

<p>Publishing in <i>Animal Genetics</i></p>
--

Organised by a standing committee **no**

Date and meeting time: July 25, 2016 2pm -

Chair, name and contact email:

Editor-in-Chief, dr. Johannes A. Lenstra Email: J.A.Lenstra@uu.nl

Number of participants at meeting: Hugely contrasting with the same meeting in Xi'An it was only attended by 3 participants and we may consider if we should hold it again in Dublin.

Summary of the meeting

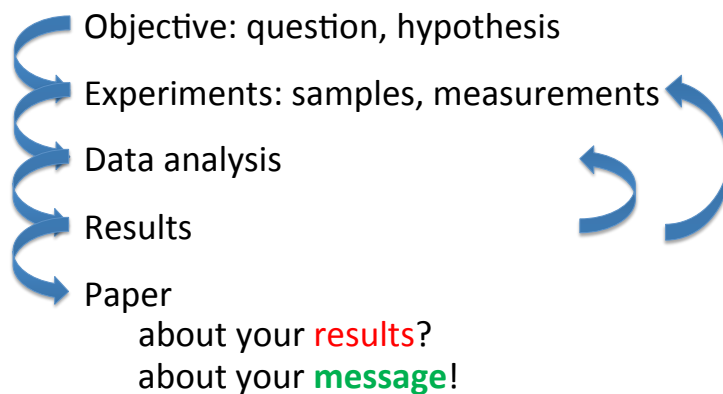
The "Animal Genetics Workshop" was held at July 25. Presentations by the Editor-in-Chief, dr. Johannes A. Lenstra and the Associate Editors dr. James Kijas and prof. Klaus Wimmers described the process of the processing of manuscripts and made several recommendations on how to organize a manuscript. Although attendance was lower than during the previous workshop in 2014, the participants responded with a lively and instructive discussion.

A manuscript, a message

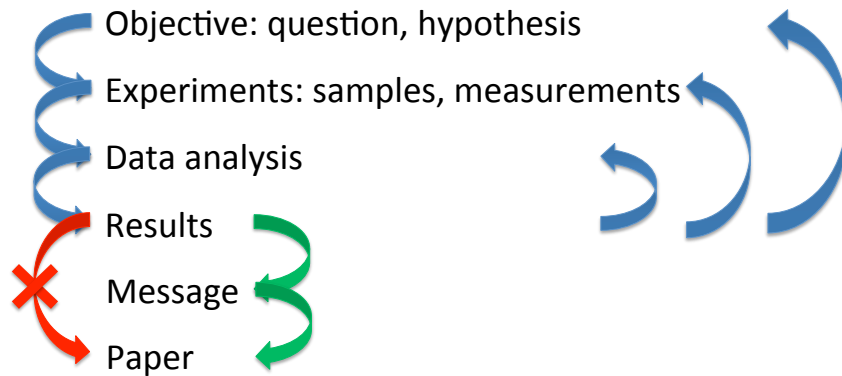
J.A. Lenstra, Utrecht University,
Editor-in-Chief, Animal Genetics

- Your work flow
- Our journal
- Our work flow
- Your manuscript

Your work flow

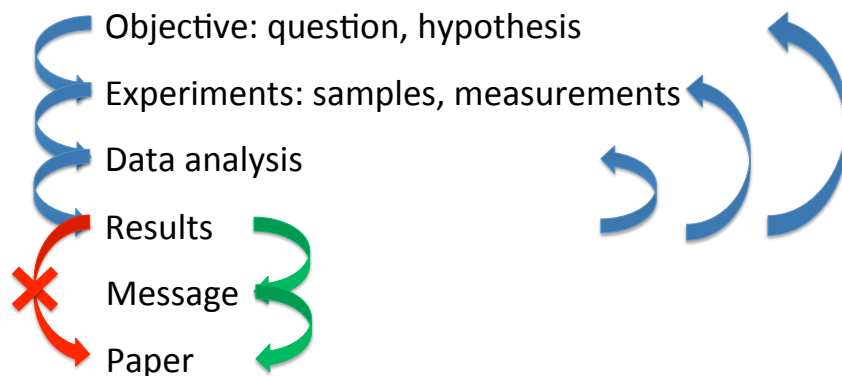


Your work flow



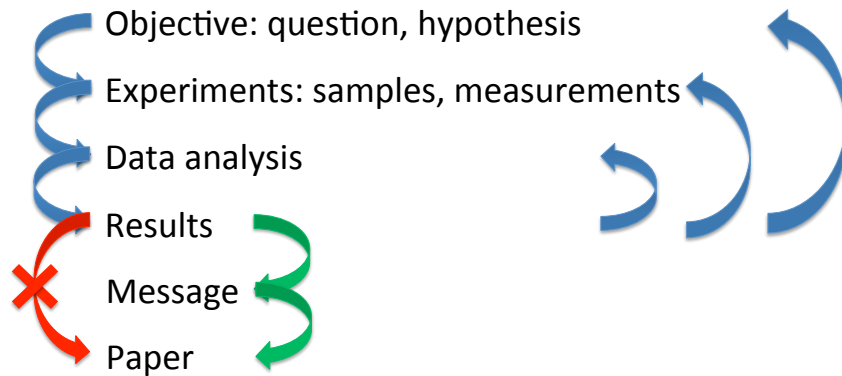
- Original question or hypothesis may blind you!
What is the **message** the results try to tell you?
It might even agree with your objective!

Your work flow



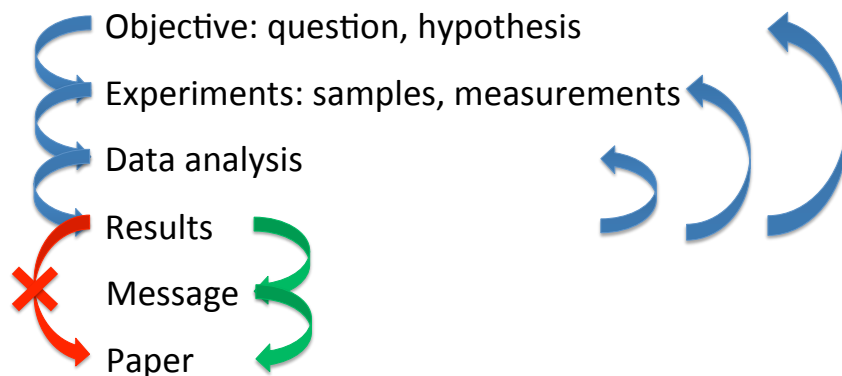
- No overinterpretation!
- Make most of it, but:
Publish now what you have now
Better now a paper than dreaming forever

Your work flow



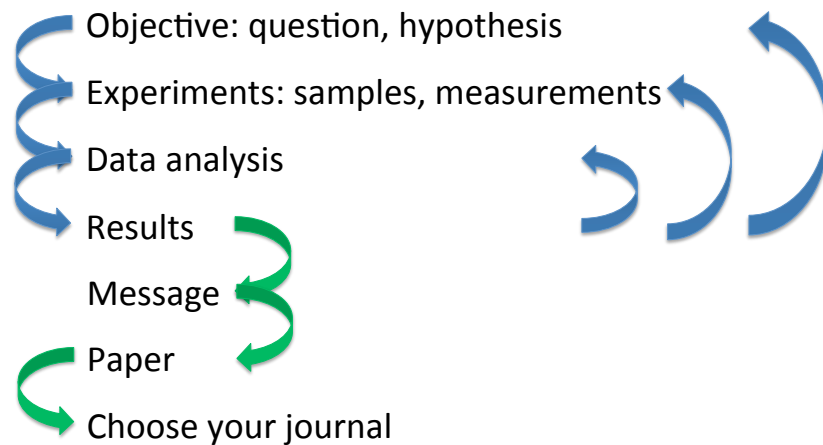
*You may sell your lousy results in an impressive presentation, but this does **never** work on paper*

Your work flow



Never walk alone: invite feedback
*Your colleagues are nasty, but useful.
They even may be right!*

Your work flow



Your journal: Animal Genetics

- Does your message fall within the **scope**?
See the *Authors' Guidelines*.
 - ☺ Supporting the breeding process:
Livestock; captive populations; aquaculture; related wild species
 - ☺ Genetics » differences between animals or populations
phenotypes vs. genotypes, QTLs, breed diversity, variable expression
- Look in a recent issue: is this your research field?

Your journal: Animal Genetics

- Does your message fall within the **scope**?
- How **important** is my message?
See the *Authors' Guidelines*.
 - ☺ Gene-oriented association studies: support of GWAS/causative mutations/more genes/more populations/300 animals
 - ☺ GWAS: more populations/follow-up on candidate genes
 - ☺ Expression studies: relevant for genetic variation
 - ☺ Diversity studies with SNPs or WGS; broad geographic coverage
- ☺ At least as important as in recent papers
- ☺ Depth and novel insights are more important than more-of-the same

Your journal: Animal Genetics

- Does your message fall within the **scope**?
- How **important** is my message?
- What is the most appropriate **format**?
 1. Full papers, <5000 words: new insight
 2. Short communications, <1500 words (GWAS without follow-up)
 3. Brief Notes, <500 words (new mutations in coat color genes)

Your journal: Animal Genetics

- Does your message fall within the **scope**?
- How **important** is my message?
- What is the most appropriate **format**?
- **Carefully** follow all instructions
 - Organization of text
 - Supplementary Files: a great invention
 - Supporting info, data for-the-record
 - References
 - Nomenclature
 - Options for Open Access
 - Public availability of datasets**

*If you do not care about the quality of your manuscript,
we will not care about you.*

Our workflow

1. Editor-in-Chief screens submission:
scope, quality, appropriate format, plagiarism,
data availability
 - Page budget of ~ 110 papers/year
 - ~66% of submissions are rejected
 - Resubmission often requested

Our workflow

2. Assignment to Associate Editor

Chief editors handles Brief Notes (without peer review) and reviews



Göran Andersson
Uppsala, Gene
identification
and function
Dog, Horse

Xhi-Qiang Du
Harbin, China
Quantitative
mapping
Pigs, chicken

James Kijas
St.Lucia, Australia
Breed diversity
Coat color
Sheep, goats

Edwige Quillet
Jouy-en-Josas,
France
Aquaculture

Tad Sonstegard
Recombinetics
USA, Genomics
Cattle

Klaus Wimmers
Dummerstorf
Functional
Genomics

Our workflow

3. Invitation of at least 2 reviewers

Recommended/opposed by authors

4. Reviewer reports

We never use a 3rd reviewer

5. Recommendation of Associate Editor

Accept (rare for original submission)

Major revision/Minor revision/Reject & Resubmit

Reject (not often if it has passed Editor-in-Chief)

6. Decision by Editor-in-Chief

Letter is signed by Associate Editor

Your manuscript

- Title
 - Abstract
 - Introduction
 - Materials
& Methods
 - Results
Figures
Tables
 - Discussion
- *This is how you write it, but not how we read it!*

Your manuscript

- Title **Clear**, well sounding **message**
but do not **shout**, **impress**, **seduce**
 - Abstract
 - Introduction
 - Materials
& Methods
 - Results
Figures
Tables
 - Discussion
- *You have only one title. Use it!*

Your manuscript

- Title **Clear**, well sounding **message**
- Abstract **Clear story:** background, approach, results, **same message**
- Introduction in different words
no speculations
- Materials & Methods Tip: start with it, forcing you to define the message
- Results Title; Abstract; what's next?
Figures
Tables
- Discussion

The abstract summarizes the paper?

The abstract explains the title!

Your manuscript

- Title **Clear**, well sounding **message**
- Abstract **Clear story:** background, approach, results, **same message**
- Introduction in different words,
no speculations
- Materials & Methods
- Results **Self-explaining**, direct link to **message**
Figures
Tables
 - Only for-the-record: supplementary
 - Tables: only essential data
 - Figures: symbols and coordinates clear without legends or main text;
- Discussion **use colors**

Your manuscript

- Title **Clear**, well sounding **message**
- Abstract **Clear story:** background, approach, results, **same message**
- Introduction in different words
no speculations
- Materials & Methods
- Results
Figures **Self-explaining:** work on it!
Tables ➤ If the **figures** explicitly support the **Abstract**, you have sold your paper!
- Discussion

One clear figure tells more than 1000 words

Your manuscript

- Title **Clear**, well sounding **message**
- Abstract **Clear story: same message**
- Introduction **Background**, from general to specific
However, - - : unknown territory
- Materials & Methods **We:** approach, outcome: **same message**
If they have read it 3 times, they will believe you!
- Results
Figures
Tables
- Discussion

Your manuscript

- Title **Clear**, well sounding **message**
- Abstract **Clear story: same message**
- Introduction **Background**, from general to specific
However, -- : unknown territory
- Materials & Methods **We**: approach, outcome: **same message**
 - Let your words count!
- Results
Figures
Tables
 - Cite all relevant literature, especially the papers of the reviewer!
- Discussion

Your manuscript

- Title **Clear**, well sounding **message**
- Abstract **Clear story: same message**
- Introduction **Background** > > **message**
- Materials & Methods Sample info!
No established methods
- Results **Self-explaining**
Figures Logical order does not always follow
Tables your notebook
- Discussion
 - *Reviewers have to read everything. Poor guys!*

Your manuscript

- Title **Clear**, well sounding **message**
 - Abstract **Clear story: same message**
 - Introduction **Background** > > **message**
 - Materials & Methods Sample info!
 No established methods
 - Results **Self-explaining**
 - Discussion Sum up/evaluate/ <-> literature/
 conclude: connect with **message**
 Implications/perspectives/speculations
- *If you still need Conclusions, it is now too late*

Your manuscript

- Title **Clear**, well sounding **message**
 - Abstract **Clear story: same message**,
 - Introduction **Background** > > **message**
 - Materials & Methods Sample info!
 No established methods
 - Results ➤ Let your words count
 - Discussion ➤ Sort your thoughts, build your case
 ➤ Informative section headings
 ➤ Logical transitions, new subject in
 new paragraph
- Finished? You are only half-way!*

Finalizing

- **Never** send out without thorough internal review.
The better is the enemy of the good
- Let your nasty colleagues look at results, analysis, presentation, **language**
Better your ego hurt than your paper rejected
We do not blame you because of your English.
*We **hate** you if you send it in!*
- **Revise** and **revise** again

Finalizing

- **Never** send out without thorough internal review.
The better is the enemy of the good
- Let your nasty colleagues look at results, analysis, presentation, **language** *English*.
- **Revise** and **revise** again

How to criticize?

Never shout!

The introduction is lousy! = Change a few commas

Better start nicely:

You make a few good points, but you have to present it in a different way = It's a mess. Clear it!

Rejected

- Heavy criticism may betray irritation because of a bad presentation
- Revise before submitting at another journal. You may get the same reviewer again!



Revision

- The reviewers are your best friends! They are more often right than your colleagues!
- Just be reasonable. Make the Editor's life easy
- Always change something, if not the argument, then the explanation

A manuscript, a message

**J.A. Lenstra, Utrecht University,
Editor-in-Chief, Animal Genetics**

- Your work flow: make it a message
- Our journal: read our guidelines
- Our work flow
- Your manuscript: build your message



ANIMAL GENETICS
Immunogenetics, Molecular Genetics and Functional Genomics

Publishing in *Animal Genetics*

James Kijas, Associate Editor

The types of manuscripts I deal with:

- **Genetic Diversity**
 - levels of genetic diversity within populations
 - relationship between populations (breeds)
 - genetic origin of breeds
- **Pigmentation Genetics**
 - genes which underpin coat colour
- **Parentage**
 - marker development and testing
- **GWAS and CNV**
 - association studies (as backup AE)
 - copy number variant surveys

Study Design

Good manuscript preparation often won't fix a bad study

- **test a hypothesis.** Genetic surveys have much less interest.
- select animals which are of interest, can test the hypothesis.
- ensure the resources being used are sufficient.
 - the animals tested per population (<20?)
 - the markers used to measure diversity (<10 microsatellites?)
- QC during genotyping
 - technical replicates, blind duplicate allele calling, inclusion of trios

Analysis

- perform analysis for a clear reason
 - if it doesn't contribute to the conclusions, don't include it
- test diversity levels against other populations
 - ISAG / FAO microsatellites are good
 - merge with existing data to provide genetic context
- if generating phylogenies:
 - clearly state what distance metric was used and how
 - bootstrap the tree for robustness and include node values

Manuscript Preparation

- Introduction:
 - assume some knowledge within the readership
 - must include reference to other key studies, even if overlapping
- Results:
 - use paragraph headings to guide the reader
 - some interpretation of results is good
 - highly descriptive material can be moved into a table
 - use the option of Supplementary Material
- Discussion:
 - provide interpretation of the key results
 - don't simply restate the results
 - relate the findings to other studies which are relevant

Things which will decrease your chances...

1. Recycling data
 - if the genotypes have been published previously:
 - essential to state how the current submission novel and new
2. Producing a Manuscript Over the Word Limit
 - ensure the length represents the weight of new findings
3. Genotyping them because they were there..
we prefer hypothesis driven science
4. Genotypic data is **not** submitted to a public database
This WILL prevent your manuscript from being published
 - Sequence into NCBI, NGS into SRA
 - SNP genotypes into Dryad or dbSNP

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3. WATCH YOUR CITATIONS GROW!
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The repository: Key features

- Flexible about data format, while encouraging the use and further development of community standards.
- Fits into the manuscript submission workflow of its partner journals, making data submission easy.
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- Contents are curated to ensure the validity of the files and metadata.
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- Long-term preservation ... by migrating common file formats when older versions become obsolete, and partnering with DataONE to guarantee access to its contents indefinitely.

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Search terms: Enter keyword, author, title, DOI, etc. Example: herbivory **Go**
Advanced search
Results/page: 20 ▾ Sort items by: relevance ▾ in order: descending ▾

Now showing items 1-7 of 7

[Dryad Data Packages \(7\)](#) [KNB \(0\)](#) [TreeBASE \(0\)](#)

Amador C, Hayes BJ, Daetwyler HD (2013) Data from: Genomic selection for recovery of original genetic background from hybrids of endangered and common breeds. *Evolutionary Applications* <http://dx.doi.org/10.5061/dryad.mn0d5>

Kijas JW, Hadfield T, Naval Sanchez M, Cockett N (2016) Data from: Genome-wide association reveals the locus responsible for four-horned ruminant. *Animal Genetics* <http://dx.doi.org/10.5061/dryad.1p7sf>

Greyenstien OFC, Reich CM, van Marle-Koster E, Riley DG, Hayes BJ (2016) Data from: Polyceraty (multi-horns) in Damara sheep maps to ovine chromosome 2. *Animal Genetics* <http://dx.doi.org/10.5061/dryad.6t34p>

Riggio V, Matika O, Pong-Wong R, Stear MJ, Bishop SC (2013) Data from: Genome-wide association and regional heritability mapping to identify loci underlying variation in nematode resistance and body weight in Scottish Blackface lambs. *Heredity* <http://dx.doi.org/10.5061/dryad.8f191>

El-Halawany NK, Zhou X, Al-Tohamy AF, El-Sayad YA, Shawky AA, Michal JJ, Jiang Z (2016) Data from: Genome-wide screening of candidate genes for improving fertility in Egyptian native Rahmani sheep. *Animal Genetics* <http://dx.doi.org/10.5061/dryad.k83b3>

KharzinoVA VR, Semyagin AA, Gladyr EA, Okhlopov IM, Brem G, Zinovieva NA (2015) Data from: A study of applicability of SNP chips developed for bovine and ovine species to whole-genome analysis of reindeer Rangifer tarandus. *Journal of Heredity* <http://dx.doi.org/10.5061/dryad.23p00>

Refine Search

Author
Hayes, Ben J. (2)
Al-Tohamy, Ahmad F. (1)
Amador, Carmen (1)
Beraldi, Dario M. (1)
Beraldi, Dario (1)
Bishop, Stephen C. (1)
Brem, Gottfried (1)
Brown, Emily A. (1)
Brown, Emily A. (1)
Brown, Emily (1)
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Subject
GWAS (2)
sheep (2)
SNP (2)
Adaptation (1)
Animal Mating/Breeding Systems (1)
body weight (1)
conservation genetics and biodiversity (1)
Conservation Genetics (1)
Damara sheep (1)
Ecological Genetics (1)
View More

Date Issued
2000 - 2019 (7)

Publication Name
Animal Genetics (3)
Evolutionary Applications (1)
Heredity (1)
Journal of Heredity (1)
Journal of Heredity (1)

	<u>Good Manuscript</u>	<u>Poor Manuscript</u>
Interest	Results are broadly relevant	Narrow focus
Mission	A question is being addressed	Survey of diversity, unlinked to any clear purpose
Introduction	Assumes knowledge in readership References past studies	Define PCR
Animals	Multiple populations, sampled to address the hypothesis	One breed from one country
Data	Data from > 1 marker type Microsatellites OK, but with allele standardisation, genotyping error estimates.	< 12 microsatellites



	<u>Good Manuscript</u>	<u>Poor Manuscript</u>
Data	Summary tables and figures Use of supplementary files	Large seq. alignments Long lists of marker data
Analysis	Diversity into a broader context Analysis answers a question	Formulaic reporting from diversity software
Tree Analysis	Topology supported by bootstrap analysis	Unsupported trees
Discussion	Highlights key findings Interprets the results Links back to the purpose	Repeats the introduction Fails to build on the results Few conclusions
Presentation	Length proportional to novelty (Short Comms can be the best!)	Long given weight of new data

Once you get an editorial decision:

- * Editors are scientists too. We get our papers rejected like anyone else.
- * Generally, implementing the reviewers suggestions moves the manuscript forward
- * Electing not to implement a reviewer's suggestion is OK, if you have a good reason
- * Electing to ignore a reviewer's suggestion is generally not OK
- * Electing to ignore an editor's suggestion is going to move the manuscript backwards

Good luck!





ANIMAL GENETICS

Immunogenetics, Molecular Genetics and Functional Genomics

Publishing in *Animal Genetics*

Klaus Wimmers

gene expression:

holistic studies: transcriptomics, microarrays, mRNA-seq

candidate genes: real time PCR, quantitative gene expression etc.

association analyses and functional studies

Material and Methods/Study Design

- Clear description
 - Number of animals per group; number of biological and technical replicates
 - Breed comparisons?!
 - Genetic aspects; implications for animal breeding
 - Factors considered in the statistical analysis; software used is relevant but not sufficient
 - Assay protocols: concentration and volume: 200µM dNTPs, 200pmol/µl

Manuscript Preparation

- Introduction:
 - assume some knowledge within the readership
 - **clear objectives**
 - hypothesis-driven vs. hypothesis generating
- Results:
 - use paragraph headings to guide the reader
 - some interpretation of results is good
 - highly descriptive material can be moved into a table
 - use the option of Supplementary Material

Manuscript Preparation (Cont.)

- Discussion:
 - provide interpretation of the key results
 - don't simply restate the results
 - relate the findings to other studies which are relevant
 - **clear statement on findings, conclusions, new hypothesis**

	<u>Good Manuscript</u>	<u>Poor Manuscript</u>
Interest	results are broadly relevant	Narrow focus
Mission	addresses aspects of genetics and breeding	just response to treatment
Introduction	Assumes knowledge in readership References past studies	Define PCR
Animals	well defined 'balanced' groups	confounding of genetic and environment
Data	quality control, multiple testing considered	bad array or NGS reads

	<u>Good Manuscript</u>	<u>Poor Manuscript</u>
Data	GEO submission, supplemental tables	just summarized data, means
Analysis	consider all relevant factors	just t-tests
Discussion	Highlights key findings Interprets the results Links back to the purpose	Repeats the introduction Fails to build on the results Few conclusions
Presentation	Length proportional to novelty (Short Comms can be the best!)	Long given weight of new data

Once you get an editorial decision:

- * Editors are scientists too. We get our papers rejected like anyone else.
- * Generally, implementing the reviewers suggestions moves the manuscript forward
- * Electing not to implement a reviewer's suggestion is OK, if you have a good reason
- * Electing to ignore a reviewer's suggestion is generally not OK
- * Electing to ignore an editor's suggestion is going to move the manuscript backwards
- * Prepare a clear response to reviewers; mark changes made to the manuscript