food system starts with better breeding

Session 25.**Methods and Tools: Genomic prediction (3)**

Room: Grote Zaal

Chair: Mario Calus, Vincent Boerner, Gregor Gorjanc

- 13:30 [Exploring the statistical nature of independent chromosome segments](#)
Hollifield, M.K.; Bermann, M.; Lourenco, D.; Misztal, I.
- 13:32 [Including local genomic breed proportions in genomic predictions for crossbred](#)
Eiriksson, J.H.; Su, G.; Christensen, O.F.
- 13:34 [Investigating the impact of APY core size and definition in single-step GBLUP evaluations](#)
Abdollahi Arpanahi, R.; Lourenco, D.; Misztal, I.
- 13:36 [Strategies for choosing core animals in APY and their impact on the accuracy of single-step genomic predictions](#)
Macciotta, N.P.P.; Dimauro, C.; Lourenco, D.; Cesarani, A.; Degano, L.; Vicario, D.
- 13:38 [Genomic prediction accuracy: how low can we go?](#)
Reverter, A.; Alexandre, P.A.; Li, Y.; Hine, B.C.; Duff, C.J.; Ingham, A.B.; Porto-Neto, L.R.
- 13:40 [Genomic prediction in smallholder tropical dairy herds: modelling milk yield in first and later lactations](#)
Negussie, E.; Lidauer, M.H.; Meseret, S.; Tera, A.; Tessema, E.; Jufar, B.; Negera, T.; Hassen, A.; Gebreyohanes, G.; Mwai, O.A.; Mrode, R.
- 13:42 [Genomic prediction of wool shedding in a composite sheep flock using pooled allele frequencies and individual genotypes](#)
Vargas Jurado, N.; Keele, J.W.; Kuehn, L.A.; Lewis, R.M.
- 13:44 Discussion
- 13:45 [Optimal core definitions for the APY model with an example in large-scale pig dataset](#)
Pocrnic, I.; Lindgren, F.; Tolhurst, D.; Herring, W.O.; Gorjanc, G.
- 14:00 [Updating the core animals in the algorithm for proven and young in the American Angus Association national evaluations](#)
Garcia, A.; Miller, S.; Tsuruta, S.; Lourenco, D.; Misztal, I.; Lu, D.; Retallick, K.
- 14:15 [A critical aspect when using APY inversion with Single-Step GBLUP](#)
Edel, C.; Pimentel, E.C.G.; Emmerling, R.; Götz, K.-U.
- 14:30 [Measures to quantify the accuracy and the erosion of genomic predicted breeding values](#)
Cuyabano, B.C.D.; Boichard, D.; Gondro, C.
- 14:45 [Model building pipeline to maximize the accuracy of breeding values prediction](#)
Jenko, J.; Nordbø, Ø.
- 15:00 [Genomic prediction in multi-breed Irish beef cattle population using a breed origin of alleles model](#)
Guillenea, A.; Lund, M.S.; Evans, R.; Karaman, E.
- 15:15 [Breed-origin-of-alleles approach using summary statistics for multi-breed genomic prediction in dairy cattle](#)
Clasen, J.B.; Fikse, W.F.; Su, G.; Karaman, E.

Session 26.

Challenges – Understanding and utilizing genetic diversity (2)

Room: Jurriaanse Zaal

Chair: Mirte Bosse, Beatriz Villanueva, Tom Druet

- 13:30 [Understanding and utilizing genetic diversity in Dual-Purpose Blue: genome-wide association for type traits](#)
Gengler, N.; Wilmot, H.; Vanderick, S.; Atashi, H.
- 13:32 [Genetic background of productive and adaptive features in the West African indigenous cattle breeds in Benin](#)
Vanvanhossou, S.F.U.; Yin, T.; Giambra, I.J.; Bruegemann, K.; Dossa, L.H.; Koenig, S.
- 13:34 [Genetic diversity and population structure of Slovenian local breed Drežnica goat](#)
Pogorevc, N.; Simčič, M.; Khayatzaadeh, N.; Sölkner, J.; Berger, B.; Bojkovski, D.; Zorc, M.; Dovč, P.; Medugorac, I.; Horvat, S.
- 13:36 [Genetic architecture of a composite beef cattle population](#)
Hay, E.A.; Toghiani, S.; Roberts, A.J.; Paim, T.; Kuehn, L.A.; Blackburn, H.D.
- 13:38 [Variation in patterns of recombination result in genetic variation in intrachromosomal shuffling in the domestic pig](#)
Brekke, C.; Johnston, S.E.; Gjuvslund, A.B.; Berg, P.
- 13:40 [Identification of runs of homozygosity islands and functional analysis for Caqueteño Creole cattle](#)
Toro-Ospina, A.M.; Silva, J.A.I.I.V.; Schettini, G.P.; Vallejo, V.H.; Ortiz, E.G.
- 13:42 [Candidate genes related to signatures of selection for body weight and harvest length in American mink](#)
Do, D.N.; Karimi, K.; Hu, G.; Miar, Y.
- 13:44 Discussion
- 13:45 [Maintenance of genetic diversity in subdivided populations using different genomic coancestry matrices](#)
Morales-González, E.; Villanueva, B.; Toro, M.Á.; Fernández, J.
- 14:00 [Long-term changes in genetic mean and genic variance and underlying allele frequencies in breeding programmes](#)
De Oliveira Junior, G.A.; Spehar, M.; Schenkel, F.S.; Baes, C.F.; Gorjanc, G.
- 14:15 [The long-term effects of genomic selection: allele frequency changes and fixation of loci](#)
Wientjes, Y.C.J.; Bijma, P.; Van Den Heuvel, J.; Zwaan, B.J.; Vitezica, Z.G.; Calus, M.P.L.
- 14:30 [The effect of recombination rate on genomic selection in simulation](#)
Johnsson, M.; Johansson, A.M.; Klingström, T.; Rius-Vilarrasa, E.
- 14:45 [Fine-scale study of meiotic recombination in cattle](#)
Oget-Ebrad, C.; Moreira, G.C.M.; Karim, L.; Coppieters, W.; Charlier, C.; Georges, M.; Druet, T.
- 15:00 [Sex differences in recombination maps are associated with differential hotspot usage in sheep](#)
Vassilief, H.; Id Bella, M.; Hazard, D.; Tortereau, F.; Faraut, T.; Johnston, S.E.; Servin, B.
- 15:15 [Is it possible to differentiate meat products of a local breed from those of its sister breed based on genotypes?](#)
Wilmot, H.; Glorieux, G.; Hubin, X.; Gengler, N.

Session 27.

Novel traits: Health and well-being (1)

Room: Van Cappellen Zaal

Chair: Jan ten Napel, Rachel Rupp, Georg Thaller, Bjorg Heringstad

- 13:30 [Resilience indicators based on individual feed intake from a high-health swine nucleus](#)
Bierman, C.D.; Kemp, R.A.; Dekkers, J.C.M.

- 13:32 [Comparison of milk yield based resilience indicators across dairy cattle breeds](#)
Bonekamp, G.; Poppe, M.; Ten Napel, J.; Kamphuis, C.; De Haas, Y.; Adriaens, I.
- 13:34 [Genotype-by-environment interactions for health traits across productivity level or health status of herds in Normandie](#)
Aguerre, S.; Vinet, A.; Mattalia, S.
- 13:36 [In search of a new tool for phenotyping tick resistance in cattle](#)
Matika, O.; Foster, S.; Githaka, N.; Mwendia, C.; Brown, H.; Watson, K.; Djikeng, A.; Birkett, M.
- 13:38 [Lameness in Genomic Evaluation for Foot and Claw disorders in Czech Holstein cows](#)
Zavadilová, L.; Kašná, E.; Krupová, Z.
- 13:40 [The lasting effect of udder inflammation on milk lactose content in dairy cows](#)
Costa, A.; Bovenhuis, H.; Egger-Danner, C.; Fuerst-Waltl, B.; Penasa, M.
- 13:42 [Estimation of genetic parameters for milk-related traits derived from automatic milking systems in Holstein cattle](#)
Gloria, L.S.; Boerman, J.P.; Pedrosa, V.B.; Chen, S.Y.; Montes Gonzalez, M.E.; Doucette, J.S.; Brito, L.F.
- 13:44 [Identification of genome regions and promising candidate genes linked to innate immune capacity on young Holstein calves](#)
Martin, P.; Fresco, S.; Jouneau, L.; Taussat, S.; Vinet, A.; Lefebvre, R.; Descamps, D.; Ferret, C.; Chottin, C.; Pietralunga, V.; Pezier, T.; Lacroix-Lamandé, S.; Boussaha, M.; Barbey, S.; Denizot, V.; Boichard, D.; Riffault, S.; Laurent, F.
- 13:46 [Assessment of miRNAs in plasma and leucocytes as potential biomarkers for rumen health in cows fed forage and high-grain](#)
Ojo, O.E.; Pacifico, C.; Johanns, S.; Ricci, S.; Rivera-Chacon, R.; Sener-Aydemir, A.; Castillo-Lopez, E.; Reisinger, N.; Zebeli, Q.; Kreuzer-Redmer, S.
- 13:48 [Variance component estimation of longitudinal alpha diversity metrics of the ocular microbiome in preweaned beef cattle](#)
Lakamp, A.D.; Neujahr, A.C.; Hille, M.M.; Loy, J.D.; Fernando, S.C.; Spangler, M.L.
- 13:50 [Gene expression patterns observed from the skin of selected cattle breeds infested with *Amblyomma hebraeum* ticks](#)
Letuka, M.; Wragg, D.; Bester-Van Der Merwe, A.; Dzama, K.; Nesengani, L.T.; Matika, O.; Dube, B.; Mapholi, N.O.
- 13:52 [Combined effect of genetics and gut microbiota on variations in vaccine response in hens](#)
Lecoeur, A.; Blanc, F.; Gourichon, D.; Bruneau, N.; Burlot, T.; Calenge, F.; Pinard-Van Der Laan, M.H.
- 13:54 Discussion
- 14:00 [Resilience indicators based on daily milk yield data for genetic selection in dairy cattle](#)
Poppe, M.; Mulder, H.A.; Hogeveen, H.; Kamphuis, C.; Bonekamp, G.; Van Pelt, M.L.; Mullaart, E.; Veerkamp, R.F.
- 14:15 [Genetic evaluation of heat tolerance in Italian Holstein breed](#)
Finocchiato, R.; Galluzzo, F.; Van Kaam, J.B.C.H.M.; Marusi, M.; Cassandro, M.
- 14:30 [Inferring genetic parameters for prenatal heat stress effects on calf diseases and cow productivity](#)
Yin, T.; Halli, K.; Vanvanhossou, S.F.; Bohlouli, M.; König, S.
- 14:45 [A genetic evaluation for calf health: preliminary analysis](#)
Lynch, C.; Schenkel, F.S.; Houlahan, K.; Van Staaveren, N.; Miglior, F.; Baes, C.F.
- 15:00 [Development of a single step genomic evaluation of health traits and relationships with dairy traits in French Holsteins](#)
Leclerc, H.; Barbat-Leterrier, A.; Vallée, R.; Guillaume, F.; Manciaux, L.; Davière, J.-B.; Philippe, M.
- 15:15 [Genetic selection for reduced susceptibility to subclinical ketosis using mid-infrared predicted traits](#)
Köck, A.; Dale, L.M.; Werner, A.; Mayerhofer, M.; Auer, F.J.; Egger-Danner, C.

Session 28.

Epigenetics, structural variants and exploiting transcriptome (1)

Room: Eduard Flipse Zaal

Chair: Ole Madsen, Jens Vanselow, Oscar Gonzalez, Christa Kühn

- 13:30 [A functional copy number gain at indicine cattle footprint modulates actin-myosin and immune response genes in muscle](#)
Da Silva, V.H.; Afonso, J.; Morosini, N.S.; Da Veiga, F.C.; Cesar, A.S.M.; Silva-Vignato, B.; Mourão, G.B.; Neto, A.Z.; Regitano, L.C.A.; Coutinho, L.L.
- 13:32 [Functional SNPs and INDELs within regulatory elements associated with mastitis in Holstein cow using -OMICs technologies](#)
Asselstine, V.; Medrano, J.F.; Stothard, P.; Miglior, F.; Karrow, N.A.; Baes, C.F.; Schenkel, F.S.; Cánovas, A.
- 13:34 [Allele specific expression as an indication of ploidy in pig IPECJ2 and chicken SL-29 cell lines](#)
De Vos, J.; Crooijmans, R.P.M.A.; Derks, M.F.L.; Kloet, S.L.; Groenen, M.A.M.; Madsen, O.
- 13:36 [Segregation of the structural variant responds for mastitis resistance in re-sequencing Nordic Holstein animals](#)
Cai, Z.; Sahana, G.
- 13:38 [Rare CNVs in the bovine genome are not captured well by 50K density genotyping array SNPs](#)
Lee, Y.L.; Bosse, M.; Coppieters, W.; Veerkamp, R.K.; Karim, L.; Oget-Ebrad, C.; Druet, T.; Groenen, M.A.M.; Georges, M.; Bouwman, A.C.; Charlier, C.
- 13:40 [Genome-wide DNA methylation of Gonad in sex-biased Zebrafish families](#)
Hosseini, S.; Trakooljul, N.; Hirschfeld, M.; Wimmers, K.; Tetens, J.; Sharifi, A.R.; Brenig, B.
- 13:42 Discussion
- 13:45 [An approach to study the association between the blood cell methylome with feed efficiency traits](#)
López-Catalina, A.; Bach, A.; Gutiérrez-Rivas, M.; Ramón Peiró-Pastor, R.; González-Recio, Ó.
- 14:00 [Multi-dimensional functional annotation of bovine genome for the BovReg project](#)
Moreira, G.C.M.; Dupont, S.; Becker, D.; Salavati, M.; Clark, R.; Clark, E.L.; Plastow, G.; Kühn, C.; Charlier, C.
- 14:15 [European project AQUA-FAANG: the epigenetic landscape of the Atlantic salmon; focus on liver tissue](#)
Baudement, M.-O.; Gillard, G.B.; Podgorniak, T.; Grønvold, L.; Lien, S.; Kent, M.P.
- 14:30 [Integration of methylome and transcriptome profiles reveals candidate biomarkers for *S.uberis*-subclinical mastitis](#)
Wang, M.Q.
- 14:45 [eQTL mapping in Brown Swiss bulls to identify variants associated with male fertility](#)
Mapel, X.M.; Hiltbold, M.; Lloret-Villas, A.; Pausch, H.
- 15:00 [Bioinformatics workflow for the detection of eQTL in the cattle genome using Nextflow DSL2](#)
Chitneedi, P.K.; Hadlich, F.; Kuehn, C.
- 15:15 [Extensive functional genomics information from early developmental time points for pig and chicken](#)
Acloque, H.; Harrison, P.W.; Lakhal, W.; Martin, F.; Archibald, A.L.; Davey, M.; Djebali, S.; Foissac, S.; Guizard, S.; Guyomar, C.; Kuo, R.; Kurylo, C.; Madsen, O.; Miedzinska, K.; Smith, J.; Sokolov, A.; De Vos, J.; Giuffra, E.; Watson, M.

Session 29.

Caprine/Ovine (2)

Room: Willem Burger Zaal

Chair: Jan ten Napel, Joanne Conington, Daniel Brown, Nicolas Gengler

- 13:30 [Six years of genomic selection have increased the genetic gain in French dairy sheep](#)
Astruc, J.M.; Lagriffoul, G.; Legarra, A.; Buisson, D.

- 13:32 [Cross-validation of single-step genetic evaluation in U.S. Katahdin sheep](#)
McMillan, A.J.; Brown, D.J.; Burke, J.M.; Morgan, J.L.; Lewis, R.M.
- 13:34 [Partitioning of genetic trends by flock and gender in Istrian sheep breed](#)
Špehar, M.; Ramljak, J.; Poslon, V.; Kasap, A.
- 13:36 [Comparison of GEBV accuracies predicted using the pedigree matrix of female and male potential reference populations](#)
Carta, A.; Usai, M.G.; Casu, S.; Salaris, S.
- 13:38 [Quantification of the effect of incomplete reproduction data on the accuracy of selection](#)
Olivier, W.J.
- 13:40 [Using random regression models to model growth in sheep with irregular data](#)
Mutch, E.; Mrode, R.; Coffey, M.; Simm, G.
- 13:42 [Impact of the order of polynomials in random regression model on the accuracy of genetic evaluation for weight traits](#)
Paneru, U.; Brown, D.J.; Moghaddar, N.; Van Der Werf, J.H.J.
- 13:44 [Estimation of linkage disequilibrium in Pag and Istrian sheep breed: towards genomic optimum contribution selection](#)
Kasap, A.; Ramljak, J.; Špehar, M.
- 13:46 [Genome-wide association study for milk composition traits of Canadian Alpine and Saanen goats](#)
Massender, E.; Oliveira, H.R.; Brito, L.F.; Maignel, L.; Jafarikia, M.; Baes, C.F.; Sullivan, B.; Schenkel, F.S.
- 13:48 Discussion
- 14:00 [Evaluating performance of Suffolk, Columbia, and crossbred lambs at birth and weaning](#)
Lewis, R.M.; Vargas Jurado, N.; Brown, D.J.; Notter, D.R.; Taylor, J.B.
- 14:15 [Genetic selection for sensory eating quality of lamb using consumer assessments](#)
Guy, S.Z.Y.; Mortimer, S.I.; Pannier, L.; McGilchrist, P.; Brown, D.J.; Pethick, D.; Swan, A.A.
- 14:30 [Genetic characterization and connectedness of dairy goats in Canada, France, Italy and Switzerland](#)
Teissier, M.; Brito, L.F.; Schenkel, F.; Bruni, G.; Fresi, P.; Bapst, B.; Robert-Granié, C.; Larroque, H.
- 14:45 [Value of data from ram breeding flocks as an industry reference population for Australian sheep](#)
Alexandri, P.; Walkom, S.F.; Swan, A.A.; Van Der Werf, J.H.J.; Brown, D.J.
- 15:00 [Pairwise principal component analysis of African goat breeds identifies loci involved in meat and/or milk production](#)
Rahmatalla, S.A.; Arends, D.; Tarekegn, G.M.; Onzima, R.; Brockmann, G.A.
- 15:15 [Linking genetic merit to phenotypes: a validation of the terminal and replacement Irish sheep breeding objectives](#)
Pabiou, T.; McDermott, K.; Bohan, A.; Farrell, L.J.; Mc Hugh, N.

Session 30.

Methods and Tools: Software and Computing Strategies (1)

Room: Grote Zaal

Chair: Jeremie Vandenplas, Daniela Lourenco, Ismo Strandén, Mehdi Sargolzaei

- 16:00 [Subsetting orthogonal data augmentation for fast parallel implementation of Bayesian models for whole-genome analyses](#)
Chen, L.; Plastow, G.
- 16:02 [A simulator to evaluate gene editing assisted selection programs](#)
Yu, X.-J.; Dagnachew, B.S.; Meuwissen, T.H.E.

- 16:04 [A database structural improvement for efficient trait variation curation in Animal QTLdb and CorrDB](#)
Hu, Z.-L.; Park, C.A.; Reecy, J.M.
- 16:06 [Efficient algorithms to identify duplicated genotypes in large datasets](#)
Ferdosi, M.H.; Masoodi, S.; Khansefid, M.
- 16:08 [Genotype error correction and the accurate identification of recombination sites](#)
Hindle, M.M.; Kranis, A.
- 16:10 [A phasing algorithm targeted at dairy cattle populations having genotyped ancestors with many genotyped offspring](#)
Dahl, M.; Christensen, O.F.
- 16:12 Discussion
- 16:15 [Recent advances and future needs in genotype imputation](#)
Vanraden, P.M.; Null, D.J.; Al-Khudhair, A.S.
- 16:45 [Imputation of low coverage sequence data by utilization of pre-phased reads and HBimpute](#)
Pook, T.; Geibel, J.
- 17:00 [Quantitative trait simulation using MeSCoT software](#)
Milkevych, V.; Karaman, E.; Sahana, G.; Janss, L.; Cai, Z.; Lund, M.S.
- 17:15 [SIRE 2.0: a novel software tool to estimate host genetic variation in infectious disease transmission](#)
Pooley, C.M.; Marion, G.; Doeschl-Wilson, A.
- 17:30 [iVPSV: an intuitive visualisation platform for structural variation data](#)
Jung, H.; Jeon, B.; Hayes, B.; Ross, E.
- 17:45 [A variational Bayes method for genomic prediction increases accuracy and computing speed](#)
Cheng, J.; Cheng, H.; Fernando, R.; Maltecca, C.; Ma, L.; Dekkers, J.; Jiang, J.

Session 31. Young scientist career development (with drinks EFFAB/FABRE-TP till 19.30)

Room: Jurriaanse Zaal

Chair: Biaty Raymond, Jo Newton, Hugo Toledo Alvarado, Marta Godia

- 16:00 [History and author analysis of the World Congresses on Genetics Applied to Livestock Production](#)
Van Eenennaam, A.L.; Hermes, S.
- 16:15 [What industry needs from an animal breeding graduate](#)
Byrne, T.J.; Fennessy, P.F.; Amer, P.R.
- 16:30 [Young scientist career development: a global discussion on challenges, opportunities and solutions](#)
Newton, J.E.; Gòdia, M.; Biaty, R.; Toledo-Alvarado, M.H.O.
- 17:30 [Young scientist career development \(with EFFAB/FABRE-TP till 19.30\)](#)
Granados Chapatte, A.

Session 32.

Novel traits: Health and well-being (2)

Room: Van Cappellen Zaal

Chair: Jan ten Napel, Rachel Rupp, Georg Thaller, Bjorg Heringstad

- 16:00 [Heritability of scurs in Wagyu and tropically adapted composite beef cattle](#)
Moser, G.; Kelly, M.J.
- 16:02 [Genetic parameters for social hierarchy of Nellore cattle using data from electronic feeding system](#)
Valente, J.P.S.; Deniz, M.; De Sousa, K.T.; Canesin, R.C.; Bonilha, S.F.M.; Mercadante, M.E.Z.; Dias, L.T.

- 16:04 [Pigs' weighing order stability is favourably linked with tail biting and production: a new proxy for social structure?](#)
Gorssen, W.; Meyermans, R.; Janssens, S.; Buys, N.
- 16:06 [Application of machine learning algorithms to develop behavioural and stress phenotypes for sheep](#)
Keshavarzi, H.; Campbell, D.L.M.; Lee, C.
- 16:08 [Heritability of social interactions in dairy cattle](#)
Rönnegård, L.; Hansson, I.; Fikse, W.F.
- 16:10 [Uncertainty about the social network among dairy cows impairs estimation of indirect genetic effects](#)
Fikse, W.F.; Hansson, I.; Rönnegård, L.
- 16:12 [Genetic and phenotypic variation and consistency of cow's preference and circadian use of robotic milking units](#)
Løvendahl, P.; Buitenhuis, A.J.
- 16:14 [Genetic and environmental influences on maternal calving difficulty in South African Holstein cattle](#)
Mkhize, N.E.; Mapholi, N.O.; Dube, B.; Madilindi, M.A.; Matika, O.; Banga, C.B.
- 16:16 [Genetic evaluation of gestation length in Italian Holstein breed](#)
Galluzzo, F.; Van Kaam, J.B.C.H.M.; Finocchiaro, R.; Ferrari, V.; Marusi, M.; Cassandro, M.
- 16:18 [Genetic evaluation of cystic ovarian disease in Czech Holstein cattle](#)
Kašná, E.; Zavadilová, L.; Krupová, Z.
- 16:20 [Entropy of broiler activity: individual variation and consistency](#)
Van Der Sluis, M.; Asher, L.; Rodenburg, T.B.; De Haas, Y.; De Klerk, B.; Ellen, E.D.
- 16:22 Discussion
- 16:30 [Laying hens tweet: they also lead and follow! – implications for genetic selection against gregarious nesting](#)
Bécot, L.; Bédère, N.; Burlot, T.; Le Roy, P.
- 16:45 [Analysis of social behaviors in large groups: simulation and genetic evaluation](#)
Wang, Z.; Doekes, H.P.; Bijma, P.
- 17:00 [Divergent genetic selections for social attractiveness or tolerance toward humans in sheep](#)
Hazard, D.; Delval, E.; Douls, S.; Durand, C.; Bonnafé, G.; Foulquié, D.; Marcon, D.; Allain, C.; Parisot, S.; Boissy, A.
- 17:15 [Genetic parameters of novel behaviour traits derived from social network analysis in pigs](#)
Agha, S.; Foister, S.; Roehe, R.; Turner, S.P.; Doeschl-Wilson, A.
- 17:30 [Genetic parameter estimation of various body temperature and respiration rate in maternal-line pigs under heat stress](#)
Wen, H.; Johnson, J.; Freitas, P.; Maskal, J.; Byrd, M.; Tiezzi, F.; Huang, Y.; Schinckel, A.; Brito, L.
- 17:45 [Genetics of body weight and length of Large White piglets and relationship to maternal performance](#)
Canario, L.; Billon, Y.; Hébrard, W.; Demars, J.

Session 33. **Epigenetics, structural variants and exploiting transcriptome (2)**

Room: Eduard Flipse Zaal

Chair: Christina Rochus, Paul Stothard, Zhao Guiping, Martijn Derks, Emily Clark

- 16:00 [Demonstrating the use of a mammalian methylation microarray for epigenome wide association studies in livestock](#)
Caulton, A.; Dodds, K.G.; McRae, K.M.; Couldrey, C.; Horvath, S.; Clarke, S.M.
- 16:02 [Regulatory QTL and exon expression QTL in the mammary gland of dairy cows](#)
Prowse-Wilkins, C.; Lopdell, T.; Xiang, R.; Vander Jagt, C.; Littlejohn, M.; Chamberlain, A.; Goddard, M.

- 16:04 [H3K27me3 predicted regulation of gene expression linked to calcium quantification in Nelore muscle](#)
Afonso, J.A.
- 16:06 [Comparative analysis of CAGE-Seq across tissues reveals transcription start sites unique to cattle](#)
Salavati, M.; Clark, R.; Becker, D.; Kühn, C.; Plastow, G.; Moreira, G.C.M.; Charlier, C.; Clark, E.L.
- 16:08 [Transcriptomic characterisation of claw horn disruption lesions in the peripheral blood leucocytes of dairy cattle](#)
Dai, X.; Xai, D.; Griffiths, B.E.; Anagnostopoulos, A.; Barden, M.; Li, B.; Coffey, M.; Werling, D.; Oikonomou, G.; Banos, G.; Psifidi, A.
- 16:10 [Evidences of INFt and ISG gene expression in leukocytes of pregnant hair sheep ewes from a thermal stress experiment](#)
Gomez-Guzman, J.A.; Vazquez-Armijo, J.F.; Lara-Rivera, A.L.; Sifuentes-Rincon, A.M.; Ramirez-Valverde, R.; Nuñez-Dominguez, R.; Martinez-Gonzalez, J.C.; Arellano-Vera, W.; Parra-Bracamonte, G.M.
- 16:12 [Identification of differentially expressed transcription factors in Brangus skin infested with *Rhipicephalus australis*](#)
Mantilla Valdivieso, E.; Nguyen, L.; Ross, E.; Raza, A.; Hayes, B.; James, P.; Jonsson, N.; Tabor, A.
- 16:14 Discussion
- 16:15 [Unravelling regulatory variants affecting gene expression in four porcine tissues](#)
Gòdia, M.; Derks, M.F.L.; Harlizius, B.; Madsen, O.; Groenen, M.A.M.
- 16:30 [Unravelling the transcriptomic control of growth traits in sheep during prenatal and postnatal development](#)
Woolley, S.A.; Salavati, M.; Clark, E.L.
- 16:45 [Large-scale cis-eQTL analysis of gene expression in blood of young healthy pigs using PigGTEx](#)
Kramer, L.M.; Teng, J.; Lim, K.S.; Gao, Y.; Yin, H.; Bai, L.; Liu, G.E.; Zhang, Z.; Fang, L.; Plastow, G.S.; Tuggle, C.K.; Dekkers, J.C.M.
- 17:00 [Unravelling the structural variability in chicken genomes by long-read sequencing](#)
Geibel, J.; Schauer, J.; Weigend, A.; Reimer, C.; De Koning, D.-J.; Simianer, H.; Weigend, S.
- 17:15 [Detection and characterisation of *de novo* structural variants in pigs](#)
Steensma, M.; Lee, Y.L.; Bouwman, A.C.; Pita Barros, C.; Derks, M.F.L.; Bink, M.C.A.M.; Harlizius, B.; Huisman, A.E.; Crooijmans, R.P.M.A.; Groenen, M.A.M.; Mulder, H.A.; Rochus, C.M.
- 17:30 [Efficient detection of interchromosomal rearrangements in Holstein bulls using large SNP datasets](#)
Jourdain, J.; Pinton, A.; Barasc, H.; Barbat, A.; Hozé, C.; Philippe, M.; Boichard, D.; Capitan, A.
- 17:45 [A pan-genome of commercial pig breeds](#)
Derks, M.F.L.; Boshove, A.; Harlizius, B.; Sell-Kubiak, E.; Lopes, M.S.; Grindflek, E.; Knol, E.; Groenen, M.A.M.; Gjuvsland, A.B.

Session 34.

Caprine/Ovine (3)

Room: Willem Burger Zaal

Chair: Jan ten Napel, Joanne Conington, Daniel Brown, Nicolas Gengler

- 16:00 [Influence of a nutritional restriction in dairy ewe lambs on the response to a later inflammatory intramammary challenge](#)
Pelayo, R.; Marina, H.; Suarez-Vega, A.; Esteban-Blanco, C.; Foucras, G.; Arranz, J.J.; Gutierrez-Gil, B.
- 16:02 [Effects of breeding for scrapie resistance in Bavarian sheep breeding populations](#)
Buitkamp, J.; Semmer, J.
- 16:04 [Options for the selective breeding for resistance to gastro-intestinal nematodes of Sarda breed sheep](#)
Salaris, S.; Casu, S.; Usai, M.G.; Scala, A.; Carta, A.

- 16:06 [Investigation of the Scrapie haplotypes in the South African Merino population](#)
Reding, J.J.; Mostert, B.E.
- 16:08 [Toward a genetic evaluation for functional longevity in French dairy sheep breeds](#)
Buisson, D.; Astruc, J.M.; Doutre, L.; Palhière, I.
- 16:10 [Maturity, a new indicator to improve longevity of Saanen dairy goats in France](#)
Arnal, M.A.; Palhière, I.P.; Clément, V.C.
- 16:12 [The relevance of spermatozoal RNA and quality in livestock production](#)
Pant, S.D.
- 16:14 [Exploring the vomeronasal organ transcriptome in Rasa Aragonesa rams with different sexual behaviour](#)
Lakhssassi, K.; Ureña, I.; Marín, B.; Sarto, M.P.; Lahoz, B.; Alabart, J.L.; Folch, J.; Serrano, M.; Calvo, J.H.
- 16:16 [Elucidating transcriptomic differences in perirenal fat between male and female suckling lambs](#)
Alonso-García, M.; Arranz, J.J.; Marina, H.; Pelayo, R.; Esteban-Blanco, C.; Gutierrez-Gil, B.; Suarez-Vega, A.
- 16:18 [Measures of diversity based on autosomal and sex chromosomes of Valachian sheep](#)
Mészáros, M.; Moravčíková, N.; Mészáros, G.; Pavlík, I.; Margetin, M.; Kasarda, R.
- 16:20 Discussion
- 16:30 [The Data Quality Score: objective assessment of data quality for Australian sheep breeders](#)
Brown, D.J.; McCrabb, E.J.; Bradley, P.E.; Rose, I.J.; Banks, R.G.; Guy, S.Z.Y.
- 16:45 [Impact of genotypic information on genetic evaluation accuracy for mastitis and footrot in the UK Texel Sheep](#)
Kaseja, K.; Mucha, S.; Smith, E.; Yates, J.; Banos, G.; Conington, J.
- 17:00 [Characterization of homozygous haplotype deficiency compromising fertility traits in Manech Tête Rousse dairy sheep](#)
Ben Braiek, M.; Moreno-romieux, C.; Hozé, C.; Astruc, J.-M.; Fabre, S.
- 17:15 [Genetic analysis of colostrum and passive immune transfer in divergent goat lines selected for functional longevity](#)
Wicki, M.; Huau, C.; Fossier, T.; Rupp, R.
- 17:30 [Selection signatures in South African indigenous sheep using the HAPFLK approach](#)
Malan, I.N.; Cloete, S.W.P.; Molotsi, A.H.
- 17:45 [An across-flock genetic analysis of components of reproduction in four South African Merino resource flocks](#)
Nel, C.L.; Swan, A.A.; Dzama, K.; Olivier, W.J.; Snyman, M.A.; Cloete, S.W.P.

Session 35. Plenary 3: Discussion delivering genetic progress around the world

Room: Grote Zaal

Chair: Johan van Arendonk

- 08:30 [Panel with industry representatives, delivering genetic progress around the world](#)
Van Arendonk, J.A.M.

Session 36. Methods and Tools: Software and Computing Strategies (2)

Room: Grote Zaal

Chair: Jeremie Vandenplas, Daniela Lourenco, Ismo Strandén, Mehdi Sargolzaei

- 10:00 [Additions to the BGLR R-package: a new function for biobank size data and Bayesian multivariate models](#)
Perez-Rodriguez, P.; De Los Campos, G.

- 10:02 [SFSI: A package to solve penalized selection indices and sparse genomic prediction](#)
Lopez-Cruz, M.A.; De Los Campos, G.; Valente, B.; Chen, C.Y.; Herring, W.; Grueneberg, A.
- 10:04 [INTERGEN: An efficient and flexible tool for large-scale genetic evaluation of complex animal and plant populations](#)
Junqueira, V.S.; Campos, G.S.; Cardoso, F.F.
- 10:06 [MiXBLUP 3.0 - Software for large genomic evaluations in animal breeding programs](#)
Vandenplas, J.; Veerkamp, R.F.; Calus, M.P.L.; Lidauer, M.; Strandén, I.; Taskinen, M.; Schrauf, M.; Ten Napel, J.
- 10:08 [From raw sensor and automated data to genetic evaluation and validation in the cloud](#)
Schokker, D.; Athanasiadis, I.N.; Poppe, M.; Ten Napel, J.; Kamphuis, C.; Veerkamp, R.F.
- 10:10 [Indirect genomic prediction reduces computational costs in large-scale single-step evaluations](#)
Strandén, I.; Ten Napel, J.; Veerkamp, R.F.; Evans, R.; Naderi, S.; Mäntysaari, E.A.; Vandenplas, J.
- 16:12 Discussion
- 10:15 [Accounting for trait-specific genomic and residual polygenic covariances in multivariate single-step genomic evaluation](#)
Meyer, K.
- 10:30 [Avoiding double counting in genomic reliability calculations](#)
Ben Zaabza, H.; Taskinen, M.; Mäntysaari, E.A.; Pitkänen, T.; Aamand, G.P.; Strandén, I.
- 10:45 [JWAS version 2: leveraging biological information and high-throughput phenotypes into genomic prediction and association](#)
Cheng, H.; Fernando, R.; Garrick, D.; Zhao, T.; Qu, J.
- 11:00 [ACCF90GS2: software for fast approximation of reliabilities of estimated breeding values in single-step GBLUP](#)
Bermann, M.; Lourenco, D.; Cesarani, A.; Misztal, I.
- 11:15 [One for all: LMT – the linear models toolbox](#)
Boerner, V.
- 11:30 [Recent updates in the BLUPF90 software suite](#)
Lourenco, D.; Tsuruta, S.; Aguilar, I.; Masuda, Y.; Bermann, M.; Legarra, A.; Misztal, I.
- 11:45 [From data to genomic breeding values with the MiX99 software suite](#)
Pitkänen, T.J.; Gao, H.; Taskinen, M.; Mäntysaari, E.A.; Lidauer, M.H.; Strandén, I.

Session 37.

Society – Genetics in the tropics

Room: Eduard Flipse Zaal

Chair: Richard Crooijmans, Lucia Galvão de Albuquerque, Tadel Dessie

- 10:00 [Providing genetics for the dairy industry in the tropics - the brazilian dairy gir breeding program](#)
Panetto, J.C.C.; Silva, M.V.G.B.; Machado, M.A.; Verneque, R.S.; Fernandes, A.R.; Machado, C.H.C.; Martins, M.F.; Faza, D.R.L.R.; Borges, C.A.V.; Ventura, H.T.; Pereira, M.A.; Oliveira, J.C.; Glatzl Junior, L.A.; Garcia, A.O.; Leandro, F.D.
- 10:02 [Modelling phenotypic plasticity relative to a temperature humidity index as an indicator of adaptability in beef cattle](#)
Shaffer, W.; Moreno, J.A.H.; Bello, N.M.; Weaver, R.; Bormann, J.; Rolf, M.
- 10:04 [Differentiated genomic regions in the Afrikaner and Brahman cattle of South Africa reveal parallel adaptive mechanisms](#)
Mdyogolo, S.; MacNeil, M.D.; Neser, F.W.C.; Scholtz, M.M.; Makgahlela, M.L.
- 10:06 [Genomic analysis of milk yield and heat tolerance in small holder dairy system of sub-Saharan Africa](#)
Ekine-Dzivenu, C.C.; Mrode, R.; Oloo, R.D.; Komwihangilo, D.; Lyatuu, E.; Msuta, G.; Ojango, J.M.; Okeyo, A.M.

- 10:08 [Genetic analysis of traits needed to optimize improvement in beef cow-calf efficiency in Afrikaner cattle](#)
Scholtz, M.M.; MacNeil, M.D.; Chadyiwa, M.C.; Neser, F.W.C.
- 10:10 [Genetic diversity of the Cameroon Blackbelly sheep, an indigenous sheep from West Africa](#)
Wiener, P.; Salavati, M.; Djikeng, A.; Van Tassell, C.P.; Rosen, B.D.; Spangler, G.L.; Simo, G.; Tanya, V.; Meutchieye, F.; Clark, E.L.
- 10:12 [Phenotypic characterisation of African chickens raised in semi-scavenging conditions](#)
Morris, K.M.; Sutton, K.; Girma, M.; Esatu, W.; Dessie, T.; Vervelde, L.; Psifidi, A.; Hanotte, O.; Banos, G.
- 10:14 [Spatial modelling in genetic evaluation of South African Holstein cattle population](#)
Houaga, I.; Oliveira, T.O.; Lavrenčič, E.; Pocrnic, I.; Banga, C.B.; Gorjanc, G.
- 10:16 [Testing phenotypes for degree of resilience using fluctuations in milk yield of dairy cows in sub-Saharan Africa](#)
Oloo, R.D.; Ekine-Dzivenu, C.C.; Ojango, J.M.K.; Mrode, R.; Mwai, A.O.; Chagunda, M.G.G.
- 10:18 [Egg production and genetic parameters for Tanzanian local chickens](#)
Magwaba, T.; Mollel, E.; Mushi, J.R.; Walugembe, M.; Amuzu-Aweh, E.N.; Chiwanga, G.H.; Chouicha, N.; Msoffe, P.L.; Kelly, T.; Gallardo, R.A.; Zhou, H.; Wolc, A.; Lamont, R.J.; Muhairwa, A.P.; Dekkers, J.C.M.
- 16:20 Discussion
- 10:30 [Expanding the cattle reference graph genome](#)
Talenti, A.; Powell, J.; Wragg, D.; Paxton, E.; Chepkwony, M.; Miyunga, A.; Njeru, R.; Hemmink, J.D.; Fisch, A.; Ferreira, B.R.; Hammond, J.A.; Archibald, A.L.; Toye, P.; Connelley, T.; Morrison, L.; Prendergast, J.
- 10:45 [Genetic structure and diversity of Jersey dairy cattle in Rwanda](#)
Opoola, O.; Shumbusho, F.; Mrode, R.; Hambrook, D.; Chagunda, M.G.G.; Moran, D.; Djikeng, A.
- 11:00 [Estimation of breed admixture levels in Sri Lanka cattle and its relation to performance traits](#)
Spoelstra, M.; Sölkner, J.; Bovenhuis, H.; Babigumari, B.; Periasamy, K.; Dematawewa, C.M.B.
- 11:15 [Economic values for skin grade, days to market and number of hatchlings in the Australian saltwater crocodile industry](#)
Hermesch, S.; Isberg, S.R.
- 11:30 [Exploiting phenotypic plasticity in animal breeding](#)
Kebede, F.G.; Komen, H.; Dessie, T.; Hanotte, O.; Kemp, S.; Pita Barros, C.; Crooijmans, R.; Derks, M.; Alemu, S.W.; Bastiaansen, J.
- 11:45 [Whole genome sequencing reveals genetic diversity and heat-stress adaptation in Nigerian indigenous chickens](#)
Gheyas, A.A.; Rachman, M.; Bamidele, O.; Dessie, T.; Smith, J.; Hanotte, O.

Session 38. Challenges – Delivering genetic progress in systems around the world

Room: Jurriaanse Zaal

Chair: Johan van Arendonk, Karen Marshall, Ruiz Felipe

- 10:00 [Impact of industry effort to increase dairy heifer genomic testing in Australia](#)
Abdelsayed, M.; Axford, M.M.; Nieuwof, G.J.
- 10:02 [Weekly national dairy evaluations – a Vietnam-Australia collaboration](#)
Nieuwof, G.J.; Ong, L.T.
- 10:04 [The value proposition for using genomics to confirm parentage in Australian dairy systems](#)
Newton, J.E.; Axford, M.M.; Pryce, J.E.; Bullen, S.L.; Haile-Mariam, M.

16:06 Discussion

10:15 [Changes in genetic trends for dairy cattle in the U.S. since the implementation of genomic selection](#)
Guinan, F.L.; Wiggans, G.R.; Dürr, J.W.; Norman, H.D.; Cole, J.B.; Van Tassell, C.P.; Misztal, I.; Lourenco, D.

10:30 [Community based breeding programme for low input beef cattle production systems in the arid region of Argentina](#)
Munilla, S.; Tessi, J.M.; Maizon, D.O.

10:45 [A participatory approach to review and update the national breeding objectives for New Zealand dairy cattle](#)
Santos, B.F.S.; Jenkins, G.M.; Kok, J.; Stachowicz, K.; Amer, P.R.

11:00 [Genetic trends for carcass traits within breeds in a multi-breed evaluation](#)
Mulhall, S.A.; Sleator, R.D.; Evans, R.D.; Twomey, A.J.

11:15 [Improving growth performance for dual purpose chickens for challenging conditions in Africa](#)
Duijvesteijn, N.; Perrault, L.; Atikpakpe, R.; Garcia Martinez, N.; Renckly, J.; Arbeau, T.; Van Arendonk, J.A.M.

11:30 [Genomic Selection in the US: Where it has been and where it is going?](#)
Retallick, K.J.; Lu, D.; Garcia, A.; Miller, S.P.

11:45 [Efficient genetic progress for quantitative traits through genomic selection](#)
Tsuruta, S.; Lourenco, D.A.L.; Misztal, I.

Session 39.

Education

Room: Van Cappellen Zaal

Chair: Dieuwertje Lont, Gabor Meszaros, Ron Lewis

10:00 [Digital learning in postsecondary education: 30 transformational years](#)
Lindburg, J.J.

10:30 [A panel discussion: broadening learning by incorporating industry professionals in education](#)
Cole, J.B.; Mrode, R.A.; Olson, K.M.; Knap, P.

11:15 [Conducting a national beef cattle genetics outreach program in the USA](#)
Bullock, K.D.; Spangler, M.L.; Weaber, R.L.; Rowan, T.N.; Rolf, M.M.; Decker, J.E.; Loy, D.D.; Golden, B.L.; White, J.J.; Van Eenennaam, A.L.

11:30 [Breeding Lab: a successful industry-academia collaboration to provide MSc consultancy training](#)
Komen, J.; Van Arendonk, J.A.M.; Lont, D.E.

11:45 [How a group of Merino breeders increase the rate of genetic gain by 134% in five](#)
Granleese, T.; Van Der Werf, J.H.J.; Martin, S.J.

11:47 [YouTube applied to the education of genetics and genomics](#)
Mészáros, G.

11:49 [Creating a good learning and sharing environment for bioinformatics](#)
Klingström, T.; Ohlsson, J.I.

11:51 [European master in animal breeding and genetics \(EMABG\): A training for research, practical, and transversal skills](#)
Mészáros, G.; Berg, P.; Heams, T.; Komen, H.; Lont, D.; Simianer, H.; Sölkner, J.; Strandberg, E.; Tetens, J.

Room: Willem Burger Zaal

Chair: Renzo Bonifazi, Martino Cassandro, Fernando Cardoso

- 10:00 [Genetic prediction for growth traits in beef cattle using selected variants from imputed low-pass sequence data](#)
Russell, C.A.; Kuehn, L.A.; Snelling, W.M.; Spangler, M.L.
- 10:02 [Bos indicus genome percentage effects gene expression and differentially expressed genes in Brahman cattle whole blood](#)
Ross, E.M.; Nguyen, L.T.; Engle, B.N.; Chamberlain, A.J.; Kho, E.; Hayes, B.J.
- 10:04 [Effect of one copy of nt821 mutation in myostatin gene on ultrasound carcass traits in Senepol cattle](#)
Menezes, G.R.O.; Souza, C.B.; Lima, A.L.R.; Gondo, A.; Siqueira, F.; Egito, A.A.; Silva, L.N.; Fernandes Junior, J.A.; Torres Junior, R.A.A.
- 10:06 [Allelic diversity and effect of the intronic TBX20-191081 marker on temperament in beef cattle](#)
Del Real García, V.M.; Sifuentes Rincón, A.M.; Paredes Sánchez, F.A.; Ruiz De La Cruz, G.; Garza Brenner, E.; Parra Bracamonte, G.M.; Bernal Barragán, H.; Rodríguez Almeida, F.A.
- 10:08 [Innovative phenotyping strategies exploiting immune response to heat stress conditions](#)
Lemal, P.; Schroyen, M.; Gengler, N.
- 10:10 [Epistatic interaction networks affecting feed efficiency and methane emission in Nelore cattle](#)
Cardoso, T.F.; Bruscadin, J.J.; Diniz, W.J.S.; Banerjee, P.; Afonso, J.; Petrini, J.; Andrade, B.G.N.; Malheiros, J.M.; Porto, T.; Zerlotini, A.; Mourão, G.B.; Coutinho, L.L.; Regitano, L.C.A.
- 16:12 Discussion
- 10:15 [Host-genomically influenced ruminal microbial genes are temporally stable during the finishing phase in beef cattle](#)
Lima, J.; Martínez-Álvaro, M.; Mattock, J.; Auffret, M.D.; Duthie, C.-A.; Cleveland, M.A.; Dewhurst, R.J.; Watson, M.; Roehe, R.
- 10:30 [A hypomorphic mutation in the ATP2A1 gene increases muscle mass yet compromises meat quality of Belgian Blue cattle](#)
Rombouts, T.; Druet, T.; Gualdrón Duarte, J.L.; Ahariz, N.; Karim, K.; Coppieters, W.; De Smet, S.; Georges, M.; Charlier, C.
- 10:45 [Mitochondrial DNA copy number as a potential genetic indicator of growth and carcass traits in beef cattle](#)
Sanglard, L.P.; Kuehn, L.A.; Snelling, W.M.; Spangler, M.L.
- 11:00 [Genomic regions in Australian cattle associated with consumer satisfaction of beef](#)
Lynn, A.M.; McGilchrist, P.; Aliloo, H.; Van Der Werf, J.H.J.; Polkinghorne, R.; Clark, S.A.
- 11:15 [A genome-wide scan for signatures of selection in Hanwoo and Angus cattle using whole-genome sequence data](#)
Kim, H.J.; De Las Heras-Saldana, S.; Clark, S.; Van Der Werf, J.H.J.
- 11:30 [Genetic analyses reveal the genetic architecture of the thermotolerance – production complex in beef cattle](#)
Mateescu, R.G.; Rezende, F.M.; Sarlo Davila, K.M.; Nunez Andrade, A.N.; Hernandez, A.; Elzo, M.A.; Oltenacu, P.A.
- 11:45 [The effect of allele ancestry on hip height and body weight of tropical beef cattle](#)
Porto-Neto, L.R.; McWilliam, S.; Alexandre, P.A.; Fortes, M.R.S.; Reverter, A.

Session 41.

Lunch seminar: Illumina

Room: Van Weelde Zaal

Chair:

- 12:00 Lunchtime Satellite Symposium: From parentage to understanding the milk microbiome, the use of high throughput DNA technologies in the breeding and health of dairy cattle

Session 42.

Plenary 4

Room: Grote Zaal

Chair: Randy Borg

- 08:30 [Genetics and genomics of virus infections](#)
Koopmans, M.P.G.

Session 43.

Challenges – Across species and breed genomics genetics

Room: Jurriaanse Zaal

Chair: Irene van den Berg, Ben Hayes, Torsten Pook

- 10:00 [Application of haplotype relationship matrices for genomic prediction in purebred and crossbred cows](#)
Khansefid, M.; Ferdosi, M.H.; Goddard, M.E.; Haile-Mariam, M.; Schrooten, C.; De Jong, G.; O'Connor, E.; Daetwyler, H.D.; Pryce, J.E.; MacLeod, I.M.
- 10:02 [Bos Taurus and Bos Indicus reduced representation bisulfite sequencing comparison showed high epigenetic variability](#)
Capra, E.; Lazzari, B.; Milanesi, M.; Nogueira, G.D.P.; Garcia, J.F.; Ajmone Marsan, P.; Stella, A.
- 10:04 [Evaluating the use of genotype information for the prediction of breed composition in purebred and crossbred cattle](#)
Ryan, C.A.; Berry, D.P.; Pabiou, T.; Purfield, D.C.
- 10:06 [Genomic prediction using breed origin of alleles model accounting for probabilities in the assignment of the alleles](#)
Guillenea, A.; Su, G.; Lund, M.S.; Karaman, E.
- 10:08 [Making the most of genetic relationships between Iberian dairy sheep breeds](#)
Granado-Tajada, I.; Pineda-Quiroga, C.; Ugarte, E.; Serrano, M.; Jiménez, M.Á.; Marina, H.; Arranz, J.J.; Ramón, M.
- 10:10 [Online Mendelian inheritance in animals \(OMIA\) – future proofing of a globally used animal genetics knowledgebase](#)
Tammen, I.; Mather, M.; Li, Z.; Nothman, J.; Vanichkina, D.P.; Nicholas, F.W.
- 10:12 Discussion
- 10:15 [Predicting the purebred-crossbred genetic correlation from phenotype and genotype data of parental lines in pigs](#)
Duenk, P.; Wientjes, Y.C.J.; Bijma, P.; Lopes, M.S.; Calus, M.P.L.
- 10:30 [Multi-breed genomic predictions from commercial crossbred data](#)
Hayes, B.J.; Copley, J.; Dodd, E.; Ross, E.M.; Fordyce, G.
- 10:45 [Simultaneous mapping of quantitative trait loci in multiple subspecies using hybrid populations](#)
Warburton, C.L.; Costilla, R.C.; Engle, B.N.; Hayes, B.J.
- 11:00 [Strategies to find predictive variants that improve multi-breed genomic prediction in dairy cattle](#)
Van Den Berg, I.; Xiang, R.; Khansefid, M.; Goddard, M.E.; Pryce, J.E.; Prowse-Wilkins, C.P.; Chamberlain, A.J.; MacLeod, I.M.

- 11:30 [Impact of breed ancestry on the performance of crossbred dairy cattle](#)
Jaafar, M.A.; Heins, B.J.; Dechow, C.; Van Tassell, C.P.; Huson, H.J.
- 11:45 [DNA pooling is a cost effective method of including commercial crossbred data in selection of purebreds](#)
Aldridge, M.N.; Marjanovic, J.; Henshall, J.M.; De Klerk, B.; Peeters, K.; De Haas, Y.

Session 44. Challenges – Genetic control of infectious disease transmission and impact (1)

Room: Grote Zaal

Chair: Piter Bijma, Andrea Wilson, John McEwan

- 10:00 [Molecular mechanisms involved with influenza A nanovaccine immunogenicity in pigs](#)
Ibelli, A.M.G.; Peixoto, J.O.; Fernandes, L.T.; Haach, V.; Gava, D.; Bastos, A.P.; Fonseca, F.N.; Morés, M.A.Z.; Cantão, M.E.; Schaefer, R.; Ledur, M.C.
- 10:02 [Host variation in susceptibility to lumpy skin disease: gene expression analyses of experimentally infected cows](#)
Van Borm, S.; Klingström, T.; Niazi, A.; De Clercq, K.; Mostin, L.; Haegeman, A.; De Koning, D.J.
- 10:04 [Relationship between resistance to a *Pasteurella multocida* experimental infection and production traits in rabbits](#)
Garreau, H.; Lantier, F.; Bed'hom, B.; Guitton, E.; Helies, V.; Helloin, E.; Herbert, C.; Maupin, M.; Robert, R.; Gunia, M.
- 10:06 [Quantification of environmental management systems for U.S. Katahdin sheep producers](#)
Arisman, B.C.A.; Burke, J.M.B.; Morgan, J.L.M.; Lewis, R.M.L.
- 10:08 [Bias and heritability of the autocorrelation based on longitudinal data used as resilience indicator](#)
Mulder, H.A.
- 10:10 Discussion
- 10:15 [The possibilities of estimating relationships between traits with and without micro-genetic environmental sensitivity](#)
Madsen, M.D.; Van Der Werf, J.H.J.; Clark, S.
- 10:30 [Selective breeding for survival to *Vibrio harveyi* in European seabass is robust to different feeding environments](#)
Besson, M.; Morvezen, R.; Bestin, A.; François, Y.; Bajek, A.; Brunier, J.; Morin, T.; Vandeputte, M.; Dupont-Nivet, M.; Izquierdo, M.; Barkas, D.; Haffray, P.
- 10:45 [Can we prevent pathogen adaptation when breeding disease resistant livestock?](#)
Hulst, A.D.; Bijma, P.; De Jong, M.C.M.
- 11:00 [Indicators of disease resilience from complete blood count and *in vitro* immunoassays data from young-healthy pigs](#)
Bai, X.; Cheng, J.; Fortin, F.; Harding, J.C.S.; Dyck, M.K.; Dekkers, J.C.M.; Field, C.J.; Rogel-Gailard, C.; Blanc, F.; Plastow, G.S.
- 11:15 [Evidence of naturally occurring genetic variation in host response to challenge with a highly pathogenic PRRSV strain](#)
Dunkelberger, J.; Mathur, P.; Little, E.; Hanson, D.; Dee, S.; Knol, E.
- 11:30 [A quantitative genetic theory for infectious diseases](#)
Bijma, P.; Hulst, A.D.; De Jong, M.C.M.

Session 45.

Design of breeding programs

Room: Eduard Flipse Zaal

Chair: John Bastiaansen, Anna Sonesson, Jack Dekkers

- 10:00 [Strategies to support phenotyping for genomic selection R&D and implementation in beef and sheep industries](#)
Banks, R.
- 10:30 [The Infrastructure for cattle data at the Swedish University of Agricultural Sciences, Gigacow](#)
Klingström, T.; Ohlsson, J.I.; De Koning, D.J.
- 10:45 [Optimizing sampling strategies for sib test schemes in a broiler breeder program](#)
De Hollander, C.A.; Breen, V.P.; Henshall, J.; Lopes, F.B.; Calus, M.P.L.
- 11:00 [Plasticity of breed direct and individual heterosis effects in beef cattle under extensive conditions](#)
Pyoos-Daniels, G.M.; MacNeil, M.D.; Scholtz, M.M.; Seshoka, M.M.; Weepener, H.L.; Neser, F.W.C.
- 11:15 [Polled accelerator - a unique application of genomic technologies to address a beef breeding challenge](#)
Johnston, D.J.; Ferdosi, M.H.; Cook, J.; Savage, D.B.
- 11:30 [An approach for the design of breeding programs using genomics](#)
Dekkers, J.C.M.; Su, H.; Kramer, L.; Yu, H.
- 11:45 [Should we breed cows like pigs? a new organisation of dairy cattle breeding](#)
Kargo, M.; Nielsen, H.M.; Østergaard, S.; Kring, R.D.; Slagboom, M.; Clasen, J.B.; Thomasen, J.R.

Session 46.

Bovine Dairy - Genome informed breeding

Room: Willem Burger Zaal

Chair: Gerben de Jong, Filippo Miglior, Martin Lidauer, Mike Coffey, John Cole

- 10:00 [Understanding the genetic architecture of claw horn lesions in different lactation stages in Holstein cattle](#)
Li, B.; Barden, M.; Kapsona, V.; Molano, E.S.; Anagnostopoulos, A.; Griffiths, B.E.; Bedford, C.; Dai, X.; Coffey, M.; Psifidi, A.; Oikonomou, G.; Banos, G.
- 10:02 [Shared response pattern in the mammary transcriptome after intramammary challenge with *E. coli* or *S. aureus* pathogen](#)
Becker, D.; Heimes, A.; Weikard, R.; Hoedemaker, M.; Meyerholz, M.M.; Schuberth, H.-J.; Petzl, W.; Zerbe, H.; Schmicke, M.; Engelmann, S.; Kühn, C.
- 10:04 [Epistatic interaction between KIT and MITF causes splotchy face in Hereford × dairy crossbred calves](#)
Jivanji, S.; Yeates, A.; Harland, C.; Gray, C.; Couldrey, C.; Worth, G.; McNaughton, L.; Fransen, T.; Monehan, T.; Spelman, R.; Garrick, D.; Littlejohn, M.
- 10:06 [Searching for genes involved in heat stress response in lactating cows through transcriptomics](#)
Diaz, C.; Ramon, M.; Gonzalez-Verdejo, C.; Carabano, M.J.
- 10:08 [Genomic regions exhibiting transmission distortions and copy number variants associated with stillbirth in cattle](#)
Martin, A.A.A.; Oliveira, H.R.; Fonseca, P.A.S.; Rochus, C.M.; Miglior, F.; Id-Lahoucine, S.; Cánovas, A.; Baes, C.F.; Schenkel, F.S.
- 10:10 [Mating allocations in Nordic Red Dairy Cattle using genomic information](#)
Bengtsson, C.; Stålhammar, H.; Thomasen, J.R.; Eriksson, S.; Fikse, W.F.; Strandberg, E.
- 10:12 [Genome wide association study of blood cell count measures in Holstein cows](#)
Siberski-Cooper, C.J.; Chinchilla-Vargas, J.; Kramer, L.M.; Lim, K.S.; Mayes, M.S.; Koltes, J.E.
- 10:14 [Investigation of intestinal atresia in a jersey sire family](#)
Carthy, T.R.; Keane, O.M.; Hanrahan, J.P.; Matthews, D.; McEwan, J.; Rowe, S.; Mee, J.

- 10:16 [The genomic architecture of feed efficiency over the lactation of dairy cattle](#)
Houlahan, K.; Schenkel, F.S.; Oliveira, H.R.; Miglior, F.; Oliveira Jr., G.A.; Vandehaar, M.J.; Weigel, K.; Tempelman, R.J.; Baes, C.F.
- 10:18 Discussion
- 10:30 [Population structure and signatures of selection in Italian Holstein through genome-wide analysis of imputed SNP data](#)
Persichilli, C.; Marusi, M.; Van Kaam, J.T.; Finocchiaro, R.; Senczuk, G.; Di Civita, M.; Pilla, F.; Cassandro, M.
- 10:45 [Genome-wide association studies for maturity rate in grazing dairy cows](#)
Lopez-Villalobos, N.; Ariyaratne, H.B.P.C.; Hickson, R.E.
- 11:00 [Selection, validation, and utilization of mitogenome SNP array information in cattle breeding](#)
Brajkovic, V.; Bradic, L.; Turkalj, K.; Novosel, D.; Ristov, S.; Ajmone Marsan, P.; Colli, L.; Cubric-Curik, V.; Sölkner, J.; Curik, I.
- 11:15 [Genomewide transcriptome profiling of milk derived primary bovine mammary epithelial cells after pathogen challenge](#)
Iso-Touru, T.; Fischer, D.; Kyläniemi, M.; Tabell, J.; Virta, A.; Vilkki, J.
- 11:30 [Archetypal clustering reveals physiological mechanisms linking milk yield and fertility in dairy cattle](#)
Ooi, E.; Goddard, M.; Pryce, J.

Session 47.

Bovine Beef (2)

Room: Van Cappellen Zaal

Chair: Renzo Bonifazi, Martino Cassandro, Fernando Cardoso

- 10:00 [Mining of producer recorded data: using beef calf and cow live-weight data as a case study](#)
Walsh, S.; McHugh, N.; Evans, R.D.; Murphy, C.; Berry, D.P.
- 10:02 [Sexual precocity of purebred Charolais heifers](#)
Taussat, S.; Vinet, A.; Maupetit, D.; Dozias, D.; Chanteloup, L.; Renand, G.; Martin, P.
- 10:04 [Estimation of variance components for female longevity in Australian Angus cattle using random regression models](#)
Aliloo, H.; Clark, S.
- 10:06 [Eye muscle area and lean muscle area are genetically different traits in high marbling Wagyu carcasses](#)
McEwin, R.A.; Hebart, M.L.; Tearle, R.; Grose, J.; Pitchford, W.S.
- 10:08 [Selection on yearling days to calving improves mature fertility traits in tropically adapted cattle](#)
Facy, M.L.; Hebart, M.L.; Oakey, H.; McEwin, R.A.; Popplewell, G.I.; Pitchford, W.S.
- 10:10 [Estimation of maternal variance for slaughter traits in cattle](#)
Twomey, A.J.; Pabiou, T.
- 10:12 [Biological types, direct and maternal heterosis and recombination effects on weaning weight of composite beef cattle](#)
Ferraz, J.B.S.; Espigolan, R.; Baldi, F.S.; Eler, J.P.; Oliveira, E.C.M.; Nuñez-Dominguez, R.; Gama, L.T.
- 10:14 [Breed differences, heterosis and recombination effects for calving interval in a composite beef cattle breed](#)
Gama, L.T.; Espigolan, R.; Baldi, F.S.; Eler, J.P.; Oliveira, E.C.M.; Nuñez-Dominguez, R.; Ferraz, J.B.S.
- 10:16 [Prediction ability for growth and maternal traits using SNP arrays based on different marker density in Nellore cattle](#)
Baldi, F.
- 10:18 [Applying single step genomic evaluation and integrating local with foreign EBVs to increase calving performance](#)
Naderi Darbaghshahi, S.; Pabiou, T.; Evans, R.D.

- 10:20 [Understanding the genetics of fertility and temperament in Northern beef cattle using genomic technologies](#)
Copley, J.P.; Corbet, N.J.; Allen, J.M.; Laing, A.R.; Fordyce, G.; McGowan, M.R.; Burns, B.M.; Lyons, R.E.; Hayes, B.J.
- 10:22 [Genomic prediction with non-additive genetic effects for carcass weight and beef marbling in Japanese Black cattle](#)
Inoue, K.; Nishio, M.; Inoue, Y.; Takeda, M.; Hirooka, H.
- 10:24 [Reaction norm models contribute to the investigation of environmental sensitivity for weaning weight in Nellore cattle](#)
Carvalho Filho, I.; Alves Silva, D.; Souza Teixeira, C.; Lima Silva, T.; Galvão Albuquerque, L.; Carvalheiro, R.
- 10:26 [Investigation on inheritance transmission modes using breeding values estimated from genomic or pedigree information](#)
Hirooka, H.
- 10:28 [Genetic parameters for fatty acid traits of beef in Australian Angus](#)
Duff, C.J.; Samaraweera, A.M.; McGilchrist, P.; Clark, S.A.
- 10:30 [Integration of beef cattle international estimated breeding values in the Italian evaluation](#)
Bonifazi, R.; Calus, M.P.L.; Ten Napel, J.; Veerkamp, R.F.; Biffani, S.; Cassandro, M.; Savoia, S.; Vandenplas, J.
- 10:45 [A genomic evaluation of genotype-by-environment interactions for foot scores in American and Australian Angus cattle](#)
Alvarenga, A.B.; Retallick, K.; Garcia, A.; Oliveira, H.R.; Miller, S.P.; Byrne, A.; Brito, L.F.
- 11:00 [Single-step GBLUP evaluation for categorical traits for beef cattle](#)
Nazari-Ghadikolaei, A.; Eriksson, S.; Fikse, F.
- 11:15 [Genetic parameters for mature cow body condition scores and fat and muscle traits in finishing beef cattle](#)
Weik, F.; Hickson, R.E.; Morris, S.T.; Garrick, D.J.; Archer, J.A.
- 11:30 [Decision support tools to support a more sustainable beef -on-dairy industry](#)
Ring, S.C.; Evans, R.D.; McCarthy, J.; Cromie, A.; Berry, D.P.

Session 48.

Lunch seminar: Bayer

Room: Van Weelde Zaal

Chair:

12:00 Lunchtime Satellite Symposium: Bringing animal and plant breeding closer together

Session 49.

Challenges – Use of whole genome sequence information (1)

Room: Jurriaanse Zaal

Chair: Aniek Bouwman, Hans Daetwyler, Hubert Pausch

- 13:30 [Pangenomes of haplotype-resolved assemblies enable population-scale genotyping of cattle structural variation](#)
Leonard, A.S.; Pausch, H.
- 14:00 [Comparison of methods for building pangenome graphs](#)
Crysanto, D.; Leonard, A.; Pausch, H.
- 14:15 [Expanding the genomic toolkit: what does Oxford nanopore sequencing have to offer?](#)
Hess, A.; Caulton, A.; Clarke, R.; Brauning, R.; McRae, K.; Clarke, S.
- 14:30 [Successful trio-based reverse genetic screen in an endangered local cattle breed](#)
Häfliger, I.M.; Seefried, F.R.; Drögemüller, C.

- 14:45 [How does a harsh environment make wild and domestic animals evolve similarly?](#)
Romashov, G.; Yurchenko, A.; Yudin, N.; Larkin, D.
- 15:00 [Functional and association analyses of sequence data in a region of OAR 20 associated to paratuberculosis in sheep](#)
Casu, S.; Usai, M.G.; Sechi, T.; Maestrale, C.; Miari, S.; Salaris, S.; Ligios, C.; Carta, A.
- 15:15 [Discovery of a genetic variant in serum amyloid A that might protect chickens from amyloid arthropathy](#)
Falker-Gieske, C.; Paul, N.-F.; Spourita, M.; Gustmann, K.; Gilthorpe, J.D.; Tetens, J.

Session 50. Challenges – Genetic control of infectious disease transmission and impact (2)

Room: Grote Zaal

Chair: Piter Bijma, Andrea Wilson, John McEwan

- 13:30 [Breeding for general disease resistance: a selection experiment in rabbits](#)
Gunia, M.; Ruesche, J.; Aymard, P.; Gillet, E.; Herbert, C.; Helies, V.; Savietto, D.; Robert, R.; Warin, L.; Gilbert, H.; Garreau, H.
- 13:45 [A single step genetic evaluation including causal candidate SNPs for resistance to paratuberculosis in Holstein cattle](#)
Sanchez, M.P.; Tribout, T.; Fritz, S.; Guatteo, R.; Fourichon, C.; Schibler, L.; Delafosse, A.; Boichard, D.
- 14:00 [Genetic parameters and QTL mapping for antibody response to paratuberculosis in a natural infected flock of sheep](#)
Usai, M.G.; Casu, S.; Sechi, T.; Cancedda, M.G.; Pintus, D.; Salaris, S.; Mulas, G.; Carta, A.
- 14:15 [The genetic basis of sex differences in immune responses in wild Soay sheep \(*Ovis aries*\)](#)
Wimborne, E.A.; Sparks, A.M.; Watt, K.; Sinclair, R.; Pilkington, J.G.; Pemberton, J.M.; McNeilly, T.N.; Nussey, D.H.; Johnston, S.E.
- 14:30 [New tools and insights to enable breeding for reduced disease transmission](#)
Doeschl-Wilson, A.; Marion, G.; Pooley, C.M.
- 15:00 [Transmission experiment in turbot shows high genetic variation in host infectivity affecting disease spread and survival](#)
Prentice, J.C.; Pooley, C.M.; Tsairidou, S.; Pong Wong, R.; Anacleto, O.; Saura, M.; Bailey, R.I.; Marion, G.; Villanueva, B.; Doeschl-Wilson, A.B.
- 15:15 [Impact of selection for disease resistance on the spread of infection in a simulated aquaculture population](#)
García-Ballesteros, S.; Fernández, J.; Doeschl-Wilson, A.; Villanueva, B.

Session 51.

Breeding goals and selection strategies

Room: Eduard Flipse Zaal

Chair: John Bastiaansen, Julius van der Werf, Bruno Santos

- 13:30 [Relative importance of selection objective traits in participatory breeding programs – multiatr software](#)
Lobo, R.N.B.
- 13:32 [Validation of Angus HeiferSELECT using historical data](#)
Alexandre, P.A.; Porto-Neto, L.R.; Hine, B.; Ingham, A.B.; Samaraweera, M.; Duff, C.; Reverter, A.
- 13:34 [Full-scale simulation of the Norwegian red dairy cattle breeding programme to enable testing future breeding directions](#)
Ehsani, A.; Jenko, J.; Storlien, H.; Melbo Tajet, H.; Pocrnic, I.; Obsteter, J.; Gorjanc, G.
- 13:36 [Improving carcass value by incorporating primal weights into beef breeding objectives](#)
Sarker, N.R.; Walmsley, B.J.; Hermes, S.

- 13:38 [A method for partitioning trends in genetic mean and variance to understand breeding practices](#)
Oliveira, T.P.; Obšteter, J.; Pocrnic, I.; Gorjanc, G.
- 13:40 [A practical approach to predicting expected response to selection with a new index](#)
Zhang, X.; Amer, P.; Quinton, C.
- 13:42 Discussion
- 13:45 [Theory and tools that are needed for the design and optimization of breeding programs](#)
Amer, P.R.
- 14:15 [General properties of the optimum selection index](#)
Wellmann, R.
- 14:30 [Advantages of modularisation for industry breeding objective development](#)
Quinton, C.D.; Amer, P.R.; Byrne, T.J.; Santos, B.F.S.
- 14:45 [Enhancement of the Terminal Carcass Production index to incorporate birth weight and lambing ease in Australian sheep](#)
Dehnavi, E.; Swan, A.A.
- 15:00 [iGENDEC: a web-based decision support tool for economic index construction](#)
Spangler, M.L.; Golden, B.L.; Newman, S.; Kuehn, L.A.; Snelling, W.M.; Thallman, R.M.; Weaver, R.L.
- 15:15 [Analysis of causal structure of traits involved in sow lactation feed efficiency](#)
Mora Fenoll, M.; David, I.; Gilbert, H.; Rosa, G.J.M.; Sánchez, J.P.; Piles, M.

Session 52.

Bovine Dairy - Genetic evaluation methods

Room: Willem Burger Zaal

Chair: Gerben de Jong, Filippo Miglior, Martin Lidauer, Mike Coffey, John Cole

- 13:30 [Breed and heterosis effects for fatty acid composition of milk from dairy cows milked once- and twice-a-day](#)
Sanjayanjan, I.; López-Villalobos, N.; Blair, H.T.; Janssen, P.W.M.; Holroyd, S.E.; MacGibbon, A.K.H.,
- 13:32 [Long term effect of growth in rearing phase on reproduction and production trait in Murrah buffalo](#)
Joshi, P.; Verma, A.; Gowane, G.R.; Alex, R.; Gupta, I.D.; Worku, D.
- 13:34 [Integrating parent-of-origin effects in random regression models for milk traits](#)
Jahnel, R.E.; Blunk, I.; Reinsch, N.
- 13:36 [Recombination rate and hotspots in Holstein cattle from Mexico](#)
Mejía-Melchor, E.I.; García-Ruiz, A.; Vásquez-Peláez, C.; Toledo-Alvarado, H.O.; Ruiz-Lopez, F.J.
- 13:38 [Longevity in genetic evaluation of Holstein cows in Uruguay](#)
Silveira, N.F.; Ravagnolo, O.; Aguilar, I.
- 13:40 [Comparison of two models for dairy herd improvement data in Taiwan](#)
Lan, Y.H.; Lin, K.H.; Ting, S.H.; Su, C.L.; Tu, P.A.; Lin, E.C.
- 13:42 [Comparison of random regression test-day models for production traits of South African Jersey Cattle](#)
Kinghorn, M.G.; Cason, E.D.; Ducrocq, V.; Naser, F.W.C.
- 13:44 [ROH describes the small holder dairy systems with Holstein cattle in Mexico](#)
García-Ruiz, A.; Cortés-Hernández, J.G.; Ruiz-López, F.J.
- 13:46 Discussion
- 14:00 [How ssGBLUP became suitable for national dairy cattle evaluations](#)
Misztal, I.; Lourenco, D.; Tsuruta, S.; Aguilar, I.; Masuda, Y.; Bermann, M.; Cesarani, A.; Legarra, A.

- 14:15 [Options for evaluating multiple breeds in a single-step GBLUP for US dairy population](#)
Cesarani, A.; Lourenco, D.; Vanraden, P.M.; Nicolazzi, E.L.; Legarra, A.; Tsuruta, S.; Misztal, I.
- 14:30 [Integrating MACE breeding values into multiple-trait single step random regression test day evaluations of Aussie Reds](#)
Boerner, V.; Nguyen, T.; Nieuwhof, G.
- 14:45 [Optimum contribution selection in a dairy cattle population with different relationship matrices](#)
Gautason, E.; Sahana, G.; Guldbrandtsen, B.; Berg, P.
- 15:00 [The rising popularity of embryo transfer in U.S. dairy cattle and implications for national fertility evaluations](#)
Miles, A.M.; Hutchison, J.L.; Vanraden, P.M.
- 15:15 [Simulating technical, economic and environmental performance of a dairy herd under selection in future climate condition](#)
Burns, J.G.; Eory, V.; Mrode, R.; Wall, E.; Simm, G.

Session 53.

Bees and other insects (1)

Room: Van Cappellen Zaal

Chair: Pim Brascamp, Florence Phocas, Gertje Petersen

- 13:30 [Economic value and production characteristics of table honey](#)
Frost, E.A.; Chapman, N.C.; Banks, R.G.; Walkom, S.F.; Hermes, S.
- 13:32 [Evaluating the potential for mating control in honey bee breeding in three SE European countries – preliminary results](#)
Uzunov, A.; Andonov, S.; Dahle, B.; Kovačić, M.; Prešern, J.; Aleksovski, G.; Jaman, F.; Jovanovska, M.; Pavlov, B.; Puškadija, Z.; Wegener, J.; Büchler, R.
- 13:34 [A model for, and early implementation of, genomic selection in the Australian honey bee population](#)
Chapman, N.; Frost, E.; Banks, R.
- 13:36 [An over-time distribution map of the main *Apis mellifera* mitochondrial DNA lineage using honey as source of eDNA](#)
Taurisano, V.
- 13:38 [Using genomics to predict drone quality: why are there so many ‘dud’ male honey bees?](#)
Slater, G.P.; Harpur, B.A.
- 13:40 [Development of genomic resources in black soldier fly \(*Hermetia illucens* L.\) via throughput DNA pool sequencing](#)
Donkpegan, A.; Guigue, A.; Boulanger, F.-X.; Brard-Fudulea, S.; Haffray, P.; Sourdoux, M.; Rouger, R.
- 13:42 [The natural history of the black soldier fly, *Hermetia illucens*: insights from complete mitochondrial genome sequences](#)
Guilliet, J.G.; Filée, J.F.; Pollet, N.P.; Baudouin, G.B.
- 13:44 Discussion
- 13:45 [Impact of genetic selection in insect populations using different selection designs, a simulation study](#)
Rikkers, R.S.C.; Bastiaansen, J.W.M.; Bouwman, A.C.; Ellen, E.D.
- 14:00 [Genetic parameters of black soldier flies estimated in full sib design](#)
Bouwman, A.C.; Nugroho, J.E.; Wongso, D.; Van Schelt, J.; Pannebakker, B.A.; Zwaan, B.J.; Ellen, E.D.
- 14:15 [Towards selective breeding in insects - estimating genetic parameters through individual-level phenotypes and pedigree](#)
Hansen, L.S.; Laursen, S.F.; Bahrndorff, S.; Kargo, M.; Kristensen, T.N.; Sahana, G.; Sørensen, J.G.; Nielsen, H.M.

- 14:30 [Genetic improvement program in black soldier fly \(*H. illucens*\) for increased larval weight in industrial applications](#)
Facchini, E.; Shrestha, K.; Van Den Boer, E.; Junes, P.; Sader, G.; Peeters, K.; Schmitt, E.
- 14:45 [Tenebrio molitor genomic structure among available populations](#)
Eleftheriou, E.; Vacherie, B.; Labadie, K.; Athanassiou, C.G.; Rigaud, T.; Moret, Y.; Lefebvre, T.; Madoui, M.A.
- 15:00 [Inferring whole-genome tree sequences and population and demographic parameters of the Western honeybee](#)
Obsteter, J.; Marinc, A.; Presern, J.; Wragg, D.; Gorjanc, G.

Session 54.

Challenges – Use of whole genome sequence information (2)

Room: Jurriaanse Zaal

Chair: Aniek Bouwman, Hans Daetwyler, Hubert Pausch

- 16:00 [Genetic background of the porcine immune system using SNP chip data and whole genome sequencing data](#)
Dauben, C.M.; Große-Brinkhaus, C.; Henne, H.; Appel, A.K.; Tholen, E.
- 16:02 [Deciphering the origins of Neolithic sheep from northern Iberian Peninsula](#)
Serrano, M.; Fernández, A.; González, C.; Martínez-Blanch, J.; Moreno-García, M.; Rojo-Guerra, M.; Calvo, J.H.
- 16:04 [Prioritisation of variants from whole-genome sequence data for validation of their association with traits of interest](#)
Molinero, E.; Pena, R.N.; Estany, J.; Ros-Freixedes, R.
- 16:06 [Genome-wide association analyses and genomic prediction for pork meat quality traits using whole-genome sequence](#)
Heidaritabar, M.; Huisman, A.; Bink, M.C.A.M.; Charagu, P.; Plastow, G.
- 16:08 [A conditional multi-trait sequence GWAS of heifer fertility in tropically adapted beef cattle](#)
Forutan, M.; Engle, B.; Goddard, M.E.; Hayes, B.J.
- 16:10 [genomic prediction of purebred Merinos from an admixed terminal population using selected sequence variants](#)
Moghaddar, N.; Swan, A.A.; Gurman, P.M.; Li, L.; Van Der Werf, J.H.J.
- 16:12 [The complete mitochondrial genome of a Peruvian creole cattle \(*Bos taurus*\) and its phylogenetic analysis](#)
Arbizu, C.I.; Ferro-Mauricio, R.D.; Chávez-Galarza, J.C.; Vásquez, H.V.; Maicelo, J.L.; Poemape, C.; Gonzales, J.; Quilcate, C.; Corredor, F.A.
- 16:14 [Unravelling the effect of structural variants from whole-genome sequence for depigmentation in Nellore cattle](#)
Vargas, G.; Neves, H.H.R.; Garzón, N.A.M.; Fonseca, L.F.S.; Fernandes Júnior, G.A.; Albuquerque, L.G.; Carvalheiro, R.
- 16:16 Discussion
- 16:30 [On the advantage of identifying causal genetic variants for genomic prediction](#)
Meuwissen, T.H.E.; Goddard, M.E.
- 16:45 [Fuzzy logic strategies for combining marker statistics to optimize preselection of high-density and sequence genotypes](#)
Ling, A.; Hay, E.H.; Hartono, E.; Aggrey, S.E.; Rekaya, R.
- 17:00 [Genetic evaluations and genomic characteristics for local cattle using genome sequences, 50K and a specific SNP chip](#)
May, K.; Wolf, M.J.; Neumann, G.B.; Korkuć, P.; Brockmann, G.A.; König, S.
- 17:15 [Genomic prediction using whole-genome sequence data in intensely selected pig lines](#)
Ros-Freixedes, R.; Johnsson, M.; Whalen, A.; Chen, C.Y.; Valente, B.D.; Herring, W.O.; Gorjanc, G.; Hickey, J.M.

- 17:30 [Single and multi-breed ssGBLUP using preselected variants from whole-genome sequence data in pigs](#)
Jang, S.; Ros-Freixedes, R.; Hickey, J.M.; Chen, C.Y.; Herring, W.; Misztal, I.; Lourenco, D.
- 17:45 [Application of low-pass sequencing to genomic prediction of egg quality in laying hens](#)
Wolc, A.; Li, J.; Lubritz, D.; Arango, J.; Fulton, J.E.; Settar, P.; Rowland, K.; Cheng, H.

Session 55.

Developing countries

Room: Grote Zaal

Chair: Richard Crooijmans, Julie Ojango, Raphael Mrode, Sipke Joost Hiemstra

- 16:00 [Phylogenetic analysis of local cattle population in Northern Province of Sri Lanka](#)
Wijebandara, K.G.C.B.; Kurukulasuriya, M.S.; Bandaranayake, P.C.G.; Silva, G.L.L.P.
- 16:02 [Accounting for heterogeneity of data in implementing genomic selection models applicable to crossbred cattle in India](#)
Guintard, A.; Bourguignon, L.; Restoux, G.; Ducrocq, V.
- 16:04 [Connections among local nomenclature, phenotypes and genetic characteristics of native chickens in Cambodia: a synthesis](#)
Phem, M.; Chagunda, M.G.G.
- 16:06 [Experience in creating a female *Bos taurus* x *Bos indicus* reference population under smallholder system in India](#)
Bhave, K.G.; Joshi, S.; Gaundare, Y.; Joshi, A.; Shirsath, T.; Punde, N.; Potdar, V.; Ratnakar, V.; Swaminathan, M.
- 16:08 Discussion
- 16:15 [Learnings and experiences from a community-based goat breeding program in India](#)
Schurink, A.; Kumar, S.; Chakraborty, R.; Sawhney, T.; Nimbkar, C.; Amer, P.
- 16:30 [Response to index selection for temperate dairy cattle breeds in tropical Sri Lanka](#)
Samaraweera, A.M.; Van Der Werf, J.H.J.; Boerner, V.; Hermes, S.
- 16:45 [Challenges with creation and use of female reference populations for genomic selection under Indian smallholder systems](#)
Ducrocq, V.; Swaminathan, M.; Gibson, J.P.
- 17:00 [Bridging the gap in data from smallholder dairy systems: developing the Africa dairy genetic gains \(ADGG\) data platform](#)
Ojango, J.M.K.; Okeyo, A.M.; Mrode, R.; Chinyere, E.; Gebreyohanes, G.; Meseret, S.; Mogaka, D.; Lyatu, E.; Komwihangilo, D.; Msuta, G.; Kahumbu, S.; Gibson, J.P.; Kemp, S.
- 17:15 [Attitudes of Peruvian llama and alpaca farmers towards genetic improvement](#)
Wurzinger, M.; Gutierrez, G.
- 17:30 [Development of a low-density SNP panel for local Ghanaian and Tanzanian chicken ecotypes](#)
Walugembe, M.; Amuzu-Aweh, E.N.; Lim, K.; Wang, Y.; Chouicha, N.; Kelly, T.; Muhairwa, A.P.; Kayang, B.B.; Msoffe, P.L.M.; Naazie, A.; Otsyina, H.R.; Mushi, J.S.; Gallardo, R.A.; Zhou, H.; Lamont, S.J.; Dekkers, J.C.M.
- 17:45 [Combining demographic, production and molecular investigations in genetic improvements: case study in indigenous chicken](#)
Silva, G.L.L.P.; Kurukulasuriya, M.S.; Fernando, P.R.M.K.; Dematawewa, C.M.B.

Session 56.

Operational breeding programs

Room: Eduard Flipse Zaal

Chair: John Bastiaansen, Julius van der Werf, Bruno Santos

- 16:00 [Management of undesired alleles at multiple loci for a goat breeding program](#)
Raoul, J.; Elsen, J.M.; Rodriguez-Ramilo, S.T.; Palhière, I.

- 16:02 [Prediction of gametic variance and its use in breeding programs](#)
Hozé, C.; Baur, A.; Fritz, S.; Boichard, D.
- 16:04 [Implementing genomic management of diversity and selection in French dairy goats](#)
Palhiere, I.; Gousseau, V.; Colleau, J.J.
- 16:06 [Partition in long-term contributions of the genetic trend of Basco-Béarnaise dairy sheep](#)
Antonios, S.; Legarra, A.; Astruc, J.M.; Rodríguez-Ramilo, S.T.; Vitezica, Z.G.
- 16:08 [Introgression of prolificacy gene in Tunisian Barbarine sheep through marker-assisted selection scheme](#)
Arari, E.; Baazaoui, I.; Letayef, N.; Lahmer, M.; Hemdène, H.; Haile, A.; Rekik, M.; Bedhraf-Romdhani, S.
- 16:10 [Simulation of animal crossbreeding schemes using ADAM software](#)
Liu, H.; Nielsen, H.M.; Kargo, M.; Thomasen, J.R.; Berg, P.; Slagboom, M.; Sørensen, A.C.; Milkevych, V.
- 16:12 Discussion
- 16:15 [A tool for comprehensive implementation of simple and complex breeding programs](#)
Kinghorn, B.P.; Kinghorn, A.J.; Baller, J.L.
- 16:45 [Beyond scenarios – resource optimization for dairy cattle breeding programs \(MoBPSopti\)](#)
Hassanpour, A.; Simianer, H.; Pook, T.
- 17:00 [Predicting the outcome of a selection scheme in maternal traits](#)
Mäki-Tanila, A.V.; Pietarinen, J.
- 17:15 [Inbreeding in circular and panmictic mating systems](#)
Guldbrandsen, B.
- 17:30 [Genomic rotational crossbreeding including advanced optimum contribution selection methods in local dairy cattle breeds](#)
Stock, J.; Esfandyari, H.; Hinrichs, D.; Wellmann, R.; Bennewitz, J.
- 17:45 [Allele frequency differences at epistatic QTL explain different genetic trends in number of teats in two pig lines](#)
Sevillano, C.A.; Harlizius, B.; Derks, M.F.L.; Lopes, M.S.; Van Son, M.; Knol, E.F.

Session 57.

Bovine Dairy - Phenotype is king

Room: Willem Burger Zaal

Chair: Gerben de Jong, Filippo Miglior, Martin Lidauer, Mike Coffey, John Cole

- 16:00 [Candidate genomic regions for forage dry matter intake in Swedish dairy cows using single-step genome-wide association](#)
Tarekegn, G.M.; Karlsson, J.; Kronqvist, C.; Holtenius, K.; Andonov, S.; Berglund, B.; Strandberg, E.
- 16:02 [Stillbirth, dystocia and weaning rates in Australian dairy calves](#)
Axford, M.M.; Pryce, J.E.; Khansefid, M.; Haile-Mariam, M.
- 16:04 [The relative importance of linear type traits in determining survival increases as Holstein-Friesian dairy cows age](#)
Williams, M.; Sleator, R.D.; Murphy, C.P.; McCarthy, J.; Berry, D.P.
- 16:06 [Genetic parameters of milk composition and fertility traits in cows milked once- or twice-daily in New Zealand](#)
Jayawardana, J.M.D.R.; Lopez-Villalobos, N.; Hickson, R.E.; McNaughton, L.R.
- 16:08 [Identifying phenotypes to enhance stress resilience of dairy cows](#)
Sullivan, T.M.; Sharma, A.; Lamers, K.; While, C.; Mallard, B.A.; Cánovas, A.; Karrow, N.A.
- 16:10 [Estimation of genetic correlations between predicted energy balance and milk fatty acids of Holsteins in Japan](#)
Nishiura, A.; Sasaki, O.; Aihara, M.; Saito, Y.; Tatebayashi, R.; Takeda, H.

- 16:12 [Associations between milk protein polymorphisms and milk production in Holstein-Friesian cows](#)
Kelly, D.N.; Dunne, F.L.; Evans, R.D.; Berry, D.P.
- 16:14 [Genetic analysis of milking traits in Holstein cows based on automatic milking system data](#)
Kawakami, J.; Gotoh, Y.; Baba, T.; Yamaguchi, S.; Nakagawa, S.; Yamaguchi, S.; Oka, T.; Kawahara, T.
- 16:16 [Fertility traits of Mexican Holstein cattle: genetic parameters, correlations and changes in genetic diversity over time](#)
Durán-Alvarez, C.; García-Ruiz, A.; Alonso Morales, R.A.; Eguiarte, L.E.; Piñero, D.; Ruiz-López, F.J.
- 16:18 Discussion
- 16:30 [Genetic parameters for residual feed efficiency in three dairy cattle breeds in commercial farms using 3D cameras](#)
Manzanilla-Pech, C.I.V.; Stephensen, R.B.; Andersen, T.; Lassen, J.
- 16:45 [Insemination values to support mating decisions under dairy heifer calf herd size constraints](#)
De Vries, A.; Bliznyuk, N.; Sharma, P.; Han, Y.; Pinedo, P.
- 17:00 [Onset of heat stress and development of genomic predictions for heat tolerance in US Holsteins and Jerseys](#)
McWhorter, T.M.; Sargolzaei, M.; Sattler, C.G.; Utt, M.D.; Tsuruta, S.; Misztal, I.; Lourenco, D.
- 17:15 [Detection of genetic variability in cattle infectivity for bovine tuberculosis \(bTB\)](#)
Sánchez-Molano, E.; Madenci, D.; Tsairidou, S.; Winters, M.; Mitchell, A.P.; Banos, G.; Doeschl-Wilson, A.
- 17:30 [Dairy female fertility traits in seasonal and non-seasonal herds in Ireland](#)
Stachowicz, K.; Amer, P.R.; Kelleher, M.M.; Ring, S.C.; Evans, R.D.
- 17:45 [Genetic aspects of age at first calving in Italian Holstein dairy cows](#)
Ferrari, V.; Galluzzo, F.; Finocchiaro, R.; Van Kaam, J.B.C.H.M.; Penasa, M.; Marusi, M.; Cassandro, M.

Session 58.

Bees and other insects (2)

Room: Van Cappellen Zaal

Chair: Pim Brascamp, Florence Phocas, Gertje Petersen

- 16:00 [Heritability of disease resistance to chronic bee paralysis, chalkbrood and nosemosis in the honeybee \(*A.m.carnica*\)](#)
Hoppe, A.; Bernstein, R.; Du, M.; Bienefeld, K.
- 16:02 [Genetic analysis of royal jelly production and behaviour traits of honeybees](#)
Basso, B.; Kistler, T.; Gerez, T.; Phocas, F.
- 16:04 [Comparison of heritabilities and estimated breeding values for three honeybee traits using dam and animal models](#)
Petersen, G.E.L.; Hely, F.S.; Fennessy, P.F.; Dearden, P.K.
- 16:06 Discussion
- 16:15 [Statistics for an accurate genome wide association study on Varroa resistance trait in a French honeybee](#)
Eynard, S.E.; Vignal, A.; Agez, Y.; Basso, B.; Bouchez, O.; Le Conte, Y.; Dainat, B.; Decourtye, A.; Genestout, L.; Guichard, M.; Guillaume, F.; Labarthe, E.; Mahla, R.; Mondet, F.; Neudischko, M.; Phocas, F.; Poquet, Y.; Sann, C.; Tabet, K.; Servin, B.
- 16:30 [New approach to identify Mendelian inconsistencies between SNP and pedigree information in the honey bee](#)
Bernstein, R.; Du, M.; Hoppe, A.; Bienefeld, K.
- 16:45 [Investigation of parental meiotic contribution in honeybees \(*Apis mellifera*\)](#)
Petersen, G.E.L.; Heywood, A.; Walters, A.C.L.; Fennessy, P.F.; Dearden, P.K.
- 17:00 [SIMplyBee: stochastic simulator of honeybee populations and breeding programmes](#)
Strachan, L.; Bubnič, J.; Obšteter, J.; Gorjanc, G.

17:15 [Assessment of uncertainty in direct and maternal genetic parameters estimates for honeybee colony phenotypes](#)

Kistler, T.; Brascamp, E.W.; Basso, B.; Bijma, P.; Phocas, F.

17:30 [Very local genotype by environment interaction in Austrian honey bees](#)

Brascamp, E.W.; Rubinigg, M.; Veerkamp, R.F.; Bijma, P.

Session 59.

Plenary 5

Room: Grote Zaal
Chair: Eric Mullaart

08:30 [Discoveries and lessons from a genome-wide association study of human height in >5 million Individuals](#)
Yengo, L.

Session 60.

Statistical genetics: Machine learning, deep learning and artificial intelligence

Room: Grote Zaal
Chair: Pascal Duenk, Miguel Perez, Jared Decker

10:00 [Multivariate application of artificial neural networks for genomic prediction](#)
Peters, S.; Kizilkaya, K.; Sinecen, M.; Thomas, M.

10:02 [Comparison of GBLUP and machine learning breeding values for binary disease traits in working dogs](#)
Thorsrud, J.; Evans, K.; Holle, D.; Huson, H.

10:04 [Predicting the polled genotype of ungenotyped animals using machine learning methods](#)
Gjuvsland, A.B.

10:06 [A machine learning approach to classify high and low feed efficient or grower mink](#)
Shirzadifar, A.; Manafazhar, G.; Davoudi, P.; Do, D.N.; Hu, G.; Miar, Y.

10:08 [A machine learning approach for predicting the most and the least feed-efficient groups in beef cattle](#)
Shirzadifar, A.; Plastow, G.; Basarab, J.; Miar, Y.; Li, C.; Fitzsimmons, C.; Riazi, M.; Manafazhar, G.

10:10 [Combination of SNP markers for discrimination of a target chicken population using machine learning algorithms](#)
Cho, E.; Cho, S.; Kim, M.; Ediriweera, T.K.; Seo, D.; Lee, J.H.

10:12 [LASSO and SVM: an alternative approach to identify associated genome regions for simple and complex traits in cattle](#)
Widmer, S.; Seefried, F.R.; Drögemüller, C.; Von Rohr, P.

10:14 [Quantifying the functional conservation between human and pig using artificial neural networks](#)
Li, J.; Zhao, T.; Pan, Z.; Zhou, H.; Fang, L.; Cheng, H.

10:16 [Using a U-net architecture to develop an automated ultrasound images analysis method in a rabbit breeding program](#)
Herbert, C.; Ribas, C.; Kasheffard, K.; Flatrès-Grall, L.; Lenoir, G.

10:18 Discussion

10:30 [Machine learning and genetic improvement of animals and plants: where are we?](#)
Gianola, D.

11:00 [Predicting pig digestibility coefficients with microbial and genomic data using machine learning prediction algorithms](#)
Carillier-Jacquín, C.; Deru, V.; Tusell, L.; Bouquet, A.; Jacquín, L.; Gilbert, H.

- 11:15 [\(Quasi\) multi-task support vector regression for whole-genome prediction of carcass traits in commercial broilers](#)
Alves, A.A.C.; Fernandes, A.F.A.; Breen, V.; Hawken, R.; Rosa, G.J.M.
- 11:30 [Genomic prediction of longitudinal body weights in pigs using a neural network](#)
Ni, Z.; Fernando, R.L.; Yu, H.; Knol, E.F.; Dekkers, J.C.M.
- 11:45 [Compressing microbiota information using an autoencoder to predict growth traits in swine](#)
Maltecca, C.; Jiang, J.; Fix, J.; Schwab, C.; Shull, C.; Tiezzi, F.

Session 61.

Genetic diversity and inbreeding (1)

Room: Jurriaanse Zaal

Chair: Harmen Doekes, Christian Maltecca, Theo Meuwissen

- 10:00 [Assessing existing admixture in indigenous veld ecotypes and non-descript goat populations of Southern Africa](#)
Visser, C.; Lashmar, S.F.
- 10:02 [Estimation of sex chromosome inbreeding depression on milk production in cattle](#)
Curik, I.; Vostra-Vydrova, H.; Shihabi, M.; Sölkner, J.; Vostry, L.
- 10:04 [Assessing genomic diversity and heterozygosity-rich regions of transboundary Nguni cattle of South Africa and eSwatini](#)
Van Marle-Köster, E.; Lashmar, S.F.; Okpeku, M.; Muchadeyi, F.C.; Mapholi, N.O.; Visser, C.
- 10:06 [Infographics for management of inbreeding and kinship in small populations](#)
Schoon, M.A.; Neuteboom, M.; Hiemstra, S.J.; Danchin-Burge, C.; Fernández, J.; Windig, J.J.
- 10:08 [Y-chromosomal haplogroups from wild and domestic goats reveals ancient migrations and recent introgressions](#)
Lenstra, J.A.; Vargos Consortium, -; And 67 Coauthors, -
- 10:10 [Characterization and effect of inbreeding on growth and reproductive traits in Nellore Cattle](#)
Benfica, L.F.; Bem, R.D.; Carrara, E.R.; Brito, L.F.; Silva, D.A.; Carvalheiro, R.; Cyrillo, J.N.S.G.; Mercadante, M.E.Z.
- 10:12 [Genomic diversity of Czech and Slovak native goat breeds](#)
Vostry, L.; Vostra-Vydrova, H.; Rychtarova, J.; Hofmanova, B.; Moravcikova, N.; Kasarda, R.; Margetin, M.; Drzaic, I.; Cubric-Curik, V.; Solkner, J.; Curik, I.
- 10:14 [Population structure of U.S. Holsteins allows for a snapshot of allele frequency changes and family specific SNPs](#)
Lawlor, T.J.; Steyn, Y.; Tsuruta, S.; Masuda, Y.; Lourenco, D.A.L.; Misztal, I.
- 10:16 [Genome-wide evaluation of runs of homozygosity in Indian Sahiwal cattle](#)
Illa, S.K.; Mumtaz, S.; Mukherjee, S.; Nath, S.; Mukherjee, A.
- 10:18 [Following the hidden footsteps of past human migrations via the goat genome](#)
Manunza, A.; Ramirez Diaz, J.; Bobbo, T.; Cozzi, P.; Lazzari, B.; Biscarini, F.; Biffani, S.; Johansson, A.M.; Grøva, L.; Stella, A.
- 10:20 [Are autozygosity estimates from imputed genotypes reliable?](#)
Ferenčaković, M.; Curik, I.; Garcia, J.F.; Sölkner, J.; Carvalheiro, R.
- 10:22 [Genetic diversity and population structure for resistance to mastitis in Braunvieh cattle](#)
Trujano-Chavez, M.Z.; Sánchez-Ramos, R.; Pérez-Rodríguez, P.; Ruíz-Flores, A.
- 10:24 [Evaluation of the Istrian cattle population structure by pedigree analysis](#)
Ivanković, A.; Ramljak, J.; Šubara, G.; Pečina, M.; Šuran, E.; Ivkić, Z.; Konjačić, M.

- 10:26 [Population dynamics of a long-term selection experiment in chickens divergently selected for high or low body weight](#)
Harrison, S.J.; Siegel, P.B.; Honaker, C.F.; Lewis, R.M.
- 10:28 Discussion
- 10:30 [Genetic management meets genomics](#)
Woolliams, J.A.W.; Meuwissen, T.H.E.
- 11:00 [Genetic characterization of the indigenous Sanga cattle of Namibia](#)
Januarie, D.A.; Cason, E.D.; Naser, F.W.C.
- 11:15 [Hedging genetic diversity using a similarity matrix based on Mendelian sampling](#)
Musa, A.A.; Reinsch, N.
- 11:30 [Genetic basis of sexually divergent early life survival in red deer \(*Cervus elaphus*\)](#)
Peters, L.; Pemberton, J.M.; Johnston, S.E.
- 11:45 [Changes in genomic inbreeding over half a century in Swedish Red and Swedish Holstein cattle](#)
Eriksson, S.; Strandberg, E.; Johansson, A.M.

Session 62.

Methods and Tools: Breeding goals

Room: Eduard Flipse Zaal

Chair: Han Mulder, Mark Henryon, Hanne Marie Nielsen, Gregoire Leroy

- 10:00 [Manipulating response to selection on many traits](#)
Van Der Werf, J.H.J.; Clark, S.A.
- 10:02 [Selection for birth weight environmental variability in mice as a model to improve animal welfare in livestock species](#)
Gutierrez, J.P.; Formoso-Rafferty, N.; Ojeda-Marin, C.; El-Ouazizi El-Kahia, L.; Arias, K.D.; Cervantes, I.
- 10:04 [Sensitivity analysis for a new economic selection index for Chilean dairy cattle](#)
Chuma-Alvarez, J.L.; Montaldo, H.H.; Lourenco, D.A.L.; Ruiz-López, F.J.; Olivares, M.E.; Lizana, C.
- 10:06 Discussion
- 10:15 [Opportunities for animal genetics to foster the ecological transition of livestock farming systems](#)
Saviotto, D.; Douhard, F.; Gilbert, H.; Rupp, R.; Fortun-Lamothe, L.; Ducos, A.
- 10:45 [Defining animal breeding objectives and strategies within the framework of responsible research and innovation \(RRI\)](#)
Olesen, I.; Kettunen, A.; Rosendal, G.K.; Nielsen, H.M.
- 11:00 [On farm specific breeding goals for mating lead to higher genetic gains at herd level](#)
Bérodier Gomès, M.; Brochard, M.; Ducrocq, V.
- 11:15 [A bio-economic model to estimate the economic value of sow feed intake during lactation](#)
Thekkoot, D.M.; Kemp, R.A.; Dekkers, J.C.M.
- 11:30 [Consequences of using different economic selection index methods on greenhouse gas emissions in beef cattle](#)
Walmsley, B.J.
- 11:45 [Impact of planning horizon length on the relative emphasis of traits in economic breeding goals](#)
Valasek, H.F.; Golden, B.L.; Spangler, M.L.

Session 63.

Society – Genetic solutions to achieve net zero carbon emission in livestock systems

Room: Willem Burger Zaal

Chair: Michael Aldridge, Marcin Pszczola, Suzanne Rowe

- 10:00 [Strategies to mitigate greenhouse gas emissions from pasture-based sheep systems – an EU project consortium view](#)
Conington, J.; Lambe, N.; Tortereau, F.; McGovern, F.; Navajas, E.; De Barbieri, I.; Ciappesoni, G.; Jakobsen, J.; Smith, E.; Yates, J.; Le Graverand, Q.; McDermott, K.; Steinheim, G.; Aspehølen Aby, B.; Donnem, I.; McHugh, N.; Farrell, L.; Marie-Etancelin, C.; Johnson, P.; Rowe, S.
- 10:02 [Comparing measurements of product output when defining emissions intensity](#)
Richardson, C.M.; Hely, F.; Post, M.; Nguyen, T.T.T.; Nieuwhof, G.J.; Amer, P.R.
- 10:04 [The genetic progress has effect on greenhouse gas emission intensities from Norwegian pork production](#)
Gjerlaug Enger, E.; Bonesmo, H.; Martinsen, K.; Andersen-Ranberg, I.; Olsen, D.; Grindflek, E.
- 10:06 [An approach to the genetic parameters of methane emission in Latxa dairy sheep](#)
Pineda-Quiroga, C.; Granado-Tajada, I.; Ugarte, E.; Goiri, I.; García-Rodríguez, A.
- 10:08 Discussion
- 10:15 [Ameliorating the contribution of livestock to global greenhouse gas production: dream or deliverable?](#)
Hegarty, R.S.; McEwan, J.C.; Rowe, S.J.
- 10:45 [Genetically more efficient Australian dairy cows and sheep are higher emitters of methane per unit of food](#)
Sepulveda, B.J.; Muir, S.K.; Bolormaa, S.; MacLeod, I.M.; Knight, M.I.; Behrendt, R.; Marett, L.C.; Deighton, M.H.; Garner, J.B.; Moate, P.J.; Wales, W.J.; Williams, R.O.; Daetwyler, H.D.; Cocks, B.G.; Pryce, J.E.
- 11:00 [The role of livestock genetics in addressing national GHG mitigation requirements](#)
Cromie, A.R.; Berry, D.P.; Shalloo, L.; Kirk, T.; Evans, R.; Crowley, J.
- 11:15 [Can genomics cope with a 30% reduction of methane emission from livestock in 10 years?](#)
Gonzalez Recio, O.; López-Paredes, J.; Saborío-Montero, A.; López-García, A.; Gutiérrez-Rivas, M.; Goiri, I.; Atxaerandio, R.; Ugarte, E.; Charfeddine, N.; Jiménez-Montero, J.A.; García-Rodríguez, A.
- 11:30 [Low carbon emissions in future pig production – does a new breeding goal matter?](#)
Zira, S.; Olsen, H.F.; Rydhmer, L.
- 11:45 [Individual animal carbon footprints in a national beef database: AniPrint 1.0](#)
Crowley, J.J.; Shalloo, L.; Evans, R.D.; Herron, J.; Berry, D.P.; Owens, P.; Cromie, A.R.; Crosson, P.

Session 64.

Equine

Room: Van Cappellen Zaal

Chair: Bart Ducro, Emmeline Hill, Kathrin Stock

- 10:00 [Genetic analysis of three horse breeds of Greece](#)
Kominakis, A.; Kritikos, N.; Simpson, A.; Sdroulias, T.; Iliopoulou, E.; Karagianni, V.; Pappas, D.; Hager-Theodorides, A.L.
- 10:02 [Genetics of new conformation traits in Italian Heavy Draught Horse foals](#)
Mantovani, R.; Mancin, E.; Tuliozi, B.; Gomez Proto, G.; Pigozzi, G.; Sartori, C.
- 10:04 [Effects of selection on breed composition of the Spanish Sport Horse population](#)
Bartolomé, E.; Rodríguez-Ramilo, S.T.; Fernández, J.; Valera, M.
- 10:06 [Early selection criteria for improved longevity of jumping horses](#)
Ricard, A.; Deretz, S.; Dumont Saint Priest, B.

10:08 Discussion

10:15 [Recent advances in genomics of equine health, welfare and performance](#)

Mikko, S.C.M.

10:45 [Microsatellite alleles imputation from SNP genotypes for parental verification in sport](#)

Crichan, H.; Engler, C.; Goulas, E.; Dhorne-Pollet, S.; Addes, M.; Ricard, A.

11:00 [Equine parentage control: Bridging the gap from a microsatellite to a SNP based approach](#)

Nolte, W.; Alkoder, H.; Wobbe, M.; Vosgerau, S.; Lehner, S.; Krattenmacher, N.; Von Depka Prondzinski, M.; Reents, R.; Tetens, J.; Thaller, G.; Stock, K.F.; Kalm, E.; Kühn, C.

11:15 [Haplotype blocks and heterozygosity rich regions on ECA2 in Swedish Warmblood horses](#)

Ablondi, M.; Eriksson, S.; Mikko, S.

11:30 [Single step genomic evaluation for horses based on a multi-breed reference population](#)

Wobbe, M.; Alkoder, H.; Liu, Z.; Vosgerau, S.; Krattenmacher, N.; Von Depka-Prondzinski, M.; Kalm, E.; Reents, R.; Nolte, W.; Kühn, C.; Tetens, J.; Thaller, G.; Stock, K.F.

11:45 [Methodology to integrate pedigrees of two Belgian Warmblood studbooks and its importance for genetic evaluation](#)

Chapard, L.; Buys, N.; Janssens, S.

Session 65.

Lunch seminar: BIOSEARCH Technologies

Room: Van Weelde Zaal

Chair:

12:00 Lunchtime Satellite Symposium: Accelerating molecular breeding in livestock production

Session 66.

Statistical genetics: GWAS (1)

Room: Grote Zaal

Chair: Marco Bink, Goutam Sahana, Marie-Pierre Sanchez

13:30 [Haplotypes affecting pulmonary arterial pressure in Angus cattle](#)

Lu, D.; Garcia, A.; Miller, S.; Retallick, K.

13:32 [Detection of shared genomic regions between production and health traits in German Holstein cattle](#)

Schneider, H.; Segelke, D.; Tetens, J.; Thaller, G.; Bennewitz, J.

13:34 [Detecting the presence of genomic imprinting for carcass traits in cattle using imputed high-density genotypes](#)

Kenny, D.; Sleator, R.D.; Murphy, C.P.; Evans, R.D.; Berry, D.P.

13:36 [Evidence of genetic links between rumen bacteria and milk somatic cell score in Lacaune dairy sheep](#)

Martinez Boggio, G.; Meynadier, A.; Rupp, R.; Allain, C.; Buitenhuis, A.J.; Marie-Etancelin, C.

13:38 Discussion

13:45 [Leveraging GWAS models to map selection on complex traits in massive datasets](#)

Rowan, T.N.; Schnabel, R.D.; Decker, J.E.

14:00 [Fine-mapping young-stock survival QTL on chromosome 6 in Nordic Red dairy cattle](#)

Cai, Z.; Wu, X.; Thomsen, B.; Sahana, G.

14:15 [Multibreed sequence level genome-wide association study of semen traits in tropical Australian cattle](#)

Tan, W.L.A.; Porto-Neto, L.R.; Reverter, A.; Fortes, M.R.S.

14:30 [Improved genome-wide associations using a breed-specific 200K SNP chip for German Black Pied \(DSN\) cattle](#)

Korkuc, P.; Neumann, G.B.; Arends, D.; Wolf, M.J.; May, K.; König, S.; Brockmann, G.A.

- 14:45 [Haplotype-based single-step GWAS for yearling temperament in American Angus](#)
Araujo, A.C.; Carneiro, P.L.S.; Alvarenga, A.B.; Oliveira, H.R.; Miller, S.P.; Retallick, K.; Brito, L.F.
- 15:00 [Genome-wide association analyses for various thermotolerance indicators measured during lactation in maternal-line pigs](#)
Freitas, P.H.F.; Johnson, J.S.; Wen, H.; Maskal, J.M.; Byrd, M.K.; Tiezzi, F.; Huang, Y.; Schinckel, A.P.; Brito, L.F.
- 15:15 [Investigation of GWAS variants associated with loin depth in commercial pigs](#)
Desire, S.; Johnsson, M.; Ros-Freixedes, R.; Chen, C.; Herring, W.; Gorjanc, G.; Mellanby, R.J.; Hickey, J.; Jungnickel, M.

Session 67.

Genetic diversity and inbreeding (2)

Room: Jurriaanse Zaal

Chair: Harmen Doekes, Christian Maltecca, Theo Meuwissen

- 13:30 [Runs of homozygosity in Nguni and Bonsmara cattle populations](#)
Soma, P.O.; Kooverjee, B.B.; Scholtz, M.M.
- 13:32 [Estimation of old and new inbreeding and their effects on growth traits using pedigree and genomic information](#)
Sumreddee, P.; Ling, A.; Toghiani, S.; Hay, E.; Hartono, E.; Aggrey, S.; Rekaya, R.
- 13:34 [Genome wide characterisation of runs of homozygosity on the main indigenous goat breed of Botswana](#)
Monau, P.I.; Raphaka, K.; Nsoso, S.J.
- 13:36 [Candidate genes for disease, reproduction and meat quality traits in Portuguese native breeds](#)
Silva, M.V.G.B.; Verardo, L.L.; Machado, M.A.; Panetto, J.C.C.; Carolino, I.; Carolino, N.
- 13:38 [Runs of Homozygosity harbour genes associated with muscle growth in Pietrain but not with fertility in Large White pigs](#)
Palma-Vera, S.E.; Derežanin, L.; Fickel, J.; Reyer, H.; Reinsch, N.; Henne, H.; Schön, J.
- 13:40 [Analysis of runs of homozygosity of cattle living in different climate zones](#)
Falchi, L.; Mastrangelo, S.; Cesarani, A.; Senczuk, G.; Portolano, B.; Pilla, F.; Macciotta, N.P.P.
- 13:42 [The genomic inbreeding trend over the last 25 years in three Italian pig breeds](#)
Schiavo, G.; Bovo, S.; Ribani, A.; Tinarelli, S.; Cappelloni, M.; Gallo, M.; Fontanesi, L.
- 13:44 [Inbreeding and coancestry trends in Nordic Holstein](#)
Tenhunen, S.; Thomassen, J.R.; Sørensen, L.P.; Aamand, G.P.; Berg, P.; Kargo, M.
- 13:46 [Effect of genomic selection on genetic variability in chromosomal level in the Finnish Ayrshire](#)
Sarviaho, K.; Uimari, P.; Martikainen, K.
- 13:48 [Genomic diversity of two indigenous Croatian goat breeds](#)
Držić, I.; Orehovalić, V.; Vostrý, L.; Curik, I.; Mikulec, N.; Cubric-Curik, V.
- 13:50 [Consequences on the genome homozygosity of breeding program decisions to improve milk production in Manchega dairy sheep](#)
Rubio-De Juan, A.; Díaz, C.; Carabaño, M.J.; Fernandez-Santos, M.R.; Ramon, M.
- 13:52 Discussion
- 14:00 [Heterosis can be explained by thousands of partially recessive, deleterious mutations with very small effects](#)
Goddard, M.E.
- 14:15 [Signatures of selection and runs of homozygosity in the genome of several fancy and meat rabbit breeds](#)
Ballan, M.; Bovo, S.; Schiavo, G.; Schiavitto, M.; Negrini, R.; Fontanesi, L.
- 14:30 [Investigating genetic redundancy as a source of genetic diversity and adaptability in the U.S. Holstein breed](#)
Steyn, Y.; Lawlor, T.J.; Tsuruta, S.; Masuda, Y.; Legarra, A.; Lourenco, D.A.L.; Misztal, I.

- 14:45 [Inbreeding depression and heterosis for live-weight and carcass traits in purebred and crossbred sheep](#)
Rafter, P.; McHugh, N.; McDermott, K.; Berry, D.P.
- 15:00 [Phylogenetic analysis and nucleotide diversity of 69 cattle breeds including German Black Pied cattle using WGS](#)
Neumann, G.B.; Korkuć, P.; Arends, D.; Wolf, M.J.; May, K.; König, S.; Brockmann, G.A.
- 15:15 [Partitioning of autozygosity in different age-based classes in cattle populations with different demographic histories](#)
Druet, T.; Flori, L.; Gautier, M.

Session 68.

Porcine (1)

Room: Van Cappellen Zaal

Chair: Egbert Knol, Luca Fontanesi, Nick Serao

- 13:30 [Estimation of genetic parameters and trends of reproduction traits of Korean Landrace and Yorkshire Pigs](#)
Lee, S.S.; Alam, M.; Chang, H.K.; Choi, T.J.
- 13:32 [Genetic parameter estimates of heat tolerance in number of born alive in Landrace, Large White, and Duroc pigs](#)
Okamura, T.; Fukuzawa, Y.; Nishio, M.; Arakawa, A.; Ishii, K.; Takahashi, H.; Ogawa, S.; Satoh, M.
- 13:34 [Bayesian analysis of paternal and maternal gametic effects in a reciprocal cross between two Iberian varieties](#)
Srihi, H.; Ibañez-Escriche, N.; Casellas, J.; Noguera, J.L.; Hernández, P.; Martín De Hijas, M.; Vázquez-Gómez, M.; Negro, S.; Rosas, J.P.; Varona, L.
- 13:36 [Heritabilities and genetic correlations of litter traits at farrowing and semen production traits in Duroc pigs](#)
Ogawa, S.; Kimata, M.; Tomiyama, M.; Satoh, M.
- 13:38 [Genomic analysis of quality and morphological sperm parameters in Piétrain breeding boars](#)
Große-Brinkhaus, C.; Kröhl, Z.M.; Friedrichs, M.; Tholen, E.
- 13:40 [Differential expression in the porcine thymus upon infection by PRRSV, influenza B or their coinfection](#)
Sarfo Davila, K.M.; Sang, Y.; Ma, W.; Miller, L.C.
- 13:42 [Genetic associations between survival at different parities in commercial crossbred sows](#)
Poulsen, B.G.; Leite, N.G.; Lourenco, D.
- 13:44 [Piglet survival is lowly heritable in DanBred Landrace pigs](#)
Guo, X.; Sørensen, A.C.; Henryon, M.; Ostensen, T.
- 13:46 [Feasibility of reducing mortality of pigs from birth to slaughter by genetic selection](#)
Su, G.; Liu, T.; Christensen, O.F.; Lund, M.S.; Nielsen, B.
- 13:48 [Genotyping dead animals improves post-weaning survival of pigs in breeding programs](#)
Sharif-Islam, M.; Van Der Werf, J.H.J.; Henryon, M.; Chu, T.T.; Wood, B.J.; Hermes, S.
- 13:50 Discussion
- 14:00 [GBP5 PRRSV resistance gene had no effect on pigs' infectivity or susceptibility in a trial simulating natural infections](#)
Chase-Topping, M.E.; Plastow, G.; Dekkers, J.; Fang, Y.; Gerdts, V.; Van Kessel, J.; Harding, J.; Opriessnig, T.; Doeschl-Wilson, A.
- 14:15 [Unravelling the genetic basis governing the porcine metabolism](#)
Bovo, S.; Schiavo, G.; Fanelli, F.; Ribani, A.; Bertolini, F.; Utzeri, V.J.; Gallo, M.; Galimberti, G.; Dall'olio, S.; Martelli, P.L.; Casadio, R.; Pagotto, U.; Fontanesi, L.
- 14:30 [The value of innate sow appetite as a model trait for maternal breeding objectives](#)
Vargovic, L.; Bunter, K.L.; Hermes, S.

- 14:45 [Genomic regions associated with backfat thickness show pleiotropic effect on osteochondrosis in pig](#)
Van Son, M.; Derks, M.F.L.; Lopes, M.S.; Sevillano, C.A.; Harlizius, B.; Grindflek, E.
- 15:00 [Non-genetic correlations between production traits and litter traits in pigs are important to account for](#)
Ostensen, T.; Henryon, M.; Guo, X.; Christensen, O.F.; Su, G.; Sørensen, A.C.
- 15:15 [Breeding for component traits of litter size at day 5 increases piglet survival while maintaining litter size at day 5](#)
Henryon, M.; Ostensen, T.; Guo, X.; Su, G.; Sørensen, A.C.

Session 69.

Novel traits: Environment and greenhouse gas (1)

Room: Willem Burger Zaal

Chair: Michael Aldridge, Marcin Pszczola, Suzanne Rowe, Eileen Wall

- 13:30 [Can ruminal microbial information help improve selection for low-methane emitting dairy cows?](#)
Zetouni, L.; Roques, S.; Kar, S.K.; De Haas, Y.; Schokker, D.; Aldridge, M.
- 13:32 [Phenotypic differences and genetic parameters for methane concentration in BeefxDairy crossbred slaughtercalves](#)
Johansen, K.; Kargo, M.; Bjerring, M.; Løvendahl, P.; Buitenhuis, A.J.
- 13:34 [Genome-wide association study for mid-infrared methane predictions in Walloon dairy cows](#)
Atashi, H.; Wilmot, H.; Vanderick, S.; Hubin, X.; Soyeurt, H.; Gengler, N.
- 13:36 [Genetic parameters for feed efficiency, gas emissions, oxygen consumption and wool traits in Australian Merino](#)
Marques, C.B.; De Barbieri, I.; Velazco, J.; Navajas, E.A.; Ciappesoni, G.
- 13:38 Discussion
- 13:45 [Genetic selection of feed efficiency and methane emissions in sheep and beef in Uruguay: progress and limitations](#)
Navajas, E.A.; Ravagnolo, O.; De Barbieri, I.; Pravia, M.I.; Aguilar, I.; Lema, M.O.; Vera, B.; Peraza, P.; Marques, C.B.; Velazco, J.I.; Ciappesoni, G.
- 14:15 [Breeding for lowered methane emissions using rumen microbial profiles in sheep](#)
Bilton, T.P.; Jordan, R.; Hess, M.K.; Hickey, S.M.; Amyes, N.; Johnson, P.; Henry, H.; Baird, H.; Van Stijn, T.; Veenvliet, B.; Bain, W.; Pile, G.; Watson, T.; Sandoval, E.; Peers-Adams, J.; Bryson, B.; Hess, A.S.; Dodds, K.G.; McEwan, J.C.; Rowe, S.J.
- 14:30 [Do we estimate dairy cows' methane production precisely enough?](#)
Pszczola, M.; Strabel, T.
- 14:45 [Heritability of methane emission in Norwegian Red cows based on measures from GreenFeed in commercial herds](#)
Wethal, K.B.; Difford, G.F.; Winnberg, K.; Norberg, E.; Heringstad, B.
- 15:00 [Heritability and genetic correlations of enteric methane emissions of dairy cows measured by sniffers and GreenFeed](#)
Van Breukelen, A.E.; Aldridge, M.N.; Veerkamp, R.F.; Koning, L.; Sebek, L.B.; De Haas, Y.
- 15:15 [Methane emission has low genetic correlations to lamb growth traits in Norwegian White sheep](#)
Jakobsen, J.H.; Blichfeldt, T.; Linnefaatten, L.-B.; Gløersen, M.O.; Wallin, L.E.; McEwan, J.C.

Session 70.

Avian (1)

Room: Eduard Flipse Zaal

Chair: John Henshall, Victor Olori, Samuel Aggrey, Esther Ellen

- 13:30 [Genome-wide association studies of chicken caecal microbiota](#)
Dai, X.; Hinsu, A.T.; Dadousis, C.; Pandit, R.J.; Crotta, M.; Limon, G.; Fosso, B.; Guitian, J.; Tomley, F.M.; Koringa, P.G.; Joshi, C.G.; Blake, D.P.; Psifidi, A.

- 13:32 [Breeding for an optimised gut microbiota composition for the improvement of phosphorus utilisation in Japanese quail](#)
Haas, V.; Vollmar, S.; Camarinha-Silva, A.; Bennewitz, J.
- 13:34 [High-resolution genotyping and analysis of in-silico predicted proteins for classical MHC genes in Korean native chicken](#)
Ediriweera, T.K.; Manjula, P.; Cho, E.; Kim, M.; Cho, S.; Lee, J.H.
- 13:36 [Genetic architecture of body weight and carcass traits in Ghanaian local chickens](#)
Kanlisi, R.A.; Amuzu-Aweh, E.N.; Walugembe, M.; Naazie, A.; Otsyina, H.R.; Chouicha, N.; Kelly, T.R.; Gallardo, R.; Dekkers, J.; Lamont, S.; Zhou, H.; Kayang, B.B.
- 13:38 Discussion
- 13:45 [Estimating environmental direct-maternal covariance in real data – illustration on broilers](#)
Romé, H.; Chu, T.T.; Marois, D.; Huang, C.H.; Madsen, P.; Jensen, J.
- 14:00 [Host transcriptome response of meat-type chickens infected with *Eimeria maxima* and reared under heat stress environment](#)
Aggrey, S.E.
- 14:30 [Changes in genetic parameters for traits under genomic selection in poultry](#)
Richter, J.; Hidalgo, J.; Breen, V.; Hawken, R.; Misztal, I.; Lourenco, D.
- 14:45 [Effects of age, line and diet on the occurrence of white striping lesions in broiler breast muscle](#)
Fernandes, L.T.; Peixoto, J.O.; Dal Pizzol, M.S.; Ibelli, A.M.G.; Morés, M.A.Z.; Tavernari, F.C.; Coldebella, A.; Cantão, M.E.; Ledur, M.C.
- 15:00 [Variation in male autosomal recombination in turkeys \(*Meleagris gallopavo*\)](#)
Rochus, C.M.; Wood, B.J.; Baes, C.F.
- 15:15 [Functional annotations of regulatory elements in the chicken genome](#)
Pan, Z.; Wang, Y.; An, L.; Bi, Y.; Guan, D.; Delany, M.; Cheng, H.H.; Zhou, H.

Session 71.

Statistical genetics: GWAS (2)

Room: Grote Zaal

Chair: Marco Bink, Goutam Sahana, Marie-Pierre Sanchez

- 16:00 [Multivariate GWAS revealed a critical region on chromosome 4 for developmental and feather growth traits in ducks](#)
Tarsani, E.; Desire, S.; Matika, O.; McIntosh, K.; Rae, A.; Kranis, A.; Watson, K.A.
- 16:02 [Investigation of genes associated with maternal weaning weight in South African Bonsmara beef cattle](#)
Reding, J.J.; Van Der Westhuizen, R.R.; Berry, D.P.; Van Marle-Koster, E.
- 16:04 [Genome-wide genomic and functional association study for workability and calving traits in Holstein cattle](#)
Suchocki, T.; Kosińska-Selbi, B.; Żarnecki, A.; Jakimowicz, M.; Jagusiak, W.; Morek-Kopeć, M.; Szyda, J.
- 16:06 [Genomic region-specific association test identifies new loci for carcass traits in Hanwoo \(Korean native cattle\)](#)
Lee, D.J.; Lee, D.H.; Kang, J.M.; Kim, Y.K.; Chung, Y.J.; Lee, S.H.
- 16:08 [Genetic mechanisms underlying feet and legs malformation in Nellore cattle: prioritization of GWAS results](#)
Silva, T.L.; Gondro, C.; Fonseca, P.A.S.; Da Silva, D.A.; Vargas, G.; Neves, H.H.R.; Carvalho Filho, I.; Teixeira, C.S.; Albuquerque, L.G.; Carvalheiro, R.
- 16:10 [Genome-wide association studies for milk yield in *Bos taurus* X *Bos indicus* crossbred cattle in India](#)
Alkalaldehy, M.; Swaminathan, M.; Podtar, V.; Jhadav, S.; Dhanikachalam, V.; Joshi, A.; Gibson, J.
- 16:12 [Grouping of highly correlated variables improves performance of genomic evaluations](#)
Wittenburg, D.; Klosa, J.

- 16:14 [A Monte-Carlo approximation of the null hypothesis for genome wide association using the windows variance approach](#)
López-Carbonell, D.; Ramírez, M.; Altarriba, J.; Srihi, H.; Varona, L.
- 16:16 Discussion
- 16:30 [Sequence-based association analyses on X chromosome in six dairy cattle breeds](#)
Sanchez, M.P.; Escoufflaire, C.; Baur, A.; Hozé, C.; Capitan, A.; Fritz, S.; Boichard, D.
- 16:45 [Pleiotropic effects on carcass and meat quality traits in crossbred beef cattle](#)
Rezende, F.M.; Rodriguez, E.; Leal-Gutiérrez, J.D.; Elzo, M.E.; Johnson, D.D.; Carr, C.; Mateescu, M.G.
- 17:00 [Sequence-based multi-trait genome-wide association study for linear classification traits in Belgian Blue beef cattle](#)
Gualdron Duarte, J.L.; Gori, A.S.; Costa Monteiro Moreira, G.; Georges, M.; Charlier, C.; Druet, T.
- 17:15 [Integrating imputed structural variants and tandem repeats in a GWAS for growth and carcass traits in F2 pig crosses](#)
Blaj, I.; Tetens, J.; Bennewitz, J.; Thaller, G.; Falker-Gieske, C.
- 17:30 [Detecting QTL for two lowly correlated traits using multi-trait and meta-analysis approaches in Swiss Large White pigs](#)
Nosková, A.; Mehrotra, A.; Kadri, N.K.; Neuenschwander, S.; Hofer, A.; Pausch, H.
- 17:45 [A Forward algorithm to identify credible sets in Bayesian variable selection models](#)
De Los Campos, G.; Samaddar, A.; Valente, B.; Chen, C.-Y.; Herring, W.; Grueneberg, A.

Session 72.

Genetic diversity and inbreeding: Genebanking

Room: Jurriaanse Zaal

Chair: Kor Oldenbroek, Gwendal Restoux, Gustavo Gandini

- 16:00 [New FAO guidelines for the management of animal genetic resources](#)
Boettcher, P.J.; Ajmone-Marsan, P.; Baumung, R.; Boes, J.; Colli, L.; Ginja, C.; Honkatukia, M.; Kantanen, J.; Leroy, G.; Lenstra, J.A.
- 16:02 [Genebanks for animal genetic resources in Europe: quality management system as a tool to improve their operation](#)
Danchin, C.; Bojkovski, D.; Duclos, D.; Neuteboom, M.; Schoon, M.; Tejerina Ampudia, F.; Tixier-Boichard, M.; Hiemstra, S.J.
- 16:04 [Genetic characterization of endangered indigenous pigs of Angola](#)
Sá, P.; Santos, D.; Leitão, A.; Cordeiro, J.M.; Gama, L.T.; Amaral, A.J.
- 16:06 [Genetic diversity and inbreeding in US Jersey population and germplasm collection](#)
Srikanth, K.; Neupane, M.; Jaafar, M.A.; Wolfe, C.W.; Huson, H.J.; Van Tassell, C.P.; Blackburn, H.D.
- 16:08 Discussion
- 16:15 [Development and utilization of the United States gene bank collection](#)
Blackburn, H.D.
- 16:30 [Mapping genetic diversity in European gene banks: preliminary results on chickens for the validation of IMAGE001 array](#)
Tixier-Boichard, M.; Peynot, N.; Duclos, D.; Weigend, S.; Monteagudo, L.; Martinez Martinez, A.; Delgado, J.V.; Gonzalez Prendes, R.; Crooijmans, R.; Restoux, G.
- 16:45 [Conservation of an endangered pig breed using optimum contribution selection](#)
Nielsen, H.M.; Kargo, M.

- 17:00 [IDI: an index to assess the usefulness of cryopreserved collections for the management of animal genetic diversity](#)
Jacques, A.; Duclos, D.; Danchin-Burge, C.; Mercat, M.J.; Tixier-Boichard, M.; Restoux, G.
- 17:15 [Conservation through utilization in German Red and White dual-purpose cattle](#)
Slagboom, M.; Milkevych, V.; Liu, H.; Thomasen, J.R.; Kargo, M.; Schmidtman, C.
- 17:30 [Genetic rescue of small populations in the presence of deleterious variation](#)
Reimer, C.; Weigend, S.; Geibel, J.; Pook, T.
- 17:45 [Genebank collections in relation to risk status in livestock species](#)
Leroy, G.; Blackburn, H.; Danchin-Burge, C.; Tejerina Ampudia, F.; Hiemstra, S.J.; Ligda, C.; Boettcher, P.; Baumung, R.

Session 73.

Porcine (2)

Room: Van Cappellen Zaal

Chair: Egbert Knol, Luca Fontanesi, Nick Serao

- 16:00 [Phenotyping strategies for an efficient and holistic approach to reduced boar taint through genomic selection](#)
Markey, A.; Burgeon, C.; Gengler, N.
- 16:02 [Genome-wide association study for oxidative stress indicators in replacement gilts](#)
Breuer, S.A.; Chinchilla-Vargas, J.; Kerr, B.J.; Stalder, K.J.
- 16:04 [Genetic determinism of boar taint in the French Landrace pig breed](#)
Larzul, C.; Mercat, M.J.; Hassenfratz, C.; Carillier-Jacquín, C.; Comte, R.; Blanchet, B.; Louveau, I.; Boulot, S.; Prunier, A.
- 16:06 [A comprehensive overview of mitochondrial DNA insertions in the nuclear genome of the pig](#)
Bolner, M.; Ballan, M.; Bovo, S.; Schiavo, G.; Fontanesi, L.
- 16:08 [To Box-Cox or not to Box-Cox: phenotypic and genomic evaluation of litter size variability in Landrace pigs](#)
Cieler, G.; Knol, E.F.; Lopes, M.S.; Sell-Kubiak, E.
- 16:10 [Genetic parameters of feeding behaviour and feed efficiency traits in Pietrain](#)
Núñez, P.; Gol, S.; Reixach, J.; Ibáñez-Escriche, N.
- 16:12 [Genetic analysis of hoof colour in Duroc pigs](#)
Vila, J.; Iheshiulor, O.O.M.; Bink, M.C.A.M.; Huisman, A.E.
- 16:14 [Filling information gaps in swine crossbreeding schemes by imputing non-genotyped F1 animals to improve genetic gain](#)
See, G.M.; Fix, J.S.; Schwab, C.R.; Spangler, M.L.
- 16:16 [Distinctive gene-expression profiles characterise tail-biting precursors in pigs under dietary protein restriction](#)
Couteller, L.; Roch, L.; Kasper, C.
- 16:18 [Analyses of heat stress effects on the farrowing rate of Iberian sows](#)
Muñoz, M.; Matos, G.; Gómez, G.; García-Casco, J.M.
- 16:20 [Whole-genome screening for resilience against PRRSV outbreaks in breeding sows](#)
Laplana, M.; Ros-Freixedes, R.; Estany, J.; Fraile, L.J.; Pena, R.N.
- 16:22 Discussion
- 16:30 [Genetic relationships among immune response traits of young healthy pigs evaluated by immunoassays](#)
Bhatia, V.; Schmied, J.; Cheng, J.; Bai, X.; Mallard, B.; Fortin, F.; Harding, J.C.S.; Dyck, M.K.; Plastow, G.S.; Field, C.J.; Rogel-Gaillard, C.; Blanc, F.; Piggen Canada; Dekkers, J.C.M.
- 16:45 [Sequencing-based genome-wide association study for resilience indicators in growing pigs](#)
Laghuaouta, H.; Pena, R.N.; Ros-Freixedes, R.; Fraile, L.; Laplana, M.

- 17:00 [First parity indicator traits for longevity in crossbred sows](#)
Iversen, M.W.; Enger, E.G.
- 17:15 [protiPig: genomic analyses of traits related to nitrogen utilisation efficiency in pigs](#)
Schmid, M.; Weishaar, R.; Berghaus, D.; Haese, E.; Sarpong, N.; Kurz, A.; Seifert, J.; Camarinha-Silva, A.; Rodehutsord, M.; Bennewitz, J.
- 17:30 [Genomic prediction of ham weight loss during dry-curing in heavy pigs](#)
Bonfatti, V.; Faggion, S.; Carnier, P.
- 17:45 [Meta-analyses for boar taint compounds in two purebred maternal lines and Piétrain-sired crosses](#)
Brinke, I.; Große-Brinkhaus, C.; Roth, K.; Pröll-Cornelissen, M.J.; Schiefler, I.; Tholen, E.

Session 74.

Novel traits: Environment and greenhouse gas (2)

Room: Willem Burger Zaal

Chair: Michael Aldridge, Marcin Pszczola, Suzanne Rowe, Eileen Wall

- 16:00 [Life cycle assessment to predict individual environmental impacts: towards selection for sustainable pig production](#)
Soleimani, T.; Hermes, S.; Gilbert, H.
- 16:02 [Genetic parameters for growth, feed intake and greenhouse gasses emissions in Italian Holstein-Friesian bulls](#)
Tiezzi, F.; Finocchiaro, R.; Benzoni, L.; Van Kaam, J.B.C.H.M.; Marusi, M.; Bozzi, R.; Cassandro, M.
- 16:04 [Association of genetic resistance to internal nematodes and production traits on feed efficiency and methane emissions](#)
Navajas, E.A.; Ciappesoni, G.; Gimeno, D.; Velazco, J.I.; De Barbieri, I.
- 16:06 [Ruminal background of predisposed milk urea \(MU\) concentration in Holsteins](#)
Honerlagen, H.; Reyer, H.; Segelke, D.; Oster, M.; Ponsuksili, S.; Trakooljul, N.; Kuhla, B.; Wimmers, K.
- 16:08 [Predicting nitrogen use efficiency of individual dairy cows by mid-infrared spectra](#)
Shi, R.; Lou, W.; Ducro, B.; Van Der Linden, A.; Mulder, H.A.; Oosting, S.J.; Li, S.; Wang, Y.
- 16:10 Discussion
- 16:15 [Clearing the air between methane and commercial beef cattle in Ireland](#)
Ryan, C.V.; Kirwan, S.F.; Crowley, J.J.; Purfield, D.C.; Pabiou, T.; Evans, R.D.
- 16:30 [The impact of selection for divergence in methane emissions on alimentary tract measures of eight-month-old sheep](#)
McRae, K.M.; Hickey, S.M.; Greer, G.J.; Bryson, B.; Knowler, K.J.; Bain, W.E.; Elmes, S.N.; Young, E.A.; Wing, J.; Waller, E.; McEwan, J.C.; Rowe, S.J.
- 16:45 [Economic values for climate change responsive traits to develop a sustainable dairy cattle breeding goal in the tropics](#)
Chepsiror, C.K.; Ilatsia, E.D.; Okeno, T.O.
- 17:00 [Phenotypic and genetic trends in American Angus associated with climate variability](#)
Rovere, G.; Cuyabano, B.C.D.; Makanjuola, B.; Kelly, S.; Gondro, C.
- 17:15 [Genetic variation in resilience to climate effects on beef carcass traits](#)
Bunning, H.; Wall, E.
- 17:30 [Genetic parameters for rumination time and traits related to sustainable dairy production](#)
Lopes, L.S.F.; Houlahan, K.; Alcantara, L.; Oliveira Jr, G.A.; Tulpan, D.; Miglior, F.; Schenkel, F.S.; Baes, C.F.
- 17:45 [Genotype by temperature-humidity index interactions on milk production and udder health traits in the Montbeliarde cows](#)
Vinet, A.; Mattalia, S.; Vallée, R.; Bertrand, C.; Bertuzzi, P.; Cuyabano, B.C.D.; Boichard, D.

Room: Eduard Flipse Zaal

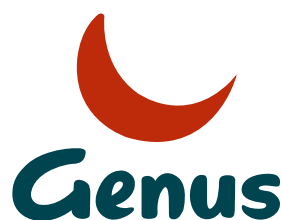
Chair: John Henshall, Victor Olori, Samuel Aggrey, Esther Ellen

- 16:00 [Time-series transcriptome analysis of broilers under *Eimeria tenella* infection reveals host-pathogen interactions](#)
Kim, M.; Chung, Y.; Manjula, P.; Seo, D.; Cho, S.; Cho, E.; Ediriweera, T.K.; Yu, M.; Nam, S.; Heo, J.M.; Lee, J.H.
- 16:02 [Genetic diversity of *Eimeria tenella* apical membrane antigen 1 in chickens from KwaZulu-Natal, South Africa](#)
Fatoba, A.J.; Zishiri, O.T.; Blake, D.P.; Peters, S.O.; Lebepe, J.; Mukaratirwa, S.; Adeleke, M.A.
- 16:04 [Chicken quantitative traits follow the omnigenic model](#)
Davoodi, P.; Ehsani, A.; Vaez Torshizi, R.; Masoudi, A.A.
- 16:06 [Association of polymorphism of MAP3K8 with egg production traits of white muscovy ducks \(*Cairina moschata*\)](#)
Bello, S.; Xu, H.; Zhang, S.; Aloryi, K.; Ahmed, R.; Bahareldin, A.; Adeola, A.; Popoola, M.; Zhu, W.; Zhang, D.; Zhang, X.; Ji, C.; Nie, Q.
- 16:08 Discussion
- 16:15 [Genetic markers associated with bone quality in Rhode Island Red laying hens](#)
Sallam, M.; McCormack, H.A.; Fleming, R.H.; Wilson, P.W.; Andersson, B.; Schmutz, M.; Benavides, C.; Dominguez-Gasca, N.; Sanchez-Rodriguez, E.; Rodriguez-Navarro, A.B.; Dunn, I.C.; De Koning, D.J.; Johnsson, M.
- 16:30 [Determining the heritability of premaxillary bone shape and size within two populations of pure line laying hens](#)
Struthers, S.; Andersson, B.; Schmutz, M.; McCormack, H.A.; Wilson, P.W.; Dunn, I.C.; Sandilands, V.; Schoenebeck, J.J.
- 16:45 [No G×E on egg qualities and body weight between cage and floor systems, implications for breeding programmes in layers](#)
Bédère, N.; Bécot, L.; Burlot, T.; Le Roy, P.
- 17:00 [Growth and laying performance of local chicken breeds and their crosses fed with faba beans](#)
Sharifi, A.R.; Nolte, T.; Jansen, S.; Weigend, S.; Mörlein, D.; Halle, I.; Link, W.; Simianer, H.
- 17:15 [Heterosis of egg-laying performance in chickens](#)
Ni, A.X.; Calus, M.P.L.; Bovenhuis, H.; Sun, Y.Y.; Chen, J.L.
- 17:30 [In vitro effects of probiotic *Bacillus* strains on adaptive immune cells of broiler chicken](#)
Larsberg, F.; Sprechert, M.; Hesse, D.; Loh, G.; Brockmann, G.A.; Kreuzer-Redmer, S.
- 17:45 [Strain and age effects, as well as genetic parameters for adult traits in ostriches](#)
Cloete, S.W.P.; Engelbrecht, A.; Brand, Z.

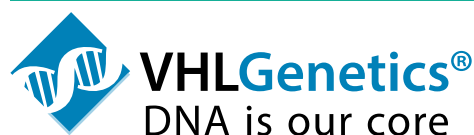
Exhibitors



Scientific sessions



Other



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