Synbreed –

Synergistic Plant and Animal Breeding

Network of excellence for interdisciplinary, genome based research

GenSAP
11 November 2014
Demands

Accelerate progress in crop and livestock breeding

Increase the number of highly qualified young breeders

Strengthen German agricultural research
  - visibility
  - competitiveness
  - cross linking
Paradigm change

Plant Breeding
Population Genetics
Quantitative Genetics
Breeding Methods

Animal Breeding
Population Genetics
Quantitative Genetics
Breeding Methods

Sequencing
Genotyping
Metabolomics
Bioinformatics

Quantitative Genetics
Population Genetics
Statistical Genetics
Breeding Methods
Synbreed partners

Technische Universität München
- Plant Breeding (C.-C. Schön, Speaker)
- Animal Breeding (H.-R. Fries)
- Genome Oriented Bioinformatics (H.-W. Mewes)
- Genetics (A. Gierl)
- Human Genetics (T. Meitinger)
- Population Genetics (A. Tellier)

Helmholtz Zentrum München
- Bioinformatics and Systems Biology/MIPS (K.F.X. Mayer)
- Human Genetics (T. Strom)

Bayerische Landesanstalt für Landwirtschaft
- Animal Breeding (K.-U. Götz)

Georg-August-Universität Göttingen
- Animal Breeding and Genetics (H. Simianer)

Universität Hohenheim
- Bioinformatics (H.-P. Piepho)
- Plant Breeding (A. E. Melchinger)
- Crop Biodiversity and Breeding Informatics (K. Schmid)

Christian-Albrechts-Universität zu Kiel
- Animal Breeding and Husbandry (G. Thaller)

Friedrich-Loeffler-Institute
- Farm Animal Genetics (S. Weigend)

KWS SAAT AG (M. Ouzunova)

Lohmann Tierzucht GmbH (R. Preisinger)
Interdisciplinary research across species:

- joint development of statistical methods and software in application projects
- shared use of data generated in technology platforms
- development of generic bioinformatic concepts for data analysis
- generation of shared biological resources in resource projects
- intensive material and data flow between partners
- integrative consolidation of results from the different projects
Progress in technology platforms

**T1 – Sequencing**
(HMGU-HG)

**Maize**
- 4 lines, 90x coverage
- 26 lines + 1 teosinte, 10x
- 9 landraces (24 S₀/pop) 2x
- 6 landraces (2 DH/pop) 5x

**Cattle**
- 140 animals, 10x

**Chicken**
- 3 Pools 20x
- 5 Individuals 25x
- 25 white layers 8x
- 25 brown layers 8x
- 40 Pools 15x

**T2 – Genotyping**
(TUM-TZ)

**Maize**
- Illumina 50k SNP-Chip
- 5305 genotypes
- Affymetrix 600k SNP-Chip
- 960 genotypes

**Cattle**
- Illumina 777k SNP-Chip
- 3072 genotypes

**Chicken**
- Affymetrix 600k SNP-Chip
- 5376 genotypes

**T4 – Biomarkers**
(TUM-GE)

Calibration for maize, milk and egg yolk completed

**Maize**
- 90 ILs
- 460 DH lines (5x)

**Cattle**
- 391 milk samples (3x)
  plus 66 checks

**Chicken**
- 1649 egg samples (3x)
Progress in application projects

**Statistical methods**
- Parametric/semi-/non-parametric and machine learning methods
- Procedures for cross-validation
  - Methods accounting for genetically heterogeneous calibration samples
  - Modeling approaches for G x E interactions
  - Development of prediction models accounting for additive effects, dominance, epistasis, imprinting and non-genetic effects

**Implementation**
- Development of genomic selection for maize and chicken breeding programs
- Implementation of genomic selection in existing breeding programs
- Optimization of breeding programs integrating genomic selection
Population genomics

- High-throughput analysis pipeline for frequency and haplotype based tests for selection
- Development of tools for the comparison of expected and observed distributions of statistics for selective sweeps by means of forward simulations
  - Analysis of LD and haplotype structure in experimental data
  - Genome-wide scans for association and selection signatures
  - Zoom into specific trait associated regions of the genome
Education and training

• **Graduate School ‘Next Generation Breeding’**
  – 14 courses on statistical inference, bioinformatics, selection theory, genome-enabled prediction

• **Summer / Winter Schools**
  – joint organization by several Synbreed partners
  – lecturers established scientists and students
  – high demand nationally and internationally
    (participants from > 20 countries)

• **Foreign scholarships**
  – 7 scientists to USA, Australia and France in high impact research groups
## Synbreed summer / winter schools

<table>
<thead>
<tr>
<th>Year</th>
<th>Title</th>
<th>Authors</th>
</tr>
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<tbody>
<tr>
<td>2010</td>
<td>Linear models and estimation of genetic parameters</td>
<td>with Larry Schaeffer</td>
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<tr>
<td>2011</td>
<td>Next generation sequence analysis: practice and departure to new frontiers</td>
<td>with Mario Caccamo, Ben Hayes, Paul Kersey, Jared Simpson</td>
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<td>2012</td>
<td>Population genomics of crop and livestock populations</td>
<td>with Michael Blum, Joachim Hermisson, Joseph Pickrell, Bertrand Servin</td>
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<td></td>
<td>→ German-French cooperation: Alain Charcosset</td>
<td></td>
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<td>2013</td>
<td>Advanced topics in plant and animal breeding</td>
<td>with Bruce Walsh</td>
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<tr>
<td>2014</td>
<td>From SNPs to gene networks</td>
<td>with Guilherme Rosa, Fabian Theis, Pascal Braun, Helge Stark, Ngoc-Thuy Ha</td>
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<tr>
<td>2015</td>
<td>Selection theory</td>
<td></td>
</tr>
</tbody>
</table>
**Contribution to consortia**

600k Chicken SNP Chip (with Roslin Institute, Affymetrix and others)

777k Cattle SNP Chip (with USDA, DPI and others)

50k and 600k Maize SNP Chip (with Illumina, Affymetrix, Trait Genetics, INRA, and others)

1,000 bull genomes project (initiated by Ben Hayes and Mike Goddard)

**Synbreed publications (2009 – 2014)**

55 papers published in peer-reviewed journals

19 joint publications of Synbreed partners

7 across species
Plant and animal synergies

- Exchange of know-how
- Joint training for young academics
- Exchange between breeding companies (KWS/Lohmann)
- Joint technology development
  - Sequencing
  - Availability of technology platforms for animals and plants
  - Chip construction
- Joint new project proposals
- Joint publications
- Mutual invitations to meetings and conferences
Synbreed – why we like it…

**Funding volume**
- strengthens position of plant and animal breeding
- reliable results due to large scale experiments

**Funding period 5 years**
- highly connected projects with mutual dependencies

**Flexibility of resource allocation**
- technological developments

**Public Private Partnership**
- immediate transfer of results into breeding

**National and international visibility**
- scientific advisory board, collaboration in chip consortia for maize/chicken/cattle, TUM-IAS, invited talks, research stays, cooperations
What’s next?

New projects
• “Selection at work” – DFG initiative
• Big Data – MDSC – Munich Data Science Center

New centers
• „Centre for integrated plant and animal breeding“ at the University of Göttingen

Education and training
• Continuation of summer schools and graduate education
• Development of an international graduate school

International collaboration
What’s next?

Synbreed –
Synergistic Plant and Animal Breeding

Understanding and predicting complex traits through genome discovery

Keynote Speakers:
Mark Cooper, DuPont Pioneer, USA
Natalia de Leon, University of Wisconsin, USA
Mike Goddard, DPI Melbourne, Australia
Pieter Knap, PIC International, Germany
Klaus Mayer, Helmholtz Zentrum, Germany
Guilherme Rosa, University of Wisconsin, USA
Carl-Johan Rubin, Uppsala University, Sweden
Maud Tenailleon, INRA, France

In addition to keynote lectures scientific findings from the Synbreed project will be presented.

04. – 06.03.2015

Technische Universität München
Campus Weihenstephan,
Freising, Germany

Application
Registration fee: 150,- Euro
Registration: www.synbreed.tum.de
Registration deadline: 15.12.2014

Organisation and Contact:
Synbreed /Hans Eisenmann-Zentrum
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Hybrid Breeding

Population 1

- crosses
- 10,000 lines
- 2,000 lines
- 50 lines

Hybrid components

Testing
- 1 location

Hybrid varieties

Population 2

- crosses
- 10,000 lines
- 2,000 lines
- 50 lines

Testing
- 5 locations
- > 10 locations

Hybrid components

Testing
- 1 location

Modified after Schmidt, 2004
Optimize Breeding Cycles

- Interconnected cycles
- Genetic subgroups
- Highly unbalanced data

Intercrossing of recombination units (RU)
Selection on line per se performance
Test-cross performance trial 1 (TC)
Test-cross trial 2
Test-cross trial 3 (factorial performance trials)

Modified after Gordillo and Geiger 2008
## Maize Advanced Cycle Breeding Populations

<table>
<thead>
<tr>
<th>Set</th>
<th>N</th>
<th>parents</th>
<th>crosses</th>
<th>Median, [min ; max]</th>
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<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>lines per parent</td>
</tr>
<tr>
<td>S1</td>
<td>928</td>
<td>52</td>
<td>173</td>
<td>21 [1; 203]</td>
</tr>
<tr>
<td>S2</td>
<td>842</td>
<td>73</td>
<td>287</td>
<td>12 [1; 129]</td>
</tr>
<tr>
<td>S3</td>
<td>1085</td>
<td>148</td>
<td>246</td>
<td>6 [1; 115]</td>
</tr>
<tr>
<td>S4</td>
<td>1017</td>
<td>58</td>
<td>130</td>
<td>13 [1; 455]</td>
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</tbody>
</table>
Predictive Abilities PBLUP and GBLUP

S1 grain yield
CV: random sampling within complete data set and tester subsets

Albrecht et al. 2014, TAG
Predictive Abilities PBLUP and GBLUP

S1 grain yield
CV: random sampling within complete data set and tester subsets

Albrecht et al. 2014, TAG
Prediction across Breeding Cycles

Albrecht et al. 2014, TAG
Prediction across Breeding Cycles

Albrecht et al. 2014, TAG
Prediction across Breeding Cycles

Auinger et al. unpublished
Summary

- GBLUP outperforms PBLUP for all traits and all genetic groups
- Introgression of unrelated material requires specific experimental designs
- Predictive abilities encouraging across cycles
- Merging data from several cycles seems favorable
Vielen Dank!
Research Visits

- **The Roslin Institute, Edinburgh University (D. Burt)**
  Research stay of S. Qanbari (UGÖ-TZ), 02/2011-04/2011, co-funded by ERF-grant

- **University of California Berkeley (R. Nielsen)**
  Research stay of S. Qanbari (UGÖ-TZ), 05/2012-11/2012

- **Cornell University (J.-L. Jannink)**
  Research stay of C. Riedelsheimer (UHO-PZ), 08/2012-12/2012, co-funded by Synbreed

- **Department of Primary Industries, Melbourne (B. Hayes)**
  Research stay of M. Erbe (UGÖ-TZ), 03/2011-08/2011, co-funded by Synbreed

- **North Carolina State University, Raleigh (T. Mackay)**

- **University of Wisconsin-Madison (D. Gianola)**
  Research stay of U. Ober (UGÖ-TZ), 08/2010-12/2010, co-funded by Synbreed
  Research stay of A. Ehret (CAU-TZ), 08/2012-12/2012, co-funded by Synbreed
Achievements

Synbreed – meeting the demands:

Accelerate progress in crop and livestock breeding

Increase the number of highly qualified young breeders

Strengthen German agricultural research
  – international visibility
  – competitiveness
  – cross linking

✓ Successful implementation by industrial partners (KWS & Lohmann Tierzucht)

✓ Currently 23 PhD students from plant/animal breeding and related fields

✓ Contributions to international consortia, flanking projects, publications, multi-species research, methodological leadership
Achievements

Sustainability of the network

• new professorial chair ‘Population Genetics’ (S3)
  TUM Center of Life and Food Sciences Weihenstephan
  Prof. Aurélien Tellier

• new professorial chair ‘Statistics in Life Sciences’ (in progress)
  TUM Center of Life and Food Sciences Weihenstephan

• concentration of expertise at Hans Eisenmann-Zentrum for Agricultural Science
  TUM Center of Life and Food Sciences Weihenstephan
  → plant breeding, population genetics (S3), biostatistics

• initiation of flanking projects

• collaborations within consortia

• strengthening of German-French collaboration:
  – GEMBAL – Multi-breed genomics of beef and dairy cattle
  – Winter school 2012 (population genetics): A. Tellier (S3) + A. Charcosset (SAB)

• interdisciplinary education and training
Synbreed objectives

Functional analysis of native biodiversity
Genetic analysis of complex traits
Development and implementation of optimal breeding strategies

→ Optimization and implementation of genomic selection and genome-based breeding in maize, chicken and cattle
International visibility

Scientific exchange

• University of Wisconsin-Madison
  Hans Fischer Senior Fellowship for Prof. Daniel Gianola (2012–2015)
  Research stay of U. Ober and A. Ehret

• North Carolina State University
  Collaboration on *Drosophila* Genetics Reference Panel using sequence data
  Research stay of U. Ober

• Edinburgh University, The Roslin Institute
  Collaboration on Affymetrix Chip development
  Research stay of S. Qanbari

• Department of Primary Industries, Melbourne
  Collaboration on 1000 bull genomes
  Research stay of M. Erbe, B. Aigner

• Institut national de la recherche agronomique, INRA Paris, Toulouse
  Collaboration on allelic diversity in European germplasm
  Research stay of C. Schön, J. Ertl, M. Gholami

• Cornell University
  Collaboration on linking allelic diversity in European and US germplasm
  Research stay of C. Riedelsheimer

• University of California Berkeley
  Research stay of S. Qanbari

• Iowa State University
  Research stay of C. Heuer

• Norwegian University of Life Sciences, Norway
  Collaboration on genomic breeding value estimation in cattle