Press Report April 2016 Andrea Acurio Biotic and abiotic factors impacting development, behavior, phenology, and reproductive biology of Drosophila suzukii J Pest Sci (published: 9 April 2016) Hamby et al (doi 10.1007/s10340-016-0756-5)

Review on juvenile development, adult reproduction, and seasonal variation in life history of D. suzukii.

They found Juvenile development is optimal at moderately warm temperatures, and larvae exhibit some immunity to parasitism. <u>Adults use visual</u> <u>cues and substrate-borne vibrations for courtship</u> <u>and exhibit a bimodal locomotor activity pattern</u> (except mated females).

Oviposition is consistently high in raspberry hosts and fruits with lower penetration force, and the presence of Wolbachia endosymbionts can lower fertility. Drosophila suzukii exhibit seasonal variation with a darker winter morph that is more cold tolerant. Also, <u>D. suzukii likely undergo</u> <u>reproductive diapause in the fall</u>, with colder temperatures and shorter day lengths influencing reproduction.



#### Introducing precise genetic modifications into human 3PN embryos by CRISPR/Cas-mediated genome editing

J. Assist. Rep. Gen (published: 6 April 2016) Kang et al. (*doi:10.1007/s10815-016-0710-8*)



**3PN Zygote Injection** 

8-16 Cell Stage

The purpose of this study was to evaluate the technology and establish principles for the introduction of precise genetic modifications in early human embryos. Data from 213 fertilized human eggs, donated by 87 patients (unsuitable for implantation as part of *in vitro* fertility therapy. Using <u>the CRISPR-Cas9 genome-editing technique they introduce into some of the embryos a mutation that cripples an immune-cell gene called *CCR5*. Some people naturally carry this mutation, which alters <u>the CCR5 protein in a way that prevents the HIV virus from entering the cells it tries to infect.</u> Genetic analysis showed that <u>of 26 human embryos targeted were modified with the *CCR5* mutation. But in some embryos, not all sets of chromosomes harboured the mutation; some contained the unmodified gene, whereas others had acquired different mutations.</u></u>

### Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases

# Nature biotechnology (published: 11 April 2016) Chen *et al.* (doi:10.1038/nbt.3514)

Data from 12 studies that together examined the genetic sequences of 589,306 people. The team looked for mutations in 874 genes linked to nearly 600 childhood diseases.

They whittled down the sample to 15,597 individuals who had at least one mutation associated with the 163 Mendelian diseases included in the study. After performing a series of quality-control tests, including manual review of clinical trials and more genetic sequencing of stored samples, they found 13 seemingly healthy individuals who survived to adulthood without showing any symptoms, despite carrying a genetic mutation linked to one of eight Mendelian diseases.

Authors argue that finding mutations that act as protective factors against disease is a better starting point for designing therapies than starting with the disease itself.



### Gene-edited CRISPR mushroom escapes US regulation Nature News (published: 14 April 2016) Waltz (doi:10.1038/nature.2016.19754)

Researchers at Pennsylvania University Park, engineered the common white button (*Agaricus bisporus*) mushroom to resist browning. <u>The effect is</u> <u>achieved by targeting the family of</u> <u>genes that encodes polyphenol</u> <u>oxidase (PPO)</u> — an enzyme that causes browning. By deleting just a handful of base pairs in the mushroom's genome, <u>Yang knocked</u> <u>out one of six PPO genes</u> — reducing <u>the enzyme's activity by 30%.</u>

The mushroom is one of about 30 genetically modified organisms (GMOs) to sidestep the USDA regulatory system in the past five years.



# Drosophila as a genetically tractable model for social insect behaviour

Frontiers in Ecology and Evolution (published: 19 April 2016) Camiletti & Thompson (doi.org/10.3389/fevo.2016.00040)

Despite having no parental care, division of labor, or subfertile caste, Drosophila may nonetheless offer a living test of certain sociobiological hypotheses framed around gene function. <u>Drosophila melanogaster, can</u> <u>respond to the ovary-suppressing queen pheromone of the honey bee Apis</u> <u>mellifera.</u> The authors explain the sociobiological imperative to reconcile kin theory with molecular biology, and qualify a potential role for Drosophila. Three applications for the fly-pheromone assay are proposed

- Availability and accessibility of massive mutant libraries makes immediately feasible any number of open or targeted gene screens against the ovary-inhibiting response.
- 2. Drosophila's powerful Gal4/UAS expression system can complement the pheromone assay by driving target gene expression into living tissue.
- Finally, coupling Gal4 with UAS-RNAi lines can facilitate loss-of-function experiments against perception and response to the ovary inhibiting pheromone, and do so for large numbers of candidates in systematic fashion.

### What is the Tree of Life?

PLOS Genetics (Published: 14 April 2016) Doolittle & Brunet (doi.org/10.1371/journal.pgen.1005912)

One of the several ways in which microbiology puts the neo-Darwinian synthesis in jeopardy is by the threatening to "uproot the Tree of Life (TOL)". Lateral gene transfer (LGT) is much more frequent than most biologists would have imagined up until about 20 years ago, so phylogenetic trees based on sequences of different prokaryotic genes are often different. How to tease out from such conflicting data something that might correspond to a single, universal Tree of Life becomes problematic. Moreover, since many important evolutionary transitions involve lineage fusions at one level or another, the aptness of a tree (a pattern of successive bifurcations) as a summary of life's history is uncertain.

## Recurrent specialization on a toxic fruit in an island Drosophila population

PNAS (published: 26 April 2016) Yassin, Debat, Bastide, Gidaszewski, David &Pool (doi: 10.1073/pnas.1522559113)





Around <u>30,000 years ago a population of Drosophila yakuba invaded the island of Mayotte</u> (Indian Ocean). The Mayotte population of D. yakuba began adapting to life on the rotting fruit of the Morinda citrifolia, a fruit that contains a toxin (octanonic acid), which is not tolerated by most insects.

 $\sim$  500,000 years ago a population of Drosophila simulans invaded the Seychelles Islands and subsequently evolved to specialize on the noni, this population eventually diverged -> D. sechellia.

To identify loci strongly associated with adaptation to noni, <u>Yassin et al., invented a</u> <u>modification of PBS, the Population Branch Excess (PBE) statistic, which specifically identifies</u> <u>loci evolving much more rapidly in the focal population than across other populations.</u> The PBE statistic is conservative for identifying loci underlying local adaptation in a population.

## Recurrent specialization on a toxic fruit in an island Drosophila population PNAS (published: 26 April 2016)

Yassin, Debat, Bastide, Gidaszewski, David & Pool

Yassin et al. quantified how often genomic regions known to underlie adaptation to noni in D. sechellia overlapped with regions of elevated PBE in the Mayotte D. yakuba population. They found that genomic regions underlying adaptation to noni fruit in D. sechellia and regions containing PBE peaks in Mayotte D. yakuba overlapped more often than expected by chance, suggesting a parallel genetic basis for adaptation to noni in both lineages.

This finding suggests that positive natural selection targeted the same regions of the genome in two flies that are distantly related, by 10 million y, because of the same environmental pressure (selective agent).



Fig. 3. Demographic history of and selection traces on the genome of Mavotte D. vakuba. (A) Plot of allele frequency spectrum of D. vakuba from

Size relationships of different body parts in the three dipteran species Drosophila melanogaster, Ceratitis capitata and Musca domestica Dev Gen Evol (published: 26 April 2016) Siomava, Wimmer & Posnien (doi: 10.1007/s00427-016-0543-6)

They studied <u>changes in size of pupae and adult organs in response to different rearing</u> temperatures and densities for D. melanogaster, Ceratitis capitata and Musca domestica. They confirm a clear sexual size dimorphism (SSD) for Drosophila and show that the SSD is less uniform in the other species. Moreover, the size response to changing growth conditions is sex dependent. Comparison of static and evolutionary allometries of the studied traits revealed that response to the same environmental variable is genotype specific but has similarities between species of the same order.</u> They conclude that the value of adult traits as estimators of the absolute body size may differ among species and the use of a single trait may result in wrong assumptions.



**Fig. 1** Wing outlines with landmarks and measurements. Wing length, width and outline for the manually measured area (*red line*) and landmarks from 1 to 11 in D melanogaster (a) and from 1 to 13 in C.

capitata (b) and *M. domestica* (c). The landmark coordinates were us extract wing length, width and WCS. *ACV* corresponds to anterior vein. *PCV* posterior cross vein. L2-L5 longitudinal veins

From vestigial to vestigial-like: the Drosophila gene that has taken wing Dev gen evol (published: 26 April 2016) Simon, Faucheux, Zider, Thézé, Thiébaud (doi 10.1007/s00427-016-0546-3)

The vestigial-like gene family have been identified as homologs of the Drosophila vestigial, which is essential to wing formation. All members of the family are characterized by the presence of the TONDU domain, a highly conserved sequence that mediates their interaction with the transcription factors of the TEAD family. Mammals possess four vestigial-like genes that can be subdivided into two classes, depending on the number of Tondu domains present. While vestigial proteins have been studied in great depth in Drosophila, we still have sketchy knowledge of the functions of vestigial-like proteins in vertebrates. They present the current knowledge about vestigial-like family gene members and their functions. together with their identification in different taxa.



### An Indel Polymorphism in the MtnA 3' Untranslated Region Is Associated with Gene Expression Variation and Local Adaptation in Drosophila melanogaster PLOS Genetics (published: April 27, 2016)

Catalán, Glaser-Schmitt, Argyridou, Duchen,& Parsch (doi.org/10.1371/journal.pgen.1005987)

Report that an indel polymorphism in the 3' untranslated region (UTR) of the metallothionein gene *MtnA* is associated with gene expression variation in natural populations of *Drosophila melanogaster*.

<u>A derived allele of *MtnA* with a 49-bp deletion in the 3' UTR segregates at high</u> <u>frequency in populations outside of sub-Saharan Africa.</u> The frequency of the deletion increases with latitude across multiple continents and approaches 100% in northern Europe. <u>Flies with the deletion have more than 4-fold</u> <u>higher *MtnA* expression than flies with the ancestral sequence.</u>

Using reporter gene constructs in transgenic flies, we show that the 3' UTR deletion significantly contributes to the observed expression difference. Population genetic analyses uncovered signatures of a selective sweep in the *MtnA* region within populations from northern Europe. We also find that the 3' UTR deletion is associated with increased oxidative stress tolerance. These results suggest that the 3' UTR deletion has been a target of selection for its ability to confer increased levels of *MtnA* expression in northern European populations, likely due to a local adaptive advantage of increased oxidative stress tolerance.