On the genetic improvement of parasitoids: lessons from *Nasonia*

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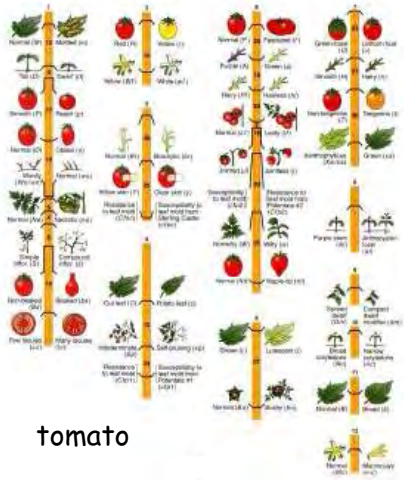
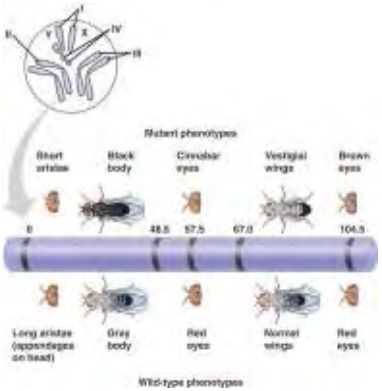
Why not parasitoids?

linkage map



tomato



D. melanogaster

Web of Knowledge™

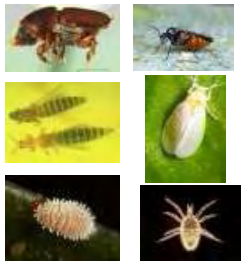
"Parasitoids" & "Genetics"	**82**	(1991-2010)
"Parasitoids" & "Ecology"	**501**	(1974-2010)
"Parasitoids" & "Behaviour"	**1734**	(1990-2010)
"Parasitoids" & "biological control"	**2705**	(1973-2010)
"Parasitoids" & "rearing"	**515**	(1977-2010)
"Parasitoids" & "quality control"	**212**	(1991-2010)

Towards the domestification of parasitoids

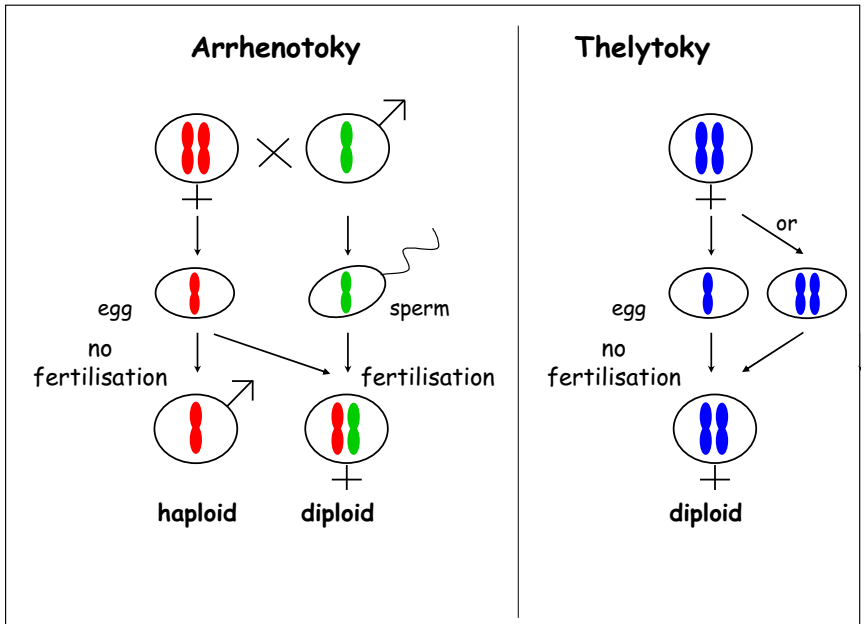
Haplodiploidy

Insects
Hymenoptera (sawflies, ants, bees, wasps)

Coleoptera (bark beetles)
Diptera (sciaridae, fungus gnats, midges)
Thysanoptera (thrips)
Hemiptera (whiteflies)
Coccoidea (scale insects)
Acari (mites)

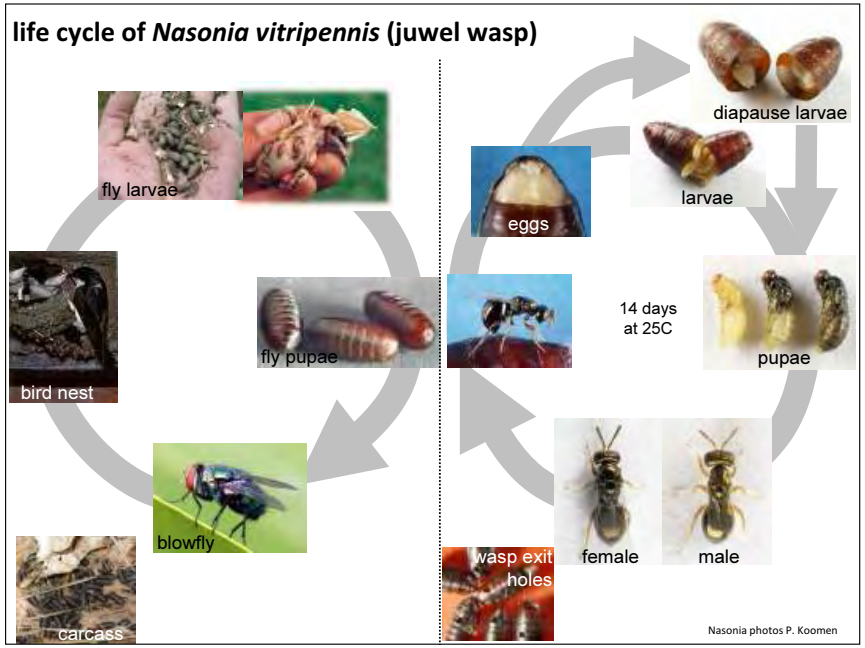


Nematodes (Oxyrudans, pinworms)
Rotifera (rotifers)

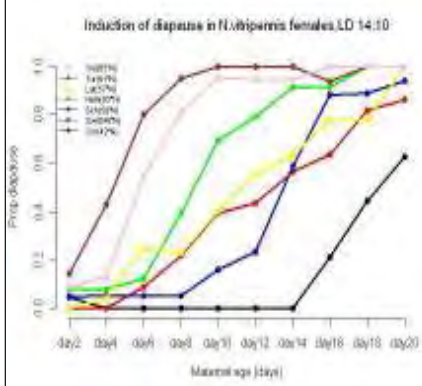


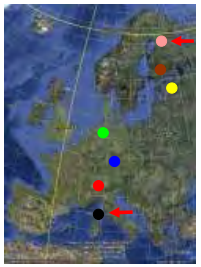
How can we genetically improve parasitoids?

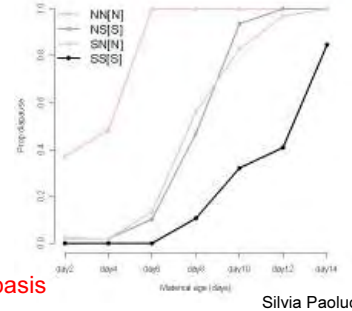
- Genetic crosses and artificial selection
- Introgression and selection
- Genetic mapping and genome sequencing
- Transformation



Genetic crosses and artificial selection: diapause



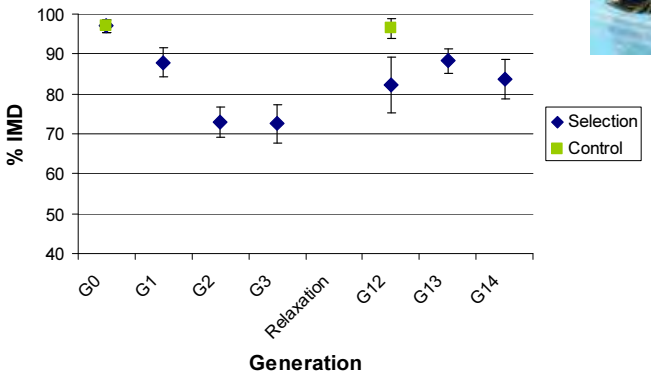




→ Diapause has a strong additive genetic basis

Silvia Paolucci

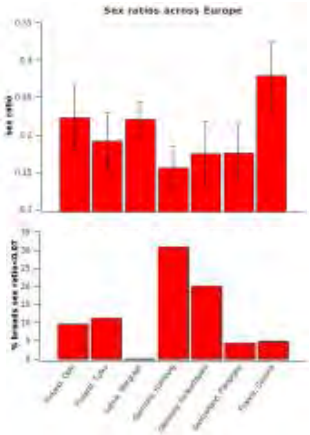
Genetic crosses and artificial selection: mate discrimination

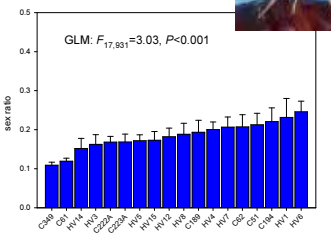


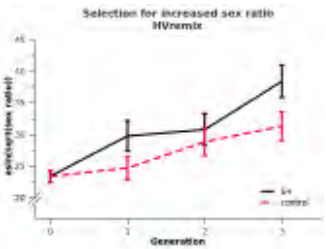
→ Selection for interspecific mate discrimination can be fast

Maartje Giesbers

Genetic crosses and artificial selection: sex ratio



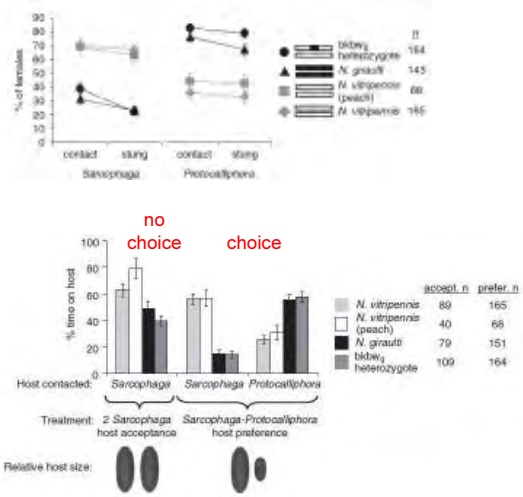


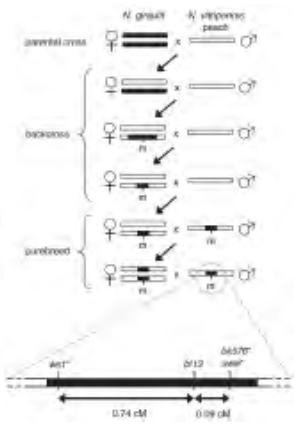


→ Genetic variation for sex ratio is large and selection for sex ratio can be fast

Pannebakker *et al*
J. Evol. Biol. in press

Introgression and selection: host preference

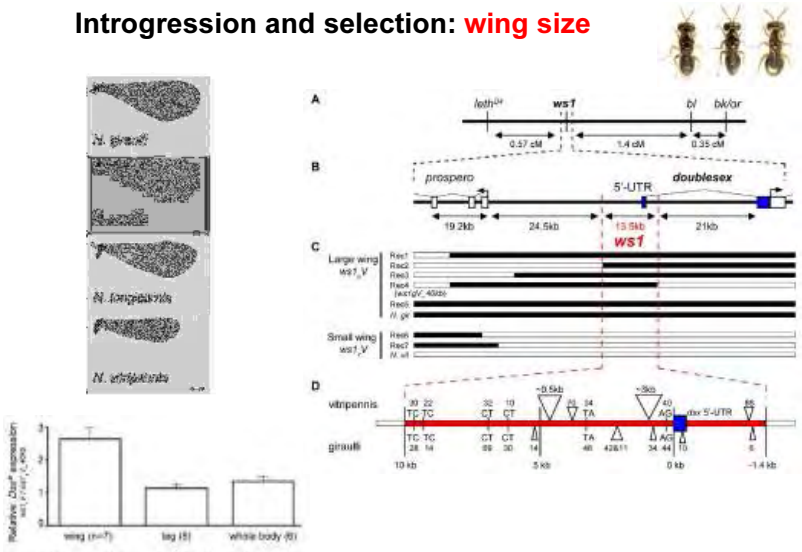




→ Host preference has a simple genetic basis: one or few major dominant genes

Desjardin *et al*
Heredity 2010

Introgression and selection: wing size



→ Wing size differences are due to the expression of a single gene: *doublesex*

Loehlin *et al*
PLoS Genetics 2010

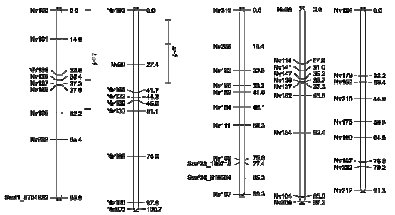
Functional and Evolutionary Insights from the Genomes of Three Parasitoid *Nasonia* Species

The *Nasonia* Genome Working Group*†

SCIENCE VOL 327 15 JANUARY 2010

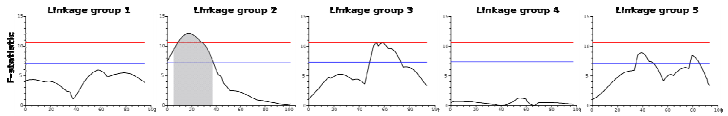
Nasonia photo P. Koomen

Genetic mapping and genome sequencing: sex ratio



Quantitative Trait Loci (QTL) for

sex ratio



→ Sex ratio and clutch size can be mapped to one or few genomic regions

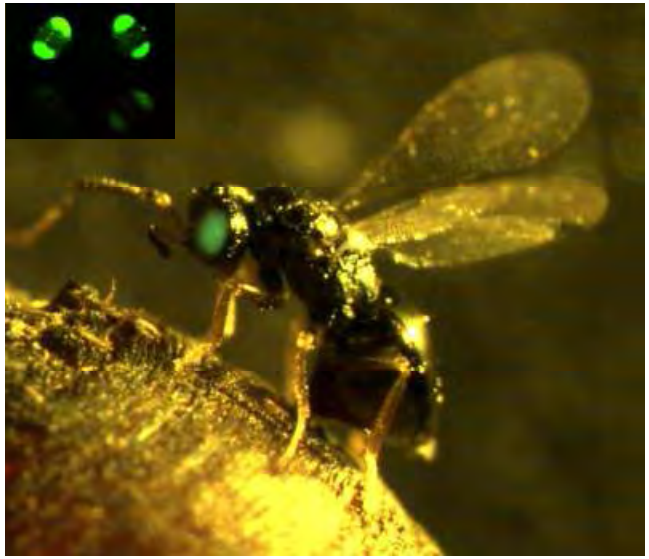
Pannebakker *et al*
J. Evol. Biol. in press

Genetic mapping and genome sequencing

High resolution mapping of:

- lifetime fecundity
- clutch size and ovariole number
- longevity
- sex ratio

Transformation?



The haplodiploid team

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Juergen Gadau & Oliver Niehuis (Tempe, AZ)

Thomas Schmidt (Freiburg, Germany)
Christoph Pietsch (Gartersleben, Germany)