NCR-204
Meeting minutes
Convened 9:00 AM Saturday, 19 February 2005 in Ventura, CA.
Adjourned 12:00 PM Sunday, 20 February 2004.

Jean-Luc Jannink	Chair
Guilherme Rosa	Secretary
Shizhong Xu	Local Host
Jean-Luc Jannink	Guest Speaker Coordinator

Participants:

Last Name	First Name	Email	Station	Member/Guest
Bastiaansen	John	john.bastiaansen@sygeninternational.com	Sygen	M
Dekkers	Jack	jdekkers@iastate.edu	Iowa State	M
Dentine	Margaret	mrdentine@cals.wisc.edu	Univ. of Wisconsin	Admin. Advisor
Ernst	Cynthia	caernst@dow.com	Dow	M
Henderson	David	dnadave@u.arizona.edu	Univ. of Arizona	M
Jannink	Jean-Luc	jjannink@iastate.edu	Iowa State	Chair
Misztal	Ignacy	ignacy@uga.edu	Univ. of Georgia	M
Muir	Bill	bmuir@purdue.edu	Purdue Univ.	M
Romero-Severson	Jeanne	jromeros@nd.edu	Notre Dame	M
Rosa	Guilherme	rosag@msu.edu	Michigan State	Secretary
Stuthman	Deon	stuth001@umn.edu	Univ. of Minnesotta	M
Xu	Shizhong	xu@genetics.usr.edu	UC Riverside	M
Wang	Dechun	wangdech@msu.edu	Michigan State	M

Minutes for 19 Feb 2005

Introductions by the Chair

Jean-Luc Jannink
Secretary in 2004, Chair in 2005
Guilherme Rosa
Secretary in 2005
Reminder of the three Objectives:

1. Develop and compare statistical methodology to map genes
   Coordinator: Guilherme Rosa
2. Examine the efficiency of incorporation molecular tools in breeding programs through theoretical modeling, computer simulations, and biological testing in actual breeding populations
   Coordinator: Jack Dekkers
3. Use molecular genetics to test hypotheses generated from the fundamental theories of population, quantitative genetics, and molecular evolutionary genetics
   Coordinator: Shizhong Xu

The business meeting was set for the last thing on Sunday
We gave time predictions for Station reports:

Jack Dekkers	25 min
Jean-Luc Jannink	15 min
Bill Muir	30 min
Shizhong Xu	45 min
Ignacy Misztal	25 min
David Henderson	20 min
Guilherme Rosa	30 min
Jeanne Romero-Severson	30 min
Dechun Wang	20 min

The order of presentation of Station reports was to be decided as we went along…

Shizhong Xu – UC Riverside
Bayesian shrinkage method for estimating QTL parameters.
Simultaneously estimation of effects and positions of several hundred QTL.
The model assumes that the maximum number of QTL is p. The positions of these QTL along the genome are disjoint and vary based on Metropolis-Hastings rule. The method can handle extremely high marker density.

Dechun Wang – Michigan State University
Results of three studies aiming the genetic mapping of quantitative trait loci underlying agronomic traits in soybean.

1. QTL underling yield in interspecific soybean backcross populations.
2. QTL conditioning waterlogging tolerance in soybean
3. Genetic mapping of genes underlying partial resistance to Sclerotinia Stem Rot in Soybean PI 391589B.

Ignacy Misztal – University of Georgia
Competitive effects for average daily gain in swine:

- 4,946 records from 2,409 litters and 362 pen-groups
- pen size ranged from 12 to 16
- models included the effects of contemporary group (farm-barn-batch), birth litter, pen-group and two additive genetic effects: direct and associative
- additive genetic variance as a function of the number of competitors in a group, the additive relationships between the animal performing the record and its pen mates, and the additive relationships between pen mates
- restricted maximum likelihood converged very slowly (flat likelihood function)
- mixed model equations can be set up directly within the BLUPF90 family of programs
- variance component estimation using REMLF90 and GIBBSF90

Estimation of competitive effects with large pen size is difficult. The magnitude of competition effects may be larger in commercial populations.

Jean-Luc Jannink – Iowa State University
Selective phenotyping for mapping QTL:
Two methods to select genotypes:

1. total number of recombination per individual
2. number of recombination as well as uniformity of its distribution across the genome

Simulations: both methods decreased the mean squared error for QTL position
Average mean squared errors were similar for the two methods and variability of mean squared error was slightly lower for the latter relative to the former method.
Most useful for QTL of small effects, or when available markers do not allow marker spacing below 10 cM.

Jack Dekkers – Iowa State University
Theoretical analysis of alternative measures of LD based on multi-allelic microsattelite markers.
Effectiveness of marker-assisted selection (MAS) using population-wide LD depends on the extent of marker-to-QTL (M-Q) LD.
Simulations: 100 generations of random mating of 100 parents; LD quantified by R^2 of regression of QTL allele on alleles at a single marker. LD evaluated using: Lewontin's D′, r^2, χ^2 and a standardized $\chi^{2\prime}$.
Extensive existed at short distances, but declined rapidly with distance. LD showed similar declines for r^2, χ^2 and $\chi^{2\prime}$, but D′ was strongly inflated.
$\chi^{2\prime}$ is a good predictor of LD between markers and QTL when LD is generated by drift alone.

Bill Muir – Purdue University
Efficiency of incorporating molecular tools in breeding programs through theoretical modeling, computer simulations, and biological testing in actual breeding populations.
Traits of low heritability: initial theoretical examination showed that MAS could increase response to selection by as much as 500%; however, more recent studies demonstrated a much more moderate response. Problem: assumption that the QTL (or closely linked makers) were known, when in reality these QTL associations are found by statistical estimation and hypothesis.
A gene level simulation to compare results of genome wide MAS (GMAS) with that using conventional methods of BLUP estimation of genetic based on pedigrees: Results showed that for a trait of heritability of .5, the accuracy of selection with GMAS reached about 88%, whereas the BLUP line only reaches 82% accuracy.
Bills sees this as the future of genomics in animal breeding, the only real issue is if we can get the price down.

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More on Station reports

David Henderson – University of Arizona
Parallel Computational and Graphical Methods for the Detection of Differential Gene Expression in Microarray Experiments:

1. Stochastic Search Variable Selection (SSVS): R code; slow (3 days)
2. Parallel Bootstrapping program: R code; slow (3 days)
3. Graphical methods for exploring array results

Software is still being improved to speed up computational time.

Guilherme Rosa – Michigan State University
Collaborative activities with other NCR-204 members. Interesting outcomes last year:

1. Book: *Genetic Analysis of Complex Traits with SAS*. Cary, NC: SAS Institute Inc., 2004. Collaboration with Arnold Saxton (Univ. Tenesse) – as the editor, and Shizhong Xu (UC Riverside).
2. Worshop: *Oligonuclotide Microarray* – University of Arizona, Tucson. Collaboration with Dave Henderson (Univ. Arizona) – who worganizes the quatitative session of the workshop.
3. Grant proposal: *Extending the net fitness components model for prediction of transgene fate to incorporate uncertainty and validation of the model*. (USDA-BRAG Program) Collaboration with Bill Muir (Purdue).

Rosa reported also on research being conducted on linear mixed models suitable for the analysis of either log ratios or log intensity values of microarray data in the presence of multiple sources of variability. These models have been used also to compare the power and efficiency of different microarray experimental designs within a hierarchical replication context.

Jeanne Romero-Severson – Notre Dame
Discussion of different microarray platforms: spotted arrays with cDNA, spotted arrays with long oligos, and high-density arrays (short oligos) such as Affymetrix. How reliable is each platform? What would be the golden standard for comparing results? RT-PCR is generally used. But it is still variable. More research should be done comparing these technologies.

Business meeting

Sending email out to NCR-204 members

Emails should be sent by using the NIMSS web page, so all members get all messages regarding NCR-204 matters; need to update emails and or email servers (SPAM blockers) to receive announcements and attachments.

Access to the NCR-204 web page

General information is available for the public; only members however can access restricted information. Access through a login system available to members (not to guests).

Preparing reports and posting them on the web

We should feature all collaborations between the NCR-204 members; reports should go only to attending members; NIMSS should be used

Attendance on the NCR-204

The attendance was the worst point on the NCR-204 review (3 reviewers); we should list not people but institutions (organizations); Gretel has some mechanisms to try to improve attendance (e.g. contacting Experiment Stations and asking them to send a representative, and to remove non attending members).

Non-attending stations in 2005:
Arkansas
Illinois
Nebraska
Utah
Virginia

Non-attending stations in 2004 and 2005:
Arkansas
Illinois
Monsanto
Nebraska
Utah
Virginia

Objective 3 of the NCR-204

We need to review and modify (rewrite) our Objective 3: Use molecular genetics to test hypotheses generated from the fundamental theories of population, quantitative genetics, and molecular evolutionary genetics

The change of NCR-204 to either NCCC-204 or NCER-204

After some explanation by Gretel regarding the differences between NCCC and NCER groups, our NCR group decided collectively ((after motion by Bill Muir) to change to NCCC-204.

Administrative Adviser

Gretel will not be the Administrative Adviser soon; reason: retirement. That's why report is so important this year.
Jean-Luc suggested a motion to acknowledge the great job Gretel's been doing as our Administrative Adviser – unanimously approved by the group.

Elect secretary

Elected John Bastiaansen - Sygen, to be secretary in 2005-2006

Next meeting

"Local Host" for NCR-204 in 2006: Cynthia Ernst (Dow Agrosciences) – pending approval by Dow Company. Suggested dates: February 16-17.

Alternative: National Breeder Round Table (1st week of May)