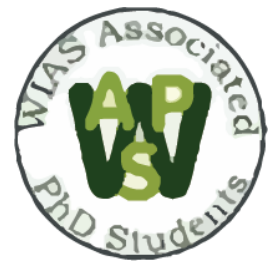




WAGENINGEN
UNIVERSITY & RESEARCH



WIAS ANNUAL CONFERENCE 2021

28 - 29 April 2021

Online COVID-friendly edition



Resilience

A warm welcome to all participants of the **WIAS Annual Conference 2021!**

The WIAS Annual Conference (WAC) or WIAS Science Day (WSD) is an annual scientific meeting organized by PhD candidates of WIAS (Wageningen Institute of Animal Sciences). The conference aims to bring together PhD-candidates, staff, and researchers from different fields within Animal Sciences to promote and present their research while encouraging interdisciplinary collaboration across the field of animal sciences.

The theme for this year's conference is: **Resilience**. It goes without being said that 2020-2021 has been an unprecedented year in many of our lives, both personally and as scientists. This year we have had to adapt to constant changes in on-campus building capacities, shipment dates for essential equipment, and access to labs and/or field sites, all while honing new techniques for communicating with each other remotely to get our projects done. As animal scientists we are accustomed to assessing resilience in our chosen animal models and we have seen how these animals cope with changes both induced by researchers or naturally occurring in their environments. This research exemplifies the variety of strategies animals use to adapt to constant change and this last year has shown us that we have a lot to learn about resilience in ourselves and in our research.

For this year's conference, we are pleased to welcome two keynote speakers. On Wednesday 28th, **Ingrid van Dixhoorn** will share with us her expertise on measuring and improving animal resilience. And on Thursday 29th, we will zoom in to a highly topical subject wherein **Bieneke Bron** will share insights on pathogen transmission and prevention strategies in relation to animal resilience. In addition, we are happy to host 32 oral presentations and 15 scientific posters from departments across WIAS, each highlighting resilience in their own field within animal sciences.

We have really enjoyed planning this unconventional, online conference in celebration of all the amazing work being done within WIAS! We hope that you find inspiration for your own work and forge new connections for future collaborations.

Stay Resilient,

The WIAS Annual Conference Committee

Tiffany Ernst (EZO)

Hongrui Cui (QVE)

Alice Scaillierez (APS)

Ilaria Minussi (ANU)

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Foreword by WIAS Science Director

Welcome the 26th WIAS annual conference!

The theme of this year is therefore aptly chosen: "Resilience". Nobody could have predicted that the world as we know it can be so disrupted by a single virus. Covid-19 has been the ultimate test for us as a species, to show our own "resilience", and it has clearly pointed out the strengths and weaknesses of our society. But Resilience is more than that. It is the ability of an ecosystem, an agricultural system, a species or even an organ inside a species, to cope with perturbations and still remain in equilibrium, performing as needed. And we, humans, are putting these systems increasingly to test, as we continue to disrupt the climate, reduce natural biodiversity, introduce new diseases and demand more of our animals by trying to make them more efficient: "Something's gotta give"

WIAS research is at the forefront of research on the role of animals in society, as exemplified by our mission: *'To improve our understanding of animals and their various roles for mankind through fundamental and strategic research and training of early-stage researchers (PhD and postdoc)'*.

Within our domain, research on resilience, and on how to make animals, animal production systems and ecosystems more resilient, is a major research theme and I am happy to see so many excellent contributions in the program. This year's conference is spread out over two days, using MS Teams, to give ample opportunity to exchange, discuss and reflect. We have invited 2 exciting speakers who will give their view on Resilience and 32 oral presentations that show what we are working on today.

All in all an exciting program covering the full breath of our research! I wish to thank the organisers for their hard work in bringing together such an interesting program and I wish you all a pleasant and fruitful WIAS science day.

To stay with the theme of this conference: **"Be resilient!"**

WIAS Scientific Director

Hans Komen

Program of the WIAS Annual Conference 2021

Day 1 – April 28th

Time	
9:00	Conference opening
9:30	Keynote speaker talk Ingrid van Dixhoorn Q&A
10:00	<i>Break: 15 minutes</i>
10:15	Oral presentations - Session 1
	<u>Ecosystem Resilience</u> <u>Agricultural Resilience</u> <u>Species Resilience</u> <u>Organismal Resilience</u>
10:15	Presentation 1 Presentation 1 Presentation 1 Presentation 1
10:35	Presentation 2 Presentation 2 Presentation 2 Presentation 2
10:55	<i>Break: 5 minutes</i>
11:00	Oral presentations - Session 2
	<u>Ecosystem Resilience</u> <u>Agricultural Resilience</u> <u>Species Resilience</u> <u>Organismal Resilience</u>
11:00	Presentation 1 Presentation 1 Presentation 1 Presentation 1
11:20	Presentation 2 Presentation 2 Presentation 2 Presentation 2
11:40	<i>Break: 5 minutes</i>
11:45	Pitch your poster - Session 1
11:55	Poster - Session 1 Virtual space chat (Wonder)
12:55	Closing remarks

Day 2 – April 29th

Time	
9:00	Conference opening
9:15	Keynote speaker talk Bieneke Bron Q&A
9:45	<i>Break: 15 minutes</i>
10:00	Oral presentations - Session 3
	<u>Ecosystem Resilience</u> <u>Agricultural Resilience</u> <u>Species Resilience</u> <u>Organismal Resilience</u>
10:00	Presentation 1 Presentation 1 Presentation 1 Presentation 1
10:20	Presentation 2 Presentation 2 Presentation 2 Presentation 2
10:40	<i>Break: 5 minutes</i>
10:45	Oral presentations - Session 4
	<u>Ecosystem Resilience</u> <u>Agricultural Resilience</u> <u>Species Resilience</u> <u>Organismal Resilience</u>
10:45	Presentation 1 Presentation 1 Presentation 1 Presentation 1
11:05	Presentation 2 Presentation 2 Presentation 2 Presentation 2
11:25	<i>Break: 5 minutes</i>
11:30	Pitch your poster - Session 2
11:40	Poster - Session 2 Virtual space chat (Wonder)
12:25	Closing remarks and awards ceremony Hans Komen & Maria Forlenza

All sessions will take place on MS Teams except for the poster sessions which will be hosted on Wonder. Concerning oral presentations, each conference theme (ecosystem resilience, agricultural resilience, species resilience and organismal resilience) will be hosted on 4 different channels. This way, you will be able to join the theme of your choice to attend oral presentations. The link for the Team containing all appropriate channels is here:

<https://teams.microsoft.com/l/team/19%3ad5cd420a427a47688981473b22e97109%40thread.tacv2/conversations?groupId=2e53e6b3-81d0-46a8-a61e-f2091dc769d9&tenantId=27d137e5-761f-4dc1-af88-d26430abb18f>

Keynote speakers



Ingrid van Dixhoorn
ingrid.vandixhoorn@wur.nl

Senior researcher at WLR

Ingrid is a veterinarian working as a senior scientific researcher at the animal health and welfare department of Wageningen Livestock Research. She namely worked on the role of housing enrichment on pig health but also on the resilience of dairy cows during the challenging transition period. As a keynote speaker, Ingrid will share with us insights on possible ways to define, measure and influence resilience in farm animals.



Bienneke, Gebbiena M. Bron
bienneke.bron@wur.nl

Post doc at QVE

Bienneke is a veterinarian turned disease ecologist working on the interface of (wild) animals and humans. She is fascinated by the eco-epidemiology of vector-borne zoonotic diseases and worked on plague, tick-borne diseases and currently Rift Valley fever virus. Thinking in a One Health framework, and mixing methodologies, she tries to better understand pathogen transmission to improve and evaluate prevention strategies.

Program of oral presentations

Day 1 - April 28th

Session 1 - from 10:15 to 10:55

Topic/channel	Time slot	Presenter name	Title	Abstract number
Ecosystem Resilience	10:15	Miriam Kuspiel	Moving out: do the costs of extra-territorial movement explain delayed dispersal in cooperative breeders?	27
	10:35	Elizabeth Phillips	Where are they now? Tracking the Mediterranean Lionfish Invasion via Local Dive Centers	31
Agricultural Resilience	10:15	Fasil Kebede	Multi-environment performance analysis to predict genotype by environment interactions (GxE) and resilience in livestock	24
	10:35	Marieke Poppe	Validation of resilience indicators based on daily milk yield in dairy cows	33
Species Resilience	10:15	Yale Deng	Impact of early-life rearing environment on gut microbiota succession, nutrient digestibility and energy balance of Nile tilapia in later life	18
	10:35	Awatif Eltijani	Characterization of mucosal B cells in common carp	19
Organismal Resilience	10:15	Benan Gulzari	Optimizing phenotypic and genomic selection schemes for integrated aquaculture genetic improvement programs	22
	10:35	Annemiek Blasweiler	The fate of duplicated genes in the Interferon stimulated pathways in the tetraploid Common Carp	7

Session 2 - from 11:00 to 11:40

Topic/channel	Time slot	Presenter name	Title	Abstract number
Ecosystem Resilience	11:00	Rainer Rauch	Effects of dietary protein oscillation on intake, production, digestibility and nitrogen metabolism in lactating dairy cows	34
	11:20	A.E. van Breukelen	Animal breeding can be used to reduce enteric methane emissions of dairy cows	39
Agricultural Resilience	11:00	L. Pisa	Bioconversion of chicken manure by housefly larvae (<i>Musca domestica</i> L.); larval performance and substrate conversion in relation to sterilization and carbohydrate addition	32
	11:20	Lotte Stokvis	Seaweed digestibility: <i>Ulva rigida</i> and <i>Solieria chordalis</i> co-products in broiler diets	37
Species Resilience	11:00	Pauline Jéhannet	What goes wrong during early development of artificially reproduced European eel <i>Anguilla anguilla</i> ? Clues from the larval transcriptome and gene expression patterns.	23
	11:20	Hugo Loning	The communication distance and singing ecology of the wild zebra finch	28
Organismal Resilience	11:00	Lisette E. van der Zande	Individual detection and tracking of group-housed pigs in their home pen using computer vision	40
	11:20	Louise Kremer	Is the Judgement Bias Task biased?	26

Day 2 – April 29th

Session 3 – from 10:00 to 10:40

Topic/channel	Time slot	Presenter name	Title	Abstract number
Ecosystem Resilience	10:00	Hongrui Cui	Evolutionary changes of a low pathogenic avian influenza virus (H9N2) in poultry under the selective pressure from inactivated vaccine	13
	10:20	Xiaoqian Gong	Understanding viral resilience to promote host resilience: A study on coronavirus endoribonuclease nsp15 as a viral antagonist of host immune responses	21
Agricultural Resilience	10:00	Eline Burgers	Revenues and costs of dairy cows with different voluntary waiting periods until first insemination	9
	10:20	Margret Wenker	Maternal bonding in dairy cattle: does type of cow-calf contact matter?	42
Species Resilience	10:00	Paraskevi Koletsis	Occurrence of mycotoxins in feedstuffs and fish feeds in Europe and the potential effects of deoxynivalenol (DON) on farmed fish species	25
	10:20	L.T.T. Phan	Effect of diet composition on energy utilisation efficiency in striped catfish (<i>Pangasius hypophthalmus</i>)	30
Organismal Resilience	10:00	Anna F. Bekebrede	Fasting reduces metabolism of intestinal epithelial cells in piglets.	6
	10:20	Jeroen Schoorl	Keeping the peace at the mucosal surface. How does host immunity control bad bugs?	36

Session 4 – from 10:45 to 11:25

Topic/channel	Time slot	Presenter name	Title	Abstract number
Ecosystem Resilience	10:45	Md. Iftakharul Alam	Synergistic effects of mangrove leaf litter and supplemental feed on water quality, growth and survival of shrimp (<i>Penaeus monodon</i> , Fabricius, 1798) post larvae.	2
	11:05	Muhammad Hunaina Fariduddin Aththar	Genetic parameters for growth and genotype by environment interaction of Nile tilapia in freshwater and brackish water	3
Agricultural Resilience	10:45	Robin E. Crossley	Dairy cattle welfare in spring-calving, pasture-based systems	12
	11:05	Tianyue Tang	Variation in birthweight, feed intake, breeding value, behaviour and skin lesions accounts for less than 45% of variation in growth rate in a multi-suckling system for pigs	38
Species Resilience	10:45	Morgina Akter	Effect of targeted feeding by varying pellet size on performance of carp-tilapia polyculture pond	1
	11:05	T.M.M. Bastiaansen	Producing resilient pellets in circular agriculture	5
Organismal Resilience	10:45	Jani de Vos	Resilience through knowledge: Molecular characterization of Pig IPECJ-2 and Chicken CRL cell lines	15
	11:05	Yun Yu	Recessive deleterious mutations in the TPO gene underlying familial thyroid follicular cell carcinoma in Dutch German longhaired pointers	44

Program of poster presentation

Day 1 - April 28th

Session 1 - from 11:45 to 13:00

Topic	Presenter name	Title	Abstract number
Ecosystem Resilience	Mariken de Wit	Data-driven modelling to improve our understanding of vector-borne disease risk: a One Health approach	17
	M. Zhou	Responses of high producing dairy cows to high ambient temperatures in the Netherlands	47
Agricultural Resilience	Cecilia Ayala	Analysing the farm-level impact of multispecies swards on Irish ruminant production systems	4
	Jacinta Bus	Individual variation in growing-finishing pig feeding patterns	10
	Emily Frehen-van Calmthout	Reinforcing resilience in broiler chickens by providing a moist, coproduct based diet	20
Species Resilience	Evelien Bos	Sources of variation in digestibility values of privately-owned dogs tested in-home	8
	Hannah De Waele	The evolution of cognition via predation: an experimental approach in guppies (<i>Poecilia reticulata</i>)	16
Organismal Resilience	Cornelius Gunter	Mucosal vaccination of fish: A whole body approach	11

Day 2 - April 29th

Session 2 - from 11:30 to 12:25

Topic	Presenter name	Title	Abstract number
Ecosystem Resilience	Marieke de Cock	The effect of urban greening on the distribution and abundance of wild rats and rat-borne zoonotic pathogens	14
Agricultural Resilience	Lonneke Noorman	Steering protein fermentation in the porcine intestinal tract by adding fermentable fibres	29
	Alice J. Scaillierez	Enlightened pigs: throwing a light on pig welfare.	35
	Chen Zheng	Practical application of fungal treatment of lignocellulosic biomass to feed ruminants in the Netherlands	46
Species Resilience	Xiaofei Yu	Genomic selection and introgression signatures resulting from adaptation to high salinity: a case study on an Indonesian farmed tilapia (Sukamandi) strain	43
Organismal Resilience	Kaylee S.E. van Dijk	Role of soluble and transmembrane TNF α during inflammation: focus on macrophage activation	41
	Yaqing Zhang	An <i>in vitro</i> model of the complex fish gill	45

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Abstracts

Abstract 1:

Effect of targeted feeding by varying pellet size on performance of carp-tilapia polyculture pond

Morgina Akter^{1,2*}, Marc Verdegem¹, Kazi Ahmed Kabir³, Mohammad Mamun-Ur-Rashid², Rodrigue Yossa⁴, Johan Schrama¹

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In fish polyculture, feed pellet size might allow targeted feeding of species that differ in size. In this study, we tested the effect of small (2mm) and large (6mm) pellet size on the production performance in ponds stocked with small Nile tilapia (*Oreochromis niloticus*) (~30 g) and large carps (~500 g). Twenty-four ponds measuring 45-m² each were assigned to test the effect of different combination of small and large pellets: S₁₀₀ (100% small pellets), S₅₀L₅₀ (50% small, 50% large), S₂₅L₇₅ (25% small, 75% large) and L₁₀₀ (100% large). There were six replicate ponds per treatment, and the growth period was 8 weeks. Each pond was stocked with 9 rohu (*Labeo rohita*), 9 catla (*Catla catla*), 9 silver carp (*Hypophthalmichthys molitrix*) and 150 Nile tilapia. Fishes were fed 15 g/kg^{0.8}/day which was lowered to 12 g/kg^{0.8}/day 6 days before harvest. Nile tilapia yield was highest in S₁₀₀ (10534 ± 1335 g) ponds and lowest in L₁₀₀ (8367 ± 565 g) ponds (P<0.05). Carp yield and survival were not affected by pellet size (P>0.05). The feed conversion ratio (FCR) increased from 2.30 in S₁₀₀ to 2.83 in L₁₀₀ (P<0.05). Results indicate that tilapia spent more energy and time in consuming large pellets which resulted in increased availability of feed for carps, but being slower eaters than tilapia, carps could not harness the benefit. Overall, tilapia dominated pond production raising their presence from 25% at stocking to 47% of total fish biomass at harvest.

Abstract 2:

Synergistic effects of mangrove leaf litter and supplemental feed on water quality, growth and survival of shrimp (*Penaeus monodon*, Fabricius, 1798) post larvae.

Md. Iftakharul Alam¹, Md. Nazmul Ahsan², Adolphe O. Debrot³, M.C.J. Verdegem^{1*}

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The present study identified the impact of mangrove leaf litter from four mangrove species (*Sonneratia apetala*, *S. caseolaris*, *Avicennia officinalis* and *Heritiera fomes*) on the production of juvenile shrimp (*Penaeus monodon*) with and without supplemental feed. Both mangrove species and feed application affected shrimp performance and water quality ($P < 0.05$). The only water quality parameters not affected were dissolved oxygen (DO), chemical oxygen demand (COD) and zooplankton concentration ($P > 0.05$). Phytoplankton concentration affected PL biomass gain ($P < 0.001$, $r = 0.681^{**}$). The average survival rate was 86-94% in the treatments with both leaf litter and feed, 75-82% in the treatments with only leaf litter and 88% in the treatment with only feed. The mean individual weight gain was 0.25-0.37g in the treatments with both leaf litter and feed, 0.03-0.10g in the treatments with only leaf litter and 0.17g in the treatment with only feed. The average specific growth rate (SGR) was 14-15% BWd⁻¹ in the treatments with both leaf litter and feed, 6-11% BWd⁻¹ in the treatments with only leaf litter and 13% BWd⁻¹ in the treatment with only feed. The treatments with addition of leaf litter had comparatively lower FCR (0.18-0.27) than the treatment with only feed (0.41). Finally, the synergistic effect of leaf litter and supplemental feed on shrimp performances and water quality was observed for all four species tested and the highest effect was recorded for *S. apetala* leaf litter followed by *A. officinalis*, *S. caseolaris* and *H. fomes*, in that order ($P < 0.05$).

Abstract 3:

Genetic parameters for growth and genotype by environment interaction of Nile tilapia in freshwater and brackish water

Muhammad Hunaina Fariduddin Aththar^{1,2*}, Priadi Setyawan^{1,3}, John Bastiaansen¹, Hans Komen¹

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The increasing salinity in coastal area is a problem that affects livelihoods of farmers in Indonesia and other parts of the world. Growing aquaculture species outside their preferred salinity range reduces growth performance. A fast growing species is needed with good adaptation to the brackish water ponds. Tilapia is a promising species with fast growth in freshwater that can also be cultivated in brackish water. However, to successfully produce tilapia in brackish water a strain with good growth over a range salinities is needed. To improve these traits, estimation of genetic parameters and genotype by environment interaction (GxE) in brackish water and freshwater is required. Objectives of this study were to investigate: 1) the genetic parameters of tilapia growth traits and 2) the presence of GxE interaction between brackish water and freshwater. For this, 91 fish families were produced following the one male to three females mating design. For each family, 20 fingerlings were randomly chosen and communally reared for grow-out in a brackish water and freshwater pond. After the grow-out period of 120-147 days, fish were harvested and recorded for harvest weight (HW) and standard length (SL). Daily growth coefficient (DGC) and length growth rate (GR) were also calculated based on weight and length data. No significant differences of trait levels were found between brackish water and freshwater. Heritabilities were moderate to high (0.35-0.72) for all trait in both environments. Genetic correlations between brackish water and freshwater for HW, SL, DGC and GR were moderate to high (0.64-0.79). In conclusion, the impact of GxE interaction between brackish water and freshwater is limited. The high value of genetic correlation between brackish water and freshwater showed that growth performance in fresh water is a good indication for growth potential in brackish water, indicating a high level of resilience in this tilapia strain to salinity stress.

Abstract 4:

Analysing the farm-level impact of multispecies swards on Irish ruminant production systems

Cecilia Ayala^{1*}, Jeroen C.J. Groot², Imke de Boer¹, Jean Kennedy³, Raimon Ripoll-Bosch¹

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Irish traditional pasture-based ruminant production is facing many challenges: agriculture is the largest contributor to Irish greenhouse gas emissions; profitability at farm level in beef and sheep farms is low and productivity of conventional permanent pastures is compromised.

Reseeding permanent pastures is a way of addressing the productivity issue with the aim of increasing farm profit, with farmers largely turning to monocultures of perennial ryegrass. These swards have high yields, but are quite dependent on nitrogen inputs, increasing production costs and greenhouse gas emissions.

Research has shown that multispecies swards have higher yields than monocultures, at lower fertilization rates, and can also reduce lamb's days to slaughter and thus, greenhouse gas emissions (per kilogram of meat).

However, whole farm-level analysis of the benefits and drawbacks of multispecies is still lacking. In this project we aim to explore the impact of reseeding with multispecies, versus perennial ryegrass, on farm greenhouse gas emission and operating profit. Using the bio-economic model FarmDESIGN and based on data from an Irish experimental farm, we built three mixed grazing farms (a traditional permanent pasture farm, a perennial ryegrass farm, and a multispecies farm).

Preliminary results show that, although both multispecies and perennial ryegrass farms could generate similar operating profits, which are higher than those of the permanent pasture farm, multispecies do so while maintaining lower greenhouse gas emissions. This suggests multispecies swards could be an ecological intensification option for farmers to address some of the socio-economic issues they face, without a negatively impacting greenhouse gas emissions.

Abstract 5:

Producing resilient pellets in circular agriculture

T.M.M. Bastiaansen^{1*}, S. de Vries¹, J. Dijkman², M. Thomas^{1,3}, W.H. Hendriks¹, G. Bosch¹

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The physical quality of feed pellets is essential for the handling properties and efficient use of feeds. To produce high quality pellets, modern pellet manufacturing processes rely heavily on the physicochemical properties of starch-rich materials such as cereals. Through addition of moisture and heat, the deformability of these materials is increased, which enhances inter-particle contacts during compaction and consequently yields stronger pellets. It is expected, however that cereals in livestock feed are to be increasingly substituted by co-products from food- and biofuel processes, as part of the transition towards a more circular agriculture. These co-products are more fibrous in nature, with low- or negligible levels of starch and, therefore, expected to be less deformable. Ergo, the substitution of cereals with co-products is expected to result in a reduced pellet quality. This project aims to develop knowledge on the inclusion of fibre-rich co-products in pelleted animal feed without compromising physical quality. Rheological-, phase transition- and viscoelastic-properties of fibrous co-products are determined under processing conditions. In addition, fibrous co-products are included in feed mashes and pelleted on pilot and industrial scale, to determine the relation between material characteristics, pellet quality and process conditions. Particle size and addition of fat impacts inter-particle binding and are therefore investigated in subsequent studies. Obtained insights are integrated into an overarching framework that is actively disseminated to the sector via the development of new teaching material. Thus, the results allow for the increased incorporation of fibrous co-products in resilient livestock feed pellets, contributing a more circular agriculture.

Abstract 6:

Fasting reduces metabolism of intestinal epithelial cells in piglets.

Anna F. Bekebrede^{1,2*}, Vincent C.J. de Boer¹, Walter J.J. Gerrits², Jaap Keijer¹

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The intestine is the primary site for absorption and digestion of food, but is also crucial for maintaining a barrier against pathogens. To support their function, intestinal epithelial cells are reliant on energy production. Insufficient energy production can diminish intestinal barrier function and thus contribute to onset of intestinal diseases such as diarrhoea, which pose a major health burden to both humans and animals. Diarrhoea is especially prevalent during the weaning transition, which is also often accompanied by decreased feed intake. We hypothesized that this decrease in feed intake causes a decrease in intestinal energy production, thereby contributing to intestinal barrier dysfunction. Therefore, we performed a pig study to investigate the effect of feed deprivation on intestinal cell metabolism. First, we optimized a technique to isolate primary intestinal epithelial cells (IECs) and measure their metabolic function using the Seahorse XF analyser, which allows for simultaneous measurement of oxidative and glycolytic metabolism. Piglets aged four and six weeks were fasted for 48 hours, to mimic feed deprivation upon weaning. Control piglets either remained with the sow (four-week-old piglets) or were fed a standard weaning diet (six-week-old piglets). IEC isolation proved to be difficult in the four-week-old fed piglets because of the thick mucus layer present, and respiration results of this group were therefore not taken into account. In six-week-old piglets, fasting resulted in significant reduction of metabolism. Both basal oxidative and glycolytic function were halved in the fasted piglets. The spare respiratory capacity, as well as compensatory glycolysis, which are measures for metabolic flexibility of a cell, were reduced by about a third in fasted piglets. Interestingly, there was no difference in contribution of either glycolysis or oxidative function to total metabolic function. Our results show that IEC metabolic function is decreased upon fasting in young piglets.

Abstract 7:

The fate of duplicated genes in the Interferon stimulated pathways in the tetraploid Common Carp

Annemiek Blasweiler^{1*}, Hendrik-Jan Megens^{1,2}, Geert Wiegertjes¹

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After the event of a whole genome duplication, duplicated genes are often lost over time. In the common carp (*Cyprinus carpio*) the duplication event is so recent that most of the genome is still in duplicated state. Following interbreeding of two diploid species, the common carp contains two subgenomes from different ancestral origin and can be called an allotetraploid (n=50). Progressively, advances in next generation sequencing technology are providing methods to reliably characterize recently duplicated genomes. Here, we present a new carp genome assembly, combining Illumina short read sequencing, Nanopore long read sequencing and HiC, a proximity ligation method that captures the three-dimensional organizational structure of chromatin. This combination of methods allows the disentanglement of the two subgenomes to reflect the two ancestral, interbreeding species. Correct interpretation of ploidy effects on immune responses requires detailed knowledge of the degree of functional divergence between duplicated genes, and their role in molecular pathways. We zoomed in on interferon-stimulated genes (ISGs) commonly expressed in response to viral infection. Binding of interferon (IFN) to cell surface receptors initiates protein signalling pathways within the cell and leads to the expression of a subset of ISG genes involved in responses of the innate immune system. We show that the carp has an ancestral set of ISGs active on both sub genomes, suggesting a complex organization of immune responses not easily explained by single subgenome dominance.

Abstract 8:

Sources of variation in digestibility values of privately-owned dogs tested in-home

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In-home digestibility testing can be advantageous compared to testing using dog panels in a kennel facility, but will likely yield more variable results as the study population's characteristics and living conditions are more variable. We aimed to determine sources of variation related to digestibility values among privately-owned dogs, as this is key information for the development of an in-home testing protocol. In a cross-over design, 53 privately-owned dogs of various breeds (34♀19♂; 5.1±3.2 yr; 21.2±12.0 kg) received two extruded dog foods with contrasting digestibility containing 0.1% TiO₂ as a marker. Dogs were fed at maintenance level (480 kJ × kg BW^{0.75}) for 7 days. Each day, owners collected the faeces of their dogs' and filled in a diary regarding food intake and faecal consistency. Foods and faeces were analysed for dry matter, ash, nitrogen, crude fat, starch, gross energy and titanium. Sources of variation in digestibility values among dogs during dietary days 2-7 were assessed using a multifactorial analysis of variance (ANOVA, Tukey's test) by repeated measures. Variation among dogs was shown to be explained by experimental food, dog age, body weight, sex, neuter status, body condition score and housing, but not by the dogs' daily activity. Identifying sources of variation in digestibility measures in dogs assists in the development and validation of in-home testing protocols. Improved understanding of variation will allow the appropriate study populations in terms of size and composition to be determined. Future studies should focus on other sources of variation, like participant compliance and sample contamination.

Abstract 9:

Revenues and costs of dairy cows with different voluntary waiting periods until first insemination

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Based on modelling studies, a 1-yr calving interval is generally considered optimal from an economic point of view. Recently some dairy farmers are deliberately extending the voluntary waiting period for insemination (VWP) to extend the calving interval, mainly to reduce the frequency of transitions such as dry-off and calving to improve cow health and reduce labor. This study aimed to evaluate yearly revenues, costs, and the net partial cashflow in a randomized control trial for individual cows with a VWP of 50, 125, or 200 days. Revenues and costs were calculated for milk yield, calves, number of inseminations, concentrate and partially mixed ration supply, disease treatments, discarded milk due to disease treatments, and labor (for milking, calving cows, inseminations, and disease treatments). Holstein-Friesian dairy cows (N=153) within one herd were blocked for parity, calving season, and 305-d milk yield, randomly assigned within the blocks to one of 3 VWP (VWP50, VWP125, or VWP200), and monitored from wk 6 post-partum until 6 wk after the next calving. Revenues from milk and costs for roughage and concentrate contributed most to the yearly net partial cashflow. Yearly revenues were greater in VWP50 compared with VWP200 (3,141 vs 2,848 €/cow per year), mainly because of 291 € greater milk revenues. Yearly costs were also greater in VWP50 compared with VWP200 (1,837 vs 1,632 €/cow per year), mainly because of 83 € greater concentrate costs. The VWP did not affect the net partial cashflow per cow per year.

Abstract 10:

Individual variation in growing-finishing pig feeding patterns

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The feeding patterns of growing-finishing pigs, consisting of intake, duration, frequency and rate, could potentially be used to monitor pig welfare. Feeding patterns, however, contain variation across and within days that appears unrelated to pig welfare and should be considered baseline, such as an increase in intake over time while duration and frequency decrease, and a peak in feeding activity in the afternoon. Although these patterns are clear at group level, many authors have reported large standard deviations around the means, implying that individual pigs may show vastly different patterns. Little is known about the variation in patterns at individual level, nevertheless distinct individual patterns could require different monitoring (e.g. modelling) methods. Our study aimed to gain insight into the feeding patterns of individual pigs, specifically looking into the variation between pigs and within a pig over time. We collected data from electronic feeding stations of 110 pigs (11 pigs/pen) and visualised group and individual patterns. At group level, we saw similar feeding patterns to what was expected from literature. Preliminary results showed distinct feeding strategies at the individual level. Pigs varied, for example, in the time of day during which they fed most and in the balance between feeding frequency and visit size used to obtain daily intake. These individual patterns became clearer with age. We conclude that pigs indeed show individual patterns in feeding behaviour, which develop over time. These individual patterns should be taken into account when developing welfare monitoring systems based on pig feeding patterns.

Abstract 11:

Mucosal vaccination of fish: A whole body approach

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This project aims to develop novel mucosal vaccination strategies for warm water fish species. Vaccination is the most effective way to prevent and possibly eradicate diseases which affect aquaculture fish species. Currently, the most effective vaccines are generally delivered by injection, but this method is labour intensive, causes handling stress and is only viable for certain fish species at the right age. Therefore, mucosal vaccination by immersion or oral administration, targeting the gills, skin, intestines or olfactory organs, is preferred.

Mucosal vaccines have been shown to be effective if they mimic the natural route of infection, for example by crossing mucosal surfaces, and if they elicit strong and lasting immune responses. In order to achieve these requirements, this project aims to develop live-recombinant viral vectors and replicon particle vaccines, and to assess their efficacy as mucosal vaccines for fish. For a whole-body approach, we will use a variety of available transgenic zebrafish lines to select promising vaccine candidates and gain insight into the underlying mechanisms of protection. The use of zebrafish which are transparent and/or have labelled immune cells will allow us to investigate *in vivo* and in real-time the kinetics of vaccine uptake and immune cell activation. Promising vaccine candidates will further be used to provide proof-of-principle of their efficacy in commercially relevant species, carp and tilapia.

Altogether the project addresses knowledge gaps on mucosal immune responses and could provide a universal platform for mucosal vaccination of fish.

Abstract 12:

Dairy cattle welfare in spring-calving, pasture-based systems

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Little research has been conducted on dairy cattle welfare within the Irish spring-calving, pasture-based system. A welfare assessment was conducted on 82 Irish dairy farms to determine the herd-level prevalence of seven animal-based indicators of welfare and identify baseline performance benchmarks. Farms were visited during both the summer-grazing and winter-housing periods. At each visit, the 2019 milking herd was scored for body condition (BCS), locomotion, ocular and nasal discharge, tail injuries, integument damage, and avoidance response. For each indicator, the range in mean performance of the top (T) and bottom (B) 20% of farms was identified for grazing and housing. At grazing, farms displayed: 0-4% (T), 20-72% (B) of cows outside BCS targets; 1-5% (T), 15-32% (B) lameness; 0% (T), 79-96% (B) ocular discharge; 2-15% (T), 44-86% (B) nasal discharge; 0-3% (T), 2-52% (B) tail injuries; 0-2% (T), 12-29% (B) integument damage; 51-74% (T), 91-100% (B) avoidance response >1m. Similar levels of lameness, ocular discharge and tail injuries were observed between visits, however, significant differences were found for BCS, nasal discharge, integument damage and avoidance response. During housing, farms displayed: 4-12% (T), 33-71% (B) of cows outside BCS targets; 2-16% (T), 53-89% (B) nasal discharge; 4-14% (T), 29-49% (B) integument damage; 4-60% (T), 61-100% (B) avoidance response >1m. Performance of the top 20% of farms represents achievable targets that farms within the Irish dairy system should strive to meet or exceed. Continuation of this research focuses on determining risk factors for specific welfare problems to further improve dairy cattle well-being.

Abstract 13:

Evolutionary changes of a low pathogenic avian influenza virus (H9N2) in poultry under the selective pressure from inactivated vaccine

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H9N2 subtype avian influenza virus (AIV) has become endemic in poultry in several location over the world, however, it was not under the primary surveillance and control in many countries due to its low pathogenicity. Several recent outbreaks of H9N2 in vaccinated poultry in Asian countries triggered the question on its transmission dynamics and evolutionary properties under the selective pressure from vaccination.

In this research, we first mimicked the natural infection and transmission process of H9N2 virus in vaccinated and non-vaccinated chickens. The statistical (S-I-R) model indicated that the transmission is not sufficiently reduced by the inactivated H9N2 vaccine. The estimated reproduction ratio (R) in non-vaccinated and low-vaccinated chicken (antisera HIT<8) were above 1. Even with higher titers (HIT>8) virus shedding still existed which contributed to the transmission in vaccinated chicken.

We therefore analysed surveillance samples that collected from local markets in 9 provinces in south China between 2013 and 2018. The H9N2 AIV isolated after 2013 grouped into a distinct new antigenic cluster, showing more mutations and a larger antigenic distance from vaccine strains (1998). Specific amino acid mutations were identified that could be related to the antigenic changes. Our findings were based on the available surveillance information of H9N2 AIV in local markets in China during 2013-2018. However, the combination of phylogenetic and antigenic analysis gave new insights to understand the molecular changes associated with antigenic drift.

Abstract 14:

The effect of urban greening on the distribution and abundance of wild rats and rat-borne zoonotic pathogens

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Increasing the number and surface of green (vegetation-based) and blue (water-based) spaces in cities is seen as a multipurpose investment not only to combat heat, but also to enrich urban biodiversity, improve living conditions and reduce flooding. However, urban greening could create more suitable habitats for wild rats and thereby facilitate the growth of rat populations and the dispersal of rat-borne zoonotic pathogens.

Rats are a well-recognized source of multiple zoonotic pathogens responsible for significant human morbidity and mortality worldwide. They are well adapted to close cohabitation with humans and are considered synanthropic animals. The proximity of rats and humans, especially in urban areas, can create higher risks for infection with rat-borne zoonotic pathogens.

Therefore, we are currently studying the effect of urban green on rat populations and rat-borne zoonotic pathogens in three cities in the Netherlands (Amsterdam, Eindhoven and Rotterdam). Urban areas are divided into three categories: parks (high green), green residential areas (medium green) and grey residential areas (low green). Over a period of 8 months, 6 locations per month will be studied. In every location, rats will be trapped systematically, by using 20 rat snap-traps per location during one month.

The trapped rats will be used for subsequent zoonotic pathogen analyses. The results will be corrected for and linked to a list of (environmental and socio-economic) factors, in order to assess the relation between urban greening, relative rat population size and rat-borne zoonotic pathogen distribution. These results will be translated to practical advice for municipalities to decrease rat nuisance and the risk for rat-borne zoonoses.

Abstract 15:

Resilience through knowledge: Molecular characterization of Pig IPECJ-2 and Chicken CRL cell lines

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The Functional Annotation of Animal Genome (FAANG) consortium is driven by a scientific community and aims to provide functional annotation of the genome for farm and companion animals. Functional annotation of genomes in farm animals contributes to animal breeding. Knowledge of functional genomic sequences is essential to obtain insight in traits of interest as well as biological processes such as intestinal absorption, immunity, protein interaction and tumor growth. Cell lines are useful models to assay and investigate these elements in detail. In this study we investigated two cell lines which are of interest due to the uniqueness of the cells being promoted as being neither transformed nor tumorigenic in nature and the functions of the cells. The IPECJ2 cell line in pigs is an intestinal epithelial cell line which can be used to investigate e.g. intestinal transportation. The Chicken SL-29 cell line is derived from embryonic (10 days gestation) untransformed fibroblast cells and is used to gain insight into immune function. The functional genome of cell lines can be different in comparison to tissues thus it is important to characterize these cell lines. Genome structure results showed aneuploidy of various chromosomes and multiply structural variants such as duplications, insertions and deletions. Gene expression analyses showed higher gene expression for genes located on chromosomes with aneuploidy, in comparison to diploid chromosomes. In conclusion, this study establishes the molecular characteristics at various levels of each cell line to use as a reference in future research not only within the FAANG community, but the scientific community.

Abstract 16:

The evolution of cognition via predation: an experimental approach in guppies (*Poecilia reticulata*)

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A key objective in modern biology is understanding the evolutionary processes that underlie the substantial variation in behaviour and life-history traits in animals. Surprisingly, the causes for the striking variation in cognition across species are still poorly understood. Comparative studies suggest that predation pressure imposes strong selection on cognitive evolution, yet experimental tests are thus far lacking. To fill this knowledge gap, I will perform several experiments to test how predation shapes the evolution of cognition. I will use Trinidadian guppies (*Poecilia reticulata*), a species that naturally occurs in high and low predation areas and is therefore ideal to link cognitive performance to an ecological and evolutionary relevant framework. I will use selection lines developed for survival under predation, allowing me to identify the link between cognition and predation in an unprecedented way. Since cognition consists of different domains, which are likely impacted by predation in different ways, I will investigate several key domains. The fish will be subjected to state-of-the-art cognitive assays that make use of novel technology. While domain-specific results are exciting on their own, the most innovative aspect will be the opportunity to construct “cognitive landscapes”. These landscapes allow for complex comparisons, providing opportunities to uncover intricate links between cognitive domains and underlying structures of cognition. My project fills a void in modern biology by providing causal conclusions about the evolution of cognition and by contributing to our understanding of how loss of predators can have downstream effects on traits essential to cope with environmental challenges.

Abstract 17:

Data-driven modelling to improve our understanding of vector-borne disease risk:
a One Health approach

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Severe vector-borne diseases have not yet formed a major threat for Dutch public health. Sporadic cases have occurred from imported infections, but the ecosystem has been sufficiently resilient to prevent diseases from getting established. However, this resilience is decreasing under the influence of ecological changes, urbanisation, international travel, and changes in land use and water management. To be better prepared for this increasing risk, it is important to understand how these changes interact and together affect transmission risk. This project is part of 'One Health PACT' (Predicting Arbovirus Tipping Points), an interdisciplinary consortium that aims to improve understanding of and preparedness for vector-borne diseases in the Netherlands. My role as a modeller is to connect the various types of data collected in the consortium using advanced Bayesian methods to better understand what drives an outbreak, assess the probability of future outbreaks and inform surveillance and control strategies. I will develop a transmission model to simulate potential emergence and spread of (new) arboviruses in the Netherlands. The metapopulation simulation model brings together spatiotemporal dynamics of human, animal and environmental factors required for emergence to assess the probability of outbreaks, using Usutu virus as a case study initially. Subsequently, we can use these empirically grounded models to apply them to different arboviruses, compare various control strategies and improve the current surveillance system. These models can also be adapted to study the possible consequences of future change scenarios for disease risk.

Abstract 18:

Impact of early-life rearing environment on gut microbiota succession, nutrient digestibility and energy balance of Nile tilapia in later life

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Gut microbial colonization of fish starts from the first-feeding when the yolk sac is almost consumed. The gut microbiota plays an important role in nutrient digestion, immune system development and pathogens resistance of fish larvae. The microbial colonization process was mainly influenced by the feed and environmental microbial community that the fish were contacted. However, the impact of early-life rearing environment on fish gut microbiota succession and performance in the later-life stages remains largely unexplored. In this study, two different rearing conditions, namely flow-through system (FTS) and biofloc system (BFS) were applied for Nile tilapia larvae culture (0 - 14 days post hatching (dph)). After that, fish were transferred to a common recirculating system and fed with the same feed (15 - 62 dph). A grow trail (63 - 104 dph) was performed in another recirculating system and fish were fed with two types of feed containing different levels of non-starch polysaccharides (NSP). The results showed that larvae cultured in FTS and BFS exhibited different gut microbiota composition and growth. The difference in gut microbiota was still detected at 62 dph even the fish were fed with same feed and cultured in the same system. However, the imprint of early-life microbial colonization was not shown at 104 dph, and no significant impact on nutrient digestions and energy balance was detected during the growth trail. Our study implied that host selection on gut microbiota overwhelmed the effect of early-life colonization with the growth of fish.

Abstract 19:

Characterization of mucosal B cells in common carp

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Fish protect themselves from various pathogenic challenges and stay resilient in their environments, thanks to the action of various immune cells. B cells at mucosal surfaces (skin, gill and gut), secrete immunoglobulins (antibodies) that neutralize microbes and microbial toxins. In teleost fish, IgM, IgD and IgT (IgT1 and IgT2 in carp) are the main immunoglobulins produced by B cells. IgM is known for a long time to play a protective role in both mucosal and systemic organs (blood, spleen, other peripheral organs). IgT, the most recently discovered, is described as the main immunoglobulin responsible for immune response at mucosal surfaces of the skin, gills, gut, nasal cavity, pharyngeal mucosa, and buccal cavity, but its role in systemic responses has also been reported.

Due to the lack of specific tools, information with regard to carp IgT at the protein level is missing. Here, we describe the generation and validation of antibodies specific for carp IgT1 and IgT2. We used these antibodies in combination with available monoclonal antibodies against carp IgM (WCI12) to evaluate the expression of the respective soluble immunoglobulins in the serum and mucus. In addition, we evaluated the relative distribution of IgT1+, IgT2+ and IgM+ B cells in the head kidney, spleen, gut, and gills of naïve carp. Furthermore, we assessed the immune responses of IgT1+ and IgM+ B cells to a systemic infection with the blood parasite *Trypanoplasma borrelli*, by examining the serum and spleen of infected carp. Altogether our data show that also in carp, IgT may be involved in mucosal as well as systemic responses and show the utility of our newly developed tools for future studies on carp responses to infection and vaccination.

Abstract 20:

Reinforcing resilience in broiler chickens by providing a moist, coproduct based diet

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It is known that providing broiler chickens with a moist diet, effects the uptake of nutrients, resulting in positive production parameters and morphology of the gastrointestinal tract (GIT). Such effect may also occur when broilers are provided with a diet containing a moist non-human edible coproduct. Increasing the usage of coproducts in broiler feed can reduce the pressure on the competition over agricultural land for either feed or food production.

A total of 382 male Ross 308 broilers were divided over 4 different treatments (T1 to T4), with 8 repetitions. T1 birds were fed a commercial dry pelleted feed (control), T2 and T3 birds were fed a moist diet, including 20% brewers spent grain (T2) or 20% wheat yeast concentrate (T3) and water, and T4 birds were fed a feed moisturized by adding water.

Body weight gain of the broilers who were fed the brewers spent grain diet (T2) was significantly higher than those fed the wheat yeast concentrate (+12.1%; $P < 0.0001$) or the moist mash diet (+7.43%; $P = 0.013$). The diet had no significant effect on the blood levels of NK-cells, B-cells and T-cells on day 7, 14 and 35. The villi length was found to be significantly longer for T2 compared to T1 on day 7 ($P = 0.023$). On day 35 all treatment groups were found to significantly differ in villi length except between T1 and T3, both representing the shortest villi ($P < 0.001$). Providing broilers with a moist coproduct diet, is a sustainable and beneficial novel feeding strategy.

Abstract 21:

Understanding viral resilience to promote host resilience: A study on coronavirus endoribonuclease nsp15 as a viral antagonist of host immune responses

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The outcome culminating coronavirus infection is determined by mutual interactions between the viruses and the hosts. Host cells possess elaborate immune responses, such as interferons that play a central role, and stress granules that function as signalling platforms. To maintain viral replication, coronaviruses have correspondingly evolved various counterstrategies, that we refer to as 'viral resilience'. To assist the hosts to survive viral infection, it is essential to develop anti-viral therapeutics. We refer to curing a viral infection via anti-viral therapeutics as 'host resilience'. Designing appropriate targets is critical to anti-viral therapeutics, and requires understanding the mechanism of viral counterstrategies. To put it another way, improving 'host resilience' requires knowledge of 'viral resilience'. In my PhD thesis, we studied the counterstrategies of coronavirus-encoded endoribonuclease nsp15. After infection of wild type and nsp15 endoribonuclease-deficient avian coronaviruses (IBV) in chicken and mammalian cells, we found that endoribonuclease nsp15 antagonizes interferons but also stress granules during IBV infection. Further analysis showed that this antagonism is mediated by nsp15's regulation of double-stranded RNAs. In addition, we observed a crosstalk between IFNs and SGs during IBV infection. Moreover, we provided evidence that nsp15 of IBV interferes with formation of chemically-induced SGs. And this activity of nsp15 is conserved among different genera of coronaviruses. Collectively, my PhD thesis work provides a better understanding of the 'viral resilience', the counterstrategy of coronavirus endoribonuclease nsp15, and thereby promote the 'host resilience', the exploitation of this enzyme for anti-viral therapeutics.

Abstract 22:

Optimizing phenotypic and genomic selection schemes for integrated aquaculture genetic improvement programs

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Centralized breeding programs are not available for most farmed fish species. One solution to this issue is to integrate breeding programs with production.

The objective of this study was to optimize an integrated breeding program for aquaculture species, where animals produced within production environment are the selection candidates. This research investigated two alternatives to select for a difficult to measure trait (DIF). One alternative was phenotypic selection on an indicator trait (IND). The other was genomic selection for DIF. Two-stage selection scheme was used where the first stage imposed phenotypic selection on harvest weight (HW). The second stage consisted of either phenotypic selection on IND or genomic selection for DIF. We investigated the genetic gains in DIF from selecting on IND or DIF by varying accuracies of GEBVs and the selected proportion in the first stage.

Given the population parameters used in our study, selecting on an IND that is very strongly correlated (0.9) to DIF yielded a similar response with genomic selection with an accuracy of 0.5. Selecting on GEBVs with accuracy above 0.5 always outperformed indirect selection. Selecting on GEBVs with an accuracy of 0.3 outperformed selecting on a moderately correlated (0.5) IND. With GEBV accuracies below 0.9, the maximum response in DIF is obtained by first applying phenotypic selection on HW.

Genotyping only the fraction of candidates that are selected in the first stage of selection significantly reduces genotyping costs and genomic selection with low accuracy will still outperform phenotypic selection on a moderately correlated indicator trait.

Abstract 23:

What goes wrong during early development of artificially reproduced European eel *Anguilla anguilla*? Clues from the larval transcriptome and gene expression patterns.

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The European eel cannot be reproduced in captivity yet but we manage to produce larvae now on a weekly basis. Larval resilience is however low and mortality during the first week is high. Larval transcriptomes were sequenced and compared between larvae that were collected at 1 day post-hatch (dph) from batches that survived less than 3dph (non-viable larvae) and larvae that survived for at least a week (viable larvae) to understand what goes wrong during early ontogeny. Expression of genes involved in inflammation and host protection was higher in non-viable vs. viable larvae suggesting that non-viable larvae suffered from infection. Expression of genes involved in homeostasis was higher in non-viable vs. viable larvae implying that non-viable larvae were possibly damaged. Morphogenesis was reduced in non-viable vs. viable larvae, probably because non-viable larvae invested energy in the immune response and homeostasis rather than in development. Major histocompatibility complex class-I (*mhc1*), M-protein (*myom2*), the dopamine 2B receptor (*d2br*), the melatonin receptor (*mtr1*) and heat-shock protein beta-1 (*hspb1*) showed strong differential expression and were therefore studied in 1, 8 and 15 dph larvae by RT-PCR to comprehend their role during ontogeny. Expression of *d2br*, *hspb1* and *mtr1* increased during ontogeny which may reflect the increase in movement at the start of swimming (8 dph) and feed searching behavior (15 dph). Expression of *mhc1* was highly expressed at all time points reflecting an active immune system. Expression of *myom2* decreased during ontogeny reflecting the growth investment. This study revealed that microbial control and salinity reduction might enhance larvae survival.

Abstract 24:

Multi-environment performance analysis to predict genotype by environment interactions (GxE) and resilience in livestock

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Performance of the existing livestock genotypes in smallholder systems of the tropics is too low to meet growing demands for animal source proteins. One approach to enhance current levels of productivity and address food security in Africa is sourcing improved genotypes developed for medium-input systems. These imported genotypes need to be tested for their yield and adaptability in the local environment. There has been a lack of comprehensive analytical framework to evaluate performance and resilience of livestock genotypes across environments. The biophysical factors and management practices of smallholder farmers are heterogeneous and require experimental designs and analytical methods which can disentangle the genetic potential of test strains from environmental confounding factors. Machine learning approaches were followed in the present study to fit species and phenotypic distribution models and identify the most important ecological factors influencing productivity. A theoretical framework of multi-environment performance analysis (MEPA) is used in plants to analyse GxE and stability. MEPA was adapted to evaluate five chicken genotypes distributed to farmers in diverse agro-ecologies of Ethiopia. We have applied ANOVA, regression, additive main effects multiplicative interaction model (AMMI), linear mixed-effects models (LMM), and Generalized Additive Models (GAMs) to evaluate performance and stability of chicken body weight across 45 testing sites. LMM and GAMs resulted in a better model fit than ANOVA and AMMI. Our approach demonstrates the applicability of MEPA in livestock to identify genotypes with superior performance and wider adaptability.

Abstract 25:

Occurrence of mycotoxins in feedstuffs and fish feeds in Europe and the potential effects of deoxynivalenol (DON) on farmed fish species

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The first part of this study evaluates the occurrence of mycotoxins patterns in feedstuffs and fish feeds. Results were extrapolated from a large data pool derived from wheat (n=857), corn (n=725), soybean meal (n=139) and fish feed (n=44) samples in European countries and based on sample analyses by liquid chromatography/tandem mass spectrometry (LC-MS/MS) in the period between 2012-2019. Deoxynivalenol (DON) was readily present in corn (in 47% of the samples) > wheat (41%) > soybean meal (11%), and in aquafeeds (48%). Co-occurrence of mycotoxins was frequently observed in feedstuffs and aquafeed samples. For example, in corn, multi-mycotoxin occurrence was investigated by Spearman's correlations and odd ratios, and both showed co-occurrence of DON with its acetylated forms (3-AcDON, 15-AcDON) as well as with zearalenone (ZEN). A meta-analytical approach aimed to estimate to which extent DON affects feed intake and growth performance in fish. Corn was identified as the ingredient with the highest risk of contamination with DON and its acetylated forms, which often cannot be detected by commonly used rapid detection methods in feed mills. Periodical state-of-the-art mycotoxin analyses are essential to detect the full spectrum of mycotoxins in fish feeds aimed to prevent detrimental effects on farmed fish and subsequent economic losses for fish farmers. Because levels below the stated regulatory limits can reduce feed intake and growth performance, our results show that the risk of DON contamination is underestimated in the aquaculture industry.

Abstract 26:

Is the Judgement Bias Task biased?

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Mood depends on one's perception of one's living conditions, resulting from the interaction between one's personality and the hedonic quality of the environment. Animal mood is commonly inferred from individual pessimism because animals in a bad mood are more pessimistic than animals in a good mood. Mood-induced pessimism is assessed using Judgment Bias Tasks (JBTs). However, there are indications that personality influences animal pessimism in JBT, hence complicating the interpretation of JBT results. We aimed to disentangle the effects of personality and housing conditions on pessimism, before investigating consistency in pessimism across housing conditions. We assessed dimensions of personality in 48 heifers using Open-Field, Novel-Object and Runway tests. Personality effects on pessimism in JBT were examined when heifers were housed under reference conditions. Subsequently, heifers were housed under positive or negative conditions, and housing effects on pessimism in JBT were investigated while controlling for personality differences. A Principal Component Analysis revealed three personality traits: Activity, Fearfulness and Sociability. Under reference conditions, inactive/fearful heifers were more pessimistic than inactive/non-fearful heifers ($p=0.032$), questioning the generalizability of JBT across individuals. Housing did not influence cattle pessimism ($p>0.05$), potentially due to an insufficient sensitivity of the JBT or a lack of treatment efficacy. Additionally, pessimism under reference conditions tended to be associated with pessimism under both positive and negative housing conditions ($p=0.057$) - suggesting that individual pessimism in JBT depends on stable characteristics like personality. We conclude that personality-based differences in perception of the JBT set-up may hinder the detection of mood-induced shifts in pessimism.

Abstract 27:

Moving out: do the costs of extra-territorial movement explain delayed dispersal in cooperative breeders?

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Individuals in many species remain as non-breeding helpers in their natal group before they leave to reproduce themselves, which apparently contradicts evolutionary theory of maximising reproductive success. Such delayed dispersal is predicted if high-quality breeding positions are limited and costly to obtain while staying provides benefits through nepotism, group benefits or indirect fitness. Although exemplary studies support these hypotheses, their relative importance across species remains unclear. The assumption that extra-territorial movement is costly is incorporated in those explanations of delayed dispersal, yet rarely addressed or tested directly. We therefore conduct a systematic literature review on empirical evidence for costs of extra-territorial movement in cooperatively breeding vertebrates. We predict that individuals suffer from lower survival rates and worse body condition while moving through unfamiliar environments without their group. Such costs may be caused by higher predation risk, lower foraging efficiency, and more frequent aggressive interactions with territory holders. We investigate if alternative strategies such as temporarily exploring foreign territories while staying most of the time in the natal territory, or dispersing in coalitions with other individuals, are less costly than lone and potentially long wandering through territories on search or waiting for a breeding vacancy. This review will thus reveal if extra-territorial movement is indeed costly and improve our understanding of the variation of dispersal costs and their weight in the evolution of cooperative breeding.

Abstract 28:

The communication distance and singing ecology of the wild zebra finch

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Birdsong is typically seen as a long-range signal functioning in mate attraction and territory defense. Among birds, the zebra finch is the prime model organism in bioacoustics, yet almost exclusively studied in the lab. In the wild, however, zebra finch song differs strikingly from songbirds commonly studied in the wild as zebra finch males sing most after mating and in the absence of territorial behavior. In this presentation, I provide an ecological framework for a wealth of laboratory studies, while using the data from the wild to obtain unprecedented insights into the communication range of avian song. By integrating calibrated sound recordings, sound transmission experiments and social ecology of zebra finches in the wild with insights from hearing physiology we show that wild zebra finch song is a very short-range signal with an audible range of about nine meter and that even the louder distance calls do not carry much farther (up to about fourteen meter). These integrated findings indicate that the vocal communication distance of the main laboratory species for avian acoustics contrasts strikingly with the classical birdsong paradigm as a long-range advertisement signal providing a novel framework for the function of birdsong and for the interpretation of laboratory studies.

Abstract 29:

Steering protein fermentation in the porcine intestinal tract by adding fermentable fibres

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Competition with human feed resources and societal developments urge the livestock sector to include more agricultural by-products that cannot be used for human consumption, as profitable alternatives to the currently used feed ingredients for animal diets (Breewood and Garnett 2020). Due to the relatively poor protein digestibility of these by-products, more undigested protein will enter the hindgut, prone to be fermented by microbiota. Protein fermentation results in the production of metabolites (biogenic amines, volatile fatty acids, ammonia, hydrogen sulfide, indolic and phenolic compounds, and nitric oxide) that may impair intestinal health (Gilbert et al. 2018; Rist et al. 2013). The inclusion of dietary fermentable fibres, shifting N-excretion from urine to feces, can reduce the production of nitrogen (N)-derived metabolites. Microbiota use the fermentable fibres as energy source, while N is used for bacterial growth. To study the interaction between dietary fibres, protein fermentation, and intestinal health, pigs received three different fibre treatments (no, rapidly fermentable-, or slowly fermentable fibres) combined with three different protein sources varying in digestibility. Both rapidly and slowly fermentable fibres reduced the concentration of N-derived metabolites in digesta by an average of 29 mmol/kg DM ($p < 0.001$), with rapidly fermentable fibres having a slightly greater effect in the ileum and cecum, and slowly fermentable fibres having a greater effect in the proximal and distal colon. No interaction between fibre treatment and protein source, and no differences in intestinal permeability were observed.

Abstract 30:

Effect of diet composition on energy utilisation efficiency in striped catfish
(*Pangasius hypophthalmus*)

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This study aims to assess the effect of diet composition on the relationship between retained energy (RE) and digestible energy (DE) intake (*i.e.*, the maintenance energy requirements and the slope [kg_{DE}]); to quantify the energy utilisation efficiency of digestible energy intake in striped catfish (*Pangasius hypophthalmus*). To achieve these aims, a 63-day experiment was conducted on striped catfish (29.1 g). A total of 4 diets were studied at 2 feeding levels, low vs. high (12 vs. 22 $\text{g} \cdot \text{kg}^{-0.8} \cdot \text{d}^{-1}$, respectively), which resulted in a 4×2 factorial design. The four diets had contrasting inclusion levels of protein, fat and carbohydrate. Non-starch polysaccharides were digestible in striped catfish with the digestibility ranging from 33.6% to 71.0%. By conducting the regression between retained energy and digestible energy intake over diets, the energy utilisation efficiency for striped catfish was estimated at 71% through the equation: $\text{RE} = -42 (\text{se } 9.2) + 0.71 (\text{se } 0.049) \text{ DE intake}$, ($R^2 = 0.95$). Diet composition did not affect the relationship between retained energy and digestible energy intake.

Abstract 31:

Where are they now? Tracking the Mediterranean Lionfish Invasion via Local Dive Centers

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Invasive species are globally on the rise and often cause harm to their new ecosystems. Tracking the spread of invaders is crucial to better management of invasive species, and citizen science is commonly used to gather such data. While valuable, this method can be unreliable due to the general public's limited expertise in accurate species identification. We introduce a refined method of citizen science by tracking the spread of the invasive lionfish (*Pterois miles*) in the Mediterranean Sea using dive centers' expertise on local marine wildlife. We found that lionfish are observed in the eastern half of the Mediterranean, though there are recent sightings as far west as Corfu, Greece. In 2020, the invasion also expanded north on the Turkish Aegean coast to Karaburun, showing that the invasion is ongoing. The invasive range now exceeds previous invasion models, highlighting the need for additional research on lionfish to more accurately predict their potential expansion. Cognitive aspects may play a role, as we recently showed that the morphologically and ecologically similar red lionfish (*P. volitans*) possesses color vision. Color vision can aid in hunting ability, opening up opportunity for lionfish to adapt and hunt diurnally in invasive ranges rather than being restricted to crepuscular hunting typical in their native range. Continuous monitoring of invasive fronts based on dive center reports and a better understanding of what makes lionfish so invasive is crucial to mitigating their negative impact on native ecosystems.

Abstract 32:

Bioconversion of chicken manure by housefly larvae (*Musca domestica* L.); larval performance and substrate conversion in relation to sterilization and carbohydrate addition

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The larvae of the housefly can be reared on manure and used as animal feed. Larvae can utilize starch and have a largely unknown relation with manure microorganisms. Our study hypothesis was that larvae compete with microorganisms for easily digestible carbohydrates such as starch. This was tested by adding starch, digestible by both larvae and microorganisms, or fructo-oligosaccharides (fos), digestible only by microorganisms, to unsterilized or heat sterilized fresh chicken manure (CMstar, CMfos, sCMstar, sCMfos). Diets and pure manure controls (CM, sCM) were inoculated with housefly eggs and larvae were harvested after five days by flotation. Total larval mass and survival were determined, as were nitrogen and DM content of larvae, diet, and residues. The highest yield (9.7 g) and heaviest larvae (13.2 mg) were on sCMstar, followed by sCM (7.2 g and 8.1 mg). Both CMfos and sCMfos had minimal yields and larval weights (0.3 and 0.2 g, 2.9 and 1.7 mg) with CMstar intermediate (3.3 g and 7.5 mg). Survival differed between diets, sCM and CM averaged 70%, sCMstar 57%, CMstar 33% with 9% for CMfos and sCMfos. DM bioconversion decreased from CM (3.5%), sCMstar (3.1%), sCM (2.6%), CMstar (1%) to CMfos and sCMfos (0.1%). Nitrogen bioconversion was highest on sCMstar (9.9%) and CM (9.3%), lower on sCM (6.6%), CMstar (4%) and the lowest on CMfos and sCMfos (0.5%). The results concur with the study hypothesis but indicate also that sterilization and carbohydrate addition might not be ideal for optimization of chicken manure as larval diet.

Abstract 33:

Validation of resilience indicators based on daily milk yield in dairy cows

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Resilience is the ability to be minimally affected by disturbances or to quickly recover. Resilience indicators for genetic selection in cows have been proposed, which are variance and autocorrelation of daily deviations from predicted milk yield. The aim was to validate how well these traits represent resilience, by estimating genetic correlations of the resilience indicators with traits describing production response to disturbances at herd level. A dataset with daily milk yield was used to identify disturbances affecting each entire herd, by selecting dates where the mean yield of all cows in the herd dropped. Production response of ~71,000 primiparous cows was then quantified by the depth of the drop and the total yield loss in kg and the length of the drop in days. Resilience indicators were available on ~79,000 cows. Genetic correlations were estimated using a sire-maternal grandsire model in ASReml. For variance, partial genetic correlations adjusted for yield level were calculated because of strong genetic correlations with yield level. Variance had strong partial genetic correlations with drop depth (0.82) and total yield loss (0.74), but not with drop length (-0.18). This suggests that variance contains information about strength of response to disturbances that cannot be explained by yield level. Autocorrelation had weak genetic correlations with drop depth (-0.13) and total yield loss (-0.01), but a strong genetic correlation with drop length (0.97). In conclusion, variance and autocorrelation cover different aspects of resilience and should be combined to breed for improved overall resilience.

Abstract 34:

Effects of dietary protein oscillation on intake, production, digestibility and nitrogen metabolism in lactating dairy cows

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Nitrogen efficiency in growing ruminants may be increased with oscillating vs static dietary crude protein (CP). We hypothesized that nitrogen efficiency in dairy cows would be increased by feeding repeated 48-h phases of 13.4% and 17.1% dietary CP (oscillating; OS), compared to a static CP supply (15.3% CP; ST). We conducted urine sampling and total faecal collection on 12 mid-lactation multiparous cows for 8-d, after an 8-d adaptation. Urine excretion was estimated using daily dietary sodium and potassium intake. The experiment was a randomized complete block design with preceding covariate period. Fixed effects of treatment, period (repeated) and associated covariate value, and block as random effect were used for statistical analysis. Nutrient intake, milk composition and yield, and efficiency of feed and nitrogen use for milk synthesis were not treatment affected. Apparent total-tract digestibility (ATTD) of organic matter and gross energy increased, and crude fat and starch ATTD tended to increase with OS, but CP ATTD was not affected. Estimated uric acid excretion tended to increase with OS, but treatment did not affect estimated allantoin or total purine derivatives excretion, or estimated microbial protein synthesis or efficiency. Estimated urinary nitrogen excretion increased and milk nitrogen as proportion of digested nitrogen tended to decrease with OS, but estimated nitrogen balance was unaffected, indicating increased post-absorptive nitrogen losses for OS. Overall, performance and efficiency of dietary nutrient use for milk synthesis were unaffected by treatment, but OS increased ATTD and tended to reduce estimated post-absorptive nitrogen efficiency.

Abstract 35:

Enlightened pigs: throwing a light on pig welfare.

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In pig farming the role of light has been largely ignored in the debate on improving animal welfare. Available literature mainly reports the effects of photoperiod (=light period) on production aspects like growth, reproduction, health or production related behaviours such as feeding and resting. The relevance of two other light parameters, light intensity (=brightness) and light spectrum (=colour), are understudied, especially in relation to important welfare indicators such as social and exploratory behaviour and affective states. Light is used to treat affective disorders in humans and given their physiological similarities with pigs, light might be more important for pigs' mood and emotions than previously anticipated. Thus, appropriate barn light settings might positively impact the welfare status of pigs. The aim of this PhD project is to investigate the effect of light intensity and light spectrum on the welfare of growing-finishing pigs. The welfare assessment of pigs will include health, production, behavioural and affective state measurements. In a first experiment, different intensity levels will be tested in a commercial farm with modern light-emitting diode (LED) technologies. Light intensity is expected to affect the rhythmicity of pigs' activity. A second experiment, will investigate the role of visible and invisible light spectra as it might play a role in pigs' affect and the display of abnormal behaviours. In light of the previously gained knowledge, combinations of light intensities and light spectra will be studied in a third experiment to propose new lighting concepts for pig houses contributing to a better pig welfare status.

Abstract 36:

Keeping the peace at the mucosal surface. How does host immunity control bad bugs?

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The digestive tract of all animals is colonized with a complex community of microbes. In response to these colonizing bacteria, the host immune system develops (it learns to discriminate between friend and foe) and in turn the immune system can shape the microbial community by removing pathogenic species. Although most microbes are harmless, some species can be deleterious when given the opportunity. These so-called pathobionts are important members of the normal microbiome that can cause the loss of homeostasis and disease under specific conditions. Unlike pathogens that will be expelled by the host immune system, these pathobionts appear to be kept under control, but can cause disease under conditions where gut homeostasis is disturbed. In our project, we will investigate how the host immune system can suppress pathobionts, while leaving commensals in the gut alone. We will make use of the zebrafish model that has attractive advantages, including the sequential development of innate and adaptive immunity, optical transparency during early development combined with genetic engineering possibilities with fluorescently labelling cell types (eg. T cells, neutrophils). With the use of the zebrafish model, we aim to unravel the role of specific cell lineages of the innate (e.g., neutrophils) and adaptive (e.g., T-cells) arms of the immune system as well as the intestinal epithelial cells, which collectively appear to orchestrate the intestinal microbiota. In addition, since cellular proximity or direct contact between immune cells and microbes are not considered to occur, we hypothesize that mediators of the immune system might impact these distant microbes via extracellular processes.

Abstract 37:

Seaweed digestibility: *Ulva rigida* and *Solieria chordalis* co-products in broiler diets

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Seaweed could be used as feed ingredient to meet the growing demand for animal protein. This study aimed to determine nutrient digestibility of desalted seaweed co-products, and effects of enzymatic hydrolysis on nutrient digestibility. Seaweed co-products (species *Ulva rigida* and *Solieria chordalis*) were included in a 2 x 2 factorial design (species x enzymatic hydrolysis) with added control. Day old male Ross308 broilers were housed in 30 pens, 12 birds per pen, n=6 pens. Co-products were added to a control diet at 10% weight basis. Birds were weighed weekly and faeces was collected qualitatively at pen level at d 19-20-21. At d21, ileal digesta was collected, and histological parameters of the duodenum were analysed. Data were analysed using a generalized linear model, with contrast statements.

On FCR, a seaweed effect (*S. chordalis* > *U. rigida* diets; $P < 0.001$) and an enzyme effect (treated > untreated; $P = 0.004$) were observed. Seaweed co-products reduced nutrient digestibility of diets ($P < 0.001$). Digestibility was reduced in *S. chordalis* diets (Seaweed effect) and diets with enzymatically treated co-products (Enzyme effect). A reduced villus length ($P < 0.001$) and villus length: crypt depth ratio ($P = 0.006$) were observed in birds fed the *U. rigida* compared to *S. chordalis* diets.

The digestibility data indicate an interaction between seaweed co-products and basal diet, potentially related to altered viscosity of intestinal chyme. *U. rigida* is, based on this experiment, more suitable for inclusion in broiler diets compared to *S. chordalis*, whereas the digestibility needs to be increased further for optimal use of the dietary nutrients.

Abstract 38:

Variation in birthweight, feed intake, breeding value, behaviour and skin lesions accounts for less than 45% of variation in growth rate in a multi-suckling system for pigs

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Previously, variation in the growth rate of piglets in a multi-suckling system was observed to be large. The aim of this study was to explain this variation during three periods: week 2-4, 4-6, and 6-8 of age. Three batches of 5 sows and 4 focal piglets in each litter were studied. In each period, several traits were recorded for all focal piglets. Multiple regression analysis was conducted on growth rate after correcting for sex and batch, using 12 explanatory variables: birthweight, the estimated breeding value for growth rate from birth to slaughter, intake of sow and piglet feed, contacting feed during sow feeding times, the presence at front and middle pairs of teats, the presence at rear pairs of teats, the frequency of ingestive, positive, negative and explorative behaviour during the day and skin lesions. Forward selection was used to select variables that significantly affect growth. Results showed that variation in 12 variables accounted for less than 45% of variation in growth rate in each period. In week 2-4, birthweight, positive behaviour, and contacting feed during sow feeding times jointly accounted for 24.2% of variation in growth rate; in week 4-6, piglet feed intake and the presence at rear teats jointly accounted for 19.9% of its variation; in week 6-8, piglet feed intake accounted for 25.9% of its variation. In conclusion, individual differences in growth in early lactation are majorly owing to individual differences in birthweight and behaviour, while in middle and late lactation are majorly owing to solid feed.

Abstract 39:

Animal breeding can be used to reduce enteric methane emissions of dairy cows

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The Dutch agricultural sector is facing the challenge to reduce methane emissions by 1 megaton by 2030, and further by 2050. In agriculture, most methane is produced by enteric fermentation of ruminants and emitted in the air through breathing and belching. Animal breeding techniques offer potential to reduce enteric emissions, in a way that is cost-effective, cumulative, and permanent. This will increase the sustainability of dairy farming, and make the sector more resilient to possible future restrictions based on emissions per farm or animal. The aim of our study was to investigate if we can use continuously recorded methane emissions, measured with gas analysers called sniffers, to breed for reduced methane emissions of dairy cows. Sniffers were installed in the feed bin of milking robots, where methane concentrations (ppm) were measured on 14 herds from March 2019 to September 2020. In total, data from 181,597 robot visits of 1,698 Holstein Friesian cows were recorded. Genetic parameters were estimated with a univariate animal model with repeated measurements. Preliminary results show that the heritability was low to moderate and ranged between 0.08 to 0.23, and was highest for weekly mean emissions (0.23 ± 0.02). The genetic standard deviation for weekly mean emissions was 73 ppm, indicating that the genetic difference between the 1% highest and lowest emitting cows is 366 ppm. The preliminary results indicate that there is genetic variation in methane emissions between cows, and decreasing methane emissions by selection in dairy cows is a possibility in the near future.

Abstract 40:

Individual detection and tracking of group-housed pigs in their home pen using computer vision

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Modern welfare definitions not only require that the Five Freedoms are met, but animals should also be able to adapt to changes (i.e. resilience) and reach a state that the animals experience as positive. Changes in individual activity showed potential in previous studies to reflect resilience. A computer vision (CV) based tracking algorithm for pigs could potentially measure individual activity. The aim of this study was to investigate a potential CV algorithm for pig detection and tracking for individual activity monitoring in pigs. This study used a tracking-by-detection method, where pigs were first detected using You Only Look Once v3 (YOLOv3) and in the next step detections were connected using the Simple Online Real-time Tracking (SORT) algorithm to track individual pigs. Two videos, of seven hours each, recorded in a barren and an enriched environment were used to test the tracking algorithm. Up to 4000 frames were annotated to train the detection model. In both environments, a mean average precision (mAP) over 99,5% was achieved and an Intersection of Union (IOU) over 85%, indicating a good accuracy of the detection algorithm. The tracking algorithm performed better in the enriched environment compared to the barren environment, likely due to the larger space per pig. Individual pigs were tracked on average for 22.3 minutes in the barren environment and 57.8 minutes in the enriched environment. Thus, individual activity could be estimated using this algorithm and therefore be able to measure resilience, but manual corrections are needed to maintain identity in longer videos.

Abstract 41:

Role of soluble and transmembrane TNF α during inflammation: focus on macrophage activation

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Usually inflammation provides host defence against infections and supports wound healing, but inflammation can also become chronic, causing several disorders in humans and animals. Tumor necrosis factor-alpha (TNF α) is a multifunctional mediator that can be expressed in a soluble (s) or transmembrane (tm) form. While sTNF α is generally associated with inflammation, the role of tmTNF α is not well understood. Yet, both sTNF α and tmTNF α are required for a fully functional immune response and both can bind to the same two TNF α receptors. Fundamental questions remain about the relative contribution of sTNF α and tmTNF α to inflammation and through which receptors they exert their activities. We aim to dissect the function of sTNF α and tmTNF α *in vivo*, during inflammation induced by injury or infections in zebrafish, with a special focus on macrophage activation. The zebrafish has several specific advantages, including: 1) transparency of embryos that allow live, non-invasive imaging of (immune) cells in real-time, 2) availability of transgenic lines expressing fluorescent proteins under the control of macrophages-, or TNF α -specific promoters, 3) availability of a well-annotated genome for gene manipulation. All this will enable us to generate new transgenic zebrafish only expressing sTnf α or tmTnf α and use Tnf α knockout lines. In a similar manner, also the expression of both Tnf α receptors can be manipulated. Altogether, this project will address fundamental questions about the relative contribution of sTNF α and tmTNF α to inflammation, with a special focus on macrophage activation and the receptors through which sTNF α and tmTNF α exert their activities.

Abstract 42:

Maternal bonding in dairy cattle: does type of cow-calf contact matter?

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It is common practice in dairy farming to separate cows and calves within a few hours after parturition, which raises public concern with regards to animal welfare. Currently, various stakeholders are interested in alternative rearing systems that allow for prolonged cow-calf contact (CCC). When contact between the dam and her young is allowed a bond develops, but little is known about how the type of contact affects the strength of this bond. Therefore, we first assessed the motivation of dairy cows with different types of CCC to reunite with their own calf. Our results showed that the calf is a valuable resource that dairy cows are willing to work for, but that dairy cows' motivation to reunite with their calves is greatest when cows have full CCC (suckling allowed) in contrast to no (separated at birth) and partial CCC (suckling prevented). Second, we evaluated the effect of type of CCC (full contact vs partial contact) on calf-directed affiliative behaviour of dairy cows at birth and in the weeks following parturition. We found that, except in the 48 hours after calving, cows allowed full contact with their calves spent more time allogrooming and in proximity to the calf compared to partial CCC. Overall, the outcomes substantiate that full CCC strengthens the bond between cow and calf. The bonding might be reinforced by the suckling of the calf, which is known to increase oxytocin levels that mediate social bonding.

Abstract 43:

Genomic selection and introgression signatures resulting from adaptation to high salinity: a case study on an Indonesian farmed tilapia (Sukamandi) strain

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Background: Tilapia is currently the most important fish in aquaculture in the tropics and subtropics. Originally a freshwater species, it is cultured in a wide range of conditions. Among the most challenging is when high salinity is involved, e.g. culturing in estuaries or high salinity ponds in polyculture with shrimp. Optimized tilapia strains generally do not tolerate high salinity well. Although the physiological adaptation for osmoregulation is reasonably well understood, it is less clear how selection results in salinity tolerance. Here we investigate one such strain that was bred to perform well in brackish water. Specifically, we infer signatures of selections in the genome. In addition, since the salinity tolerance in the strain was hypothesized to be derived from another species, we also inferred signatures of introgression between species.

Results: The local Indonesian farmed tilapia (Sukamandi) strain, is based on four generations of selection in water salinity varying from 15 to 58 ppt. We compared the genome of this Sukamandi strain to that of Nile tilapia (*Oreochromis niloticus*) and blue tilapia (*Oreochromis aureus*), the latter a putative donor of the salinity tolerance. Our results indicate that the Sukamandi strain is genetically much more similar to Nile tilapia (*Oreochromis niloticus*) ($F_{st}=0.042$) than to blue tilapia (*Oreochromis aureus*) ($F_{st}=0.386$).

Analysis of genes located in genetically differential regions showed significant involvement of ion transmembrane transport processes, such as MAPK3 activity, potassium ion homeostasis, ATPase activity and response to calcium ions. Combining genome-scale scanning for selection and introgression revealed that salinity tolerance related genes, such as *caprin1a*, *nucb2a*, *abcb10*, *cacna1ab*, *ulk2*, *slc25a24* and *cdh1* were strongly selected. While the genome of the Sukamandi strain appears to be overwhelmingly of Nile tilapia origin, some introgression from blue tilapia may have conferred some of the observed salinity tolerance.

Conclusion: Artificial selection and inter-species introgression in the tilapia Sukamandi strain, have resulted in a non-random retainment of genes derived from the introgressed species. Introgression also increased standing variation in the target trait, while directional selection enhanced the adaptivity of the introgressed individuals. Our findings support further selective breeding of tilapia tolerant to high salinity conditions.

Abstract 44:

Recessive deleterious mutations in the TPO gene underlying familial thyroid follicular cell carcinoma in Dutch German longhaired pointers

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Familial thyroid cancer originating from follicular cells accounts for 5-15% of all the thyroid carcinoma cases in humans. Previously, we described thyroid follicular cell carcinomas in a large number of the Dutch German longhaired pointers (GLPs) with likely an autosomal recessive inheritance pattern. Here, we investigated the genetic causes of the disease using a combined approach of genome-wide association study, selective sweep analysis, and ROH analysis based on 170k SNP array genotype data. A region 0-5 Mb on chromosome 17 was identified to be associated with the disease. To locate the potential causal mutations/genes, 22 dogs were sequenced. In the region, two deleterious mutations in the TPO gene; chr17:800788G>A (686F>V) and chr17:805276C>T (845T>M) were identified to be candidate causal mutations. These two SNP were subsequently genotyped in 182 GLPs (54 affected and 128 unaffected) and the recessive genotypes had relative risks of 16.57 and 16.27, respectively. This study provides novel insight into the genetic causes underlying the familial thyroid follicular cell carcinoma and we were able to develop a genetic test to screen susceptible dogs

Abstract 45:

An *in vitro* model of the complex fish gill

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This project aims to study gills as a complex organ with a special focus on the interaction between gill epithelial cells with the outer mucus layer and associated microbiota as well as with the inner immune cells populating the gills. Gills of teleosts are best known as the major site for gas exchange with water, participating in important ion-osmoregulation. The large surface area and the epithelial layer separating the gill from the environment, on the one hand effectively facilitate gas exchange while on the other offer opportunity for exposure to water-borne pathogens. To limit pathogen entry, the outer side of the gill epithelium is covered by a mucus layer harbouring an associated microbiota assumed to play a local protective role, whereas on the inner side, it interacts with the so-called gill-associated lymphoid tissue (GiALT), assumed to provide overall protection against water-borne pathogens. Comprehensive studies on gills as a complex organ with an important barrier, immune function are scarce. This project aims to study gills as a complex organ with the focus on the interaction between the epithelial cell layer and the mucus, microbiota and GiALT. To this end, we will develop an *in vitro* co-culture model of gill-derived epithelial cells with immune cells and with commensal or pathogenic microbes,

Abstract 46:

Practical application of fungal treatment of lignocellulosic biomass to feed ruminants in the Netherlands

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Lignocellulosic biomass, mainly by- or waste-products from agriculture and forestry, can be used as an energy source by ruminants who have a unique digestive system where the rumen microbes can degrade carbohydrates, such as cellulose and hemicellulose. However, the presence of lignin blocks the contact of rumen microorganisms with the carbohydrates, causing a decreased digestibility, hence a low feeding value. Experiments on a laboratory scale demonstrated that white-rot fungi can selectively degrade lignin and leave a large part of the cellulose undegraded, therefore improve the nutrition value of the low-quality biomass. This project aims to solve several challenges associated with the upscaling of the fungal treatment of high lignin biomass and contribute to making the technology suitable for large scale practical application. Four experiments will be conducted: (I) Investigate the suitability of lignocellulosic biomass available in the Netherlands to be converted into valuable feed for ruminants using white-rot fungi; (II) Determine if previous colonized substrate can be used as spawn and its optimum amount, and examine how many times it can be transferred from one batch to a next one; (III) Investigate the possibilities to replace autoclaving by simple and inexpensive methods to prevent undesired contamination; (IV) Examine the effects of the metabolites generated by the fungal treatment process on the performance, health and product quality of ruminants. Fungal biotechnology is economically and environmentally-friendly and has great potential to alleviate the food and feed competition as well as to reduce air pollution by reducing the burning of lignocellulosic biomass.

Abstract 47:

Responses of high producing dairy cows to high ambient temperatures in the Netherlands

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The dairy industry in regions with moderate climates, such as Netherlands, will be increasingly challenged in the future by global warming. Heat stressed cows show increased respiration rates, sweating rates and rectal temperature. The objective of this study was to investigate the relationship between ambient climate parameters and a number of cow parameters: respiration rate (RR), rectal temperature (RT), skin temperature (ST), skin latent heat loss (LHL) and skin sensible heat loss (SHL). The study was conducted in a naturally ventilated dairy barn located in Wageningen, the Netherlands. The dataset was composed of 144 observations from 8 lactating cows under summer conditions for 33 days from July to August 2020. The climate data were collected inside and outside the barn and the average of inside Temperature Humidity Index (THI) during the experimental period was 69.4 ± 5.5 , with a maximum value of 81.7. Measurements of RR, RT, ST, LHL and SHL were conducted at 0900 and 1400 h for ± 30 min. Split-line regression of RR and RT on THI showed thresholds (above which RR and RT started to increase) of 71 and 74. During the experimental period (33 days), totally 18 days were observed with more than 4 hours a day above the THI threshold for RR. Indoor temperature showed moderate correlations with SHL ($R^2=0.29$) and LHL ($R^2=0.28$). When the indoor air temperature increased from 17 to 31°C the sensible heat transfer decreased, on average, from 200.2 to -12.8 Wm⁻², while the LHL by skin evaporation increased from 5.2 to 411.2 W m⁻². ST showed a moderate relationship with LHL ($R^2=0.35$), and this relationship may support the use of ST data to mitigate heat stress in dairy cows.

Notes