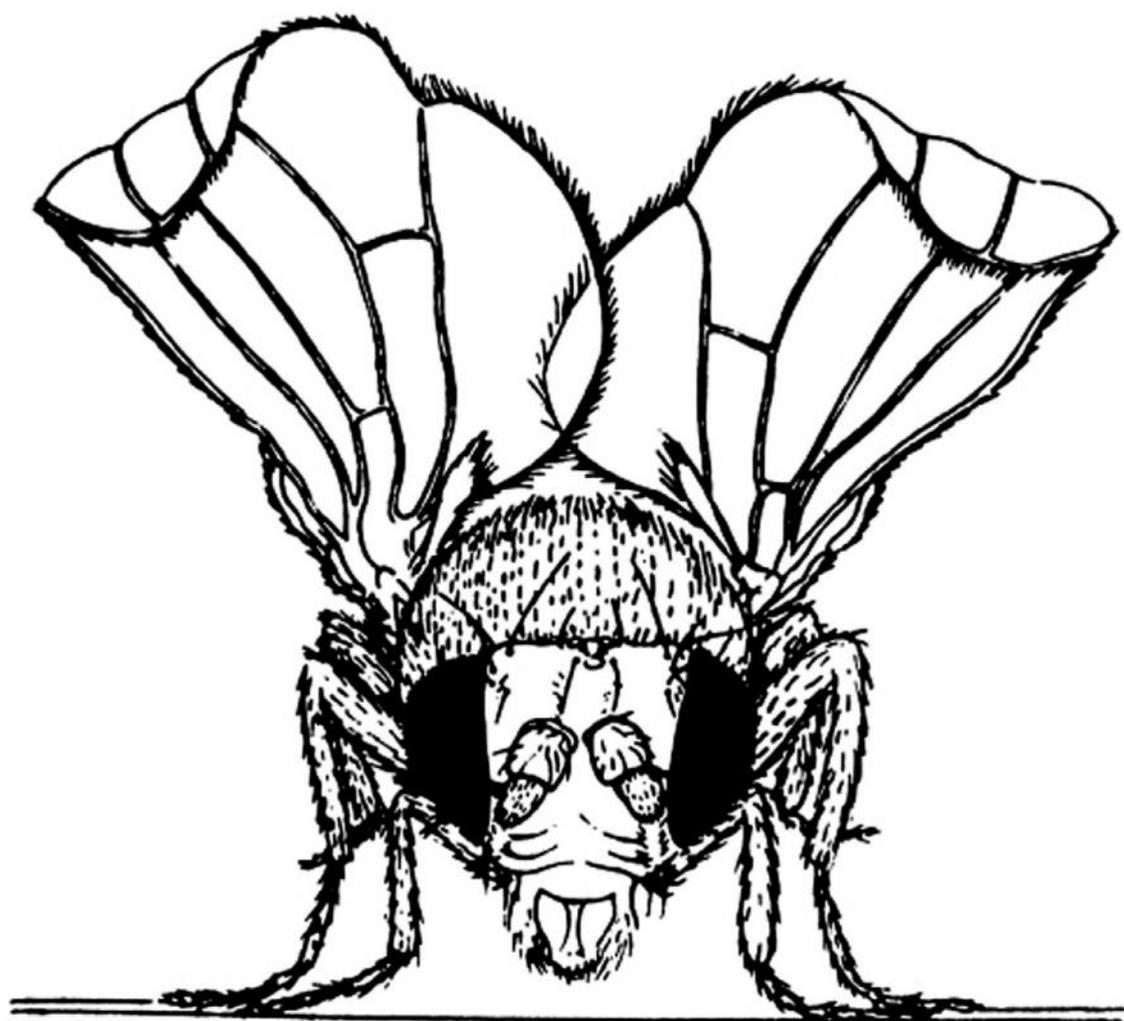


Atlas of
Drosophila
Morphology



Atlas of **Drosophila** **Morphology**

Wild-type and classical mutants



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We dedicate this book to Marta (Sylwester),
and to Elora and Ingrid (Nicolas)

Foreword

Of course, there is hardly anything that has missed the digital revolution. FlyBase has come to dominate those of us who do fly genetics so much that it is hard to recall the old days. I first started thinking it was time to switch to *Drosophila* in about 1971 and I went to Madrid to be taught fly lore by Antonio Garcia Bellido and his students such as Ginés Morata and Pedro Ripoll. The “Red Book” by Lindsley and Grell (later Lindsley and Zimm) was our bible, copies were so much used that they fell apart after a year or so. The wonderful drawings of Edith M Wallace were an indispensable part of that book; for us they were essential to learn mutant genotypes and distinguish phenotypes. Then in the last two decades we have turned to our computers for genotypes, names, chromosomal locations, papers on particular genes, but for the mutant phenotypes, to first get to know them and to follow them through the generations, we still often rely on the tattered old Red Book and Wallace’s drawings.

Up to now photographs of *Drosophila* have lacked impact and utility, mainly because of the limited resolution and depth of focus. For the photographer, *Drosophila* is the wrong size, too big for the compound microscope and too small for the macrolens. So in the past, drawings were better able to convey and emphasize points that helped recognition. But this new book has overcome these problems. The new methods of digitally accumulating focus planes combined with the skill of the authors have made the images staggeringly sharp and precise. Now you can explain to a new student how to see *Moiré*, an elusive but useful marker, perhaps even when you have not learnt to see it reliably yourself, or the slight difference between the karmoisin and the wild-type eye color. The staging of pupae is a particularly useful example of how words can fail and pictures succeed.

Even more important, the photographs convey the beauty that lies in the intricate detail of the fly and can help us remember why we are biologists. And also can help us explain to others how the fruit fly is so much more than it first seems to the naked eye. I know of no better way of illustrating this by quoting a great *Drosophila* geneticist, Curt Stern:

For more than 25 years I have looked at the little fly Drosophila and each time I am delighted anew. When I see it under moderate magnification of a binocular microscope I marvel at the clear-cut form of the head with giant red eyes, the antennae, the elaborate mouth parts; at the arch of the sturdy thorax bearing a pair of beautifully iridescent, transparent wings and three pairs of legs; at the design of the simple abdomen composed of ringlike segments. A shining waxed armor of chitin covers the whole body of the insect. In some regions this armor is bare; in other regions there arise short or long outgrowths, strong and wide at the base and gently tapering to a fine point. These are the bristles. Narrow grooves, as in fluted columns with a slightly baroque twist, extend along their lengths

Two or Three Bristles, American Scientist, 42, 213–247, 1954

You only need to glance at this lovely book to see what he meant.

Peter A. Lawrence
Cambridge, England



Introduction

*When, in 1910, a white-eyed mutant of *Drosophila ampelophila* (as the species was then called) appeared, there was nothing known at the time to indicate that this species gives rise frequently to mutant types, since these had not been seen in the numerous experiments previously made.*

**T.H. Morgan, C.B. Bridges and A.H. Sturtevant,
The Genetics of *Drosophila*, 1925**

Few could have predicted the career of a 3 mm long, tropical fly that was introduced into the United States by accident in the late nineteenth century and by the end of the following century had “invaded” biological laboratories worldwide. Even fewer would have envisaged the experimental power of this insect, and the universal knowledge it would bring to humanity. It has helped us understand heredity, genes, chromosomes, developmental patterns, immunity, physiological processes, population genetics, evolution, and has served as an experimental model to study human disease.

The quote above comes from one of the very first books on *Drosophila*, containing beautiful and precise pencil sketches by E.M. Wallace (like one reproduced here on the frontispiece). The Atlas you have in front of you takes advantage of the power of the digital photography available today. But the flies remain the same. In fact, many of the mutants illustrated in this Atlas were obtained within the first 5 years of work with *Drosophila* in the famous Fly Room (Sturtevant, 1965) at Columbia University, under the supervision of T.H. Morgan, and bred as stocks since. Numerous other mutants were induced following the discovery of the mutagenic effects of irradiation by H.J. Muller (Muller, 1930), another colorful member of the Morgan laboratory.

While the early publications on *Drosophila* are often accompanied by the illustration plates depicting the mutant phenotypes, this trend has progressively disappeared, and this information has become difficult to find as books went out of print. The rationale of this Atlas is to provide a modern version of this increasingly difficult to find information.

We hope this Atlas will become a useful resource in many genetics laboratories and help train students. If we managed to make entry into the *Drosophila* research even a bit easier then our goal has been achieved.

Sylwester Chyb and Nicolas Gompel
Cambridge, England
July 2012

How to use this book

Wild-type morphology

The external morphology of the wild-type flies is limited to the body parts affected by the mutant phenotypes. It also provides information on sexing flies and staging pupae. The information on anatomy is extracted, to a large extent from Demerec (1950) but we aimed to adhere to the current terminology by following the FlyBase guidelines.

Markers

The main part of the Atlas is devoted to about 70 mutants commonly used as markers. Their selection was based on our personal experiences, those of our colleagues who run stock collections as well as the availability of stocks expressing a single phenotype.

Markers are compiled into sections dealing with bristles, wings, appendages, eye shape, eye color, and body. Within each section, we introduce the markers in an alphabetical order based on the gene symbol. In a few instances, we have given preference to the traditional name of the mutant (e.g., *Hu*, *If*, *Sco*) rather than that of the gene, because of its more common use.

Below the marker name is the FlyBase gene or aberration number, together with available information on its location: chromosome (X, 2, 3 or 4), chromosome arm (L or R), cytological band, recombination map, and genomic coordinates (FB2012_04, released July 6, 2012).

A short description of the phenotype follows, highlighting the diagnostic morphological features of each mutant. Where abbreviations are used, these have already been explained in the wild-type morphology section.

The photograph plates face the text and illustrate phenotypes. Images were not intended to be exhaustive, as many markers are pleiotropic, but again sufficient in scope and details to show the key features of the phenotype(s). Most marker plates deal with a single allele, the most commonly used one if possible. On most plates we provide the images of the corresponding wild-type character (WT) serving as a reference.

We often show different magnifications and levels of details of the same character. The region shown at high resolution is boxed with a dashed line on the corresponding lower resolution image. We also highlight relevant details and morphological changes with arrowheads.

Many mutant phenotypes may be subject to modification with age, temperature, or genetic background and, accordingly, we attempted to illustrate the range of observable phenotypes. Phenotypes may also vary between individuals. These variations are described by the notions of *penetrance* and *variation in expressivity*.

Penetrance refers to the number of individuals of a given genotype that have the mutant phenotype. It can be complete (100% penetrance, i.e., expressed by all flies carrying the mutation) or incomplete (<100%). We have annotated the markers on an arbitrary scale of penetrance as full (100%), partial (<100%) and low (<<100%). This is only indicative and meant to prepare the users not to be surprised to find only a few flies of a given genotype displaying the expected phenotype.

Variation in expressivity refers to the extent to which the morphology is affected by a mutation. For instance, a mutation affecting wing size can result in no wing at all, a small wing, or a nearly normal wing, depending on genetic background and the rearing conditions. Here too, we ranked the markers on an arbitrary scale using a fly icon:



All flies displaying the phenotype look alike



The phenotype shows some variability, in a narrow range



The phenotype is extremely variable

In the last entry for a marker we indicate whether it is easy to score (identify) or requires experience; we also comment on any overlap between the marker phenotype and that of the wild-type or any other mutants.

Summary plates

The marker section is followed by several summary plates where various mutants affecting the same body part are presented on one plate for easy comparison.

Balancer chromosomes

As markers are most often encountered via the use of balancer stocks, we included a section listing the most common balancers: their markers (dominant and recessive) as well as basic information on their structure (breakpoints and diagrams). We also illustrate a selection of double-balancer stocks most commonly ordered from the Bloomington Stock Center (K. Matthews, personal communication). For more information on the use of balancer chromosomes refer to Greenspan (2004). For general information on balancers and other rearrangements, see Lindsley and Zimm (1992) or flybase.org.

***Drosophila melanogaster* subgroup species**

Finally, we illustrated the 9 species that together constitute the *Drosophila melanogaster* species subgroup. With the genomes of most of these species available, more and more researchers are starting to use other *Drosophila* species for their studies, which we felt warranted inclusion of a separate section.

Resources

Literature cited

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Other printed resources:

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Online resources

- | | |
|--|---|
| www.flybase.org | Drosophila genes and genome |
| www.taxodros.uzh.ch | Drosophila systematics |
| www.flystocks.bio.indiana.edu/ | Bloomington Stock Center |
| www.stockcenter.ucsd.edu | San Diego Drosophila Species Stock Center |
| www.dgrc.kit.ac.jp/en/ | DGRC, Kyoto Stock Center |
| www.gen.cam.ac.uk/department/flylab/flyculture.html | Fly Culture |

Technical notes

NOTES ON FLY STOCKS

Flies shown in this book were obtained from various sources: our personal collection, the Department of Genetics Fly Lab at Cambridge and the Bloomington Stock Center.

All flies were raised on cornmeal medium at 25°C, unless otherwise indicated. The staging was generally not taken into account, unless it was known to affect the phenotype, as for instance with eye color.

On several plates, the reader will notice variation in the color of the cuticle pigmentation, or the hue of the eye shade that is not highlighted in the text, or referred to as a particular phenotype. The origin of this variation is likely related to variation in the genetic background of the stocks.

NOTES ON PHOTOGRAPHY

Fly mounting

Adult flies and larvae were briefly anesthetized in vapors of ethyl acetate and mounted (glued) on a microscope slide. The appendages of adult flies were spread for esthetic needs, and the flies were further briefly anesthetized. The slide was placed on the microscope stage and the fly immediately imaged.

Lighting

To obtain an even, shadow-free illumination and maximize the contrast, a custom lighting system was made out of the conical shade of a desk lamp. The smaller top opening allowed the object to be seen from above. The inside of the cone was covered with strips of white light LEDs connected together, making a total of 96 uniformly distributed light points. The cone was placed above the object to be photographed, which was also surrounded by a small cylinder of tracing paper, to increase light homogeneity.

Imaging

The images in this Atlas were acquired with a ProgRes C5 camera mounted on a Leica M420 Macroscope. For each view, a stack of images of different focal plans was processed with the software Helicon Focus (HeliconSoft) to obtain an extended depth-of-field projection. The resulting projections were then enhanced using Adobe Photoshop.

Acknowledgments

The work in genetics has not been accomplished by any one individual or group of individuals, but has been worldwide and the outcome of many hands and minds.

T.H. Morgan, from his telegram read at the Nobel Banquet in Stockholm on December 10, 1933

There are numerous colleagues we would like to thank for their “hands and minds.”

First and foremost, we wish to thank John Roote of Cambridge University, who put the two of us in contact in the first place, helped us shape this Atlas, and offered advice and unflagging support throughout. Alike, Kathy Matthews of the Bloomington Stock Center went out of her way in seeking for us these photogenic flies and providing advice and feedback at different stages in the development of this work.

We acknowledge the FlyBase team for organizing, curating, and maintaining a state-of-the-art database from which we have drawn extensively in the preparation of this Atlas.

Finally, we want to thank Peter Lawrence for agreeing to write an insightful foreword with the dual perspective of a fly geneticist and a photographer.

Each of us also wants to make personal acknowledgments.

Sylwek is grateful to Professor Roger C Hardie FRS who is solely responsible for converting him to fly-pushing, Professor James L Frazier whose sabbatical at Imperial College was the intellectual spark which led to this book, and Professor Stephen J Simpson FAA for enquiring about the book's progress in his unmistakably charming way. I also want to acknowledge my sons, Adam and Szczepan, for polishing my English. Very special thanks to Professor Roger Keynes as well as Fellows and Master of the Trinity College for extending to me the status of Visiting Scholar, and to Department of Genetics, University of Cambridge for granting access to the reserved collection of the *Drosophila* literature. And finally, many thanks to Kristi Gomez, Editor at Elsevier for whom nothing was a problem.

Nicolas is grateful to François Leulier, Benjamin Prud'homme, and Ilona Grunwald-Kadow for feedback, support and inspiration, to Claude Moretti for providing technical help with the imaging setup. Also to Igor Siwanowicz for great tips on image treatment, to Yann Moreaux for having been a wonderful coach in the use of Adobe imaging softwares, to Jessica Cande for kindly proofreading the manuscript, and to Karine Grimaldi for fruitful feedback and suggestions on the layout design.

Wild-type morphology



Basics

Female and male *Drosophila melanogaster* (Meigen, 1830), dorsal view.

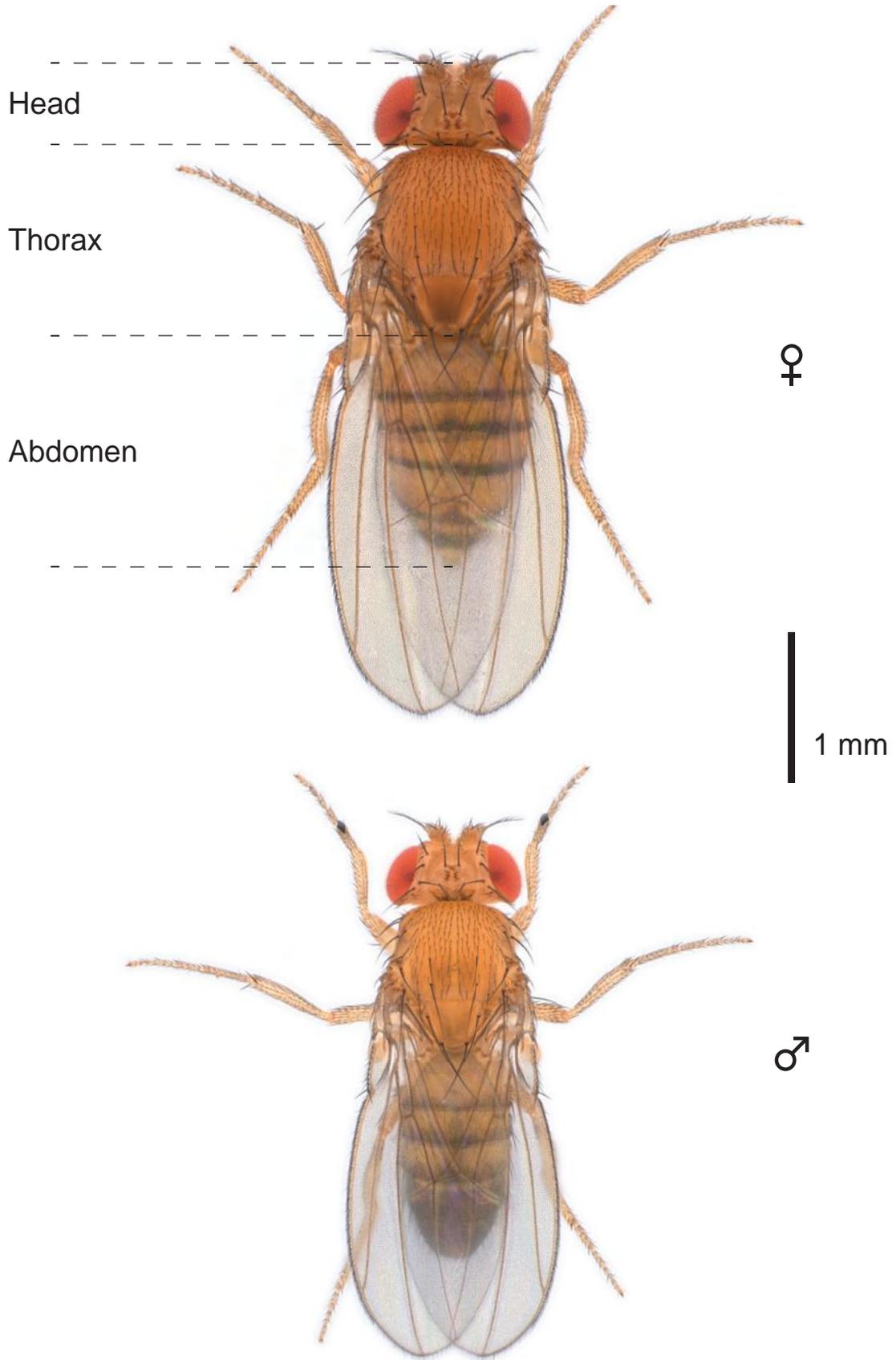
As in other insects, there are three main body parts (tagmata, *singular* tagma): head, thorax, and abdomen.

The thorax is divided into three segments:

- T1 (prothorax, anterior)
- T2 (mesothorax, middle)
- T3 (metathorax, posterior)

Different segments carry the following appendages:

- T1: one pair of legs
- T2: one pair of legs and one pair of wings
- T3: one pair of legs and one pair of halteres (modified wings)



Sexual dimorphism

Drosophila melanogaster is a sexually dimorphic species, whereby males and females can be easily distinguished on the basis of several morphological differences.

Size

Females are generally larger than males (but this may vary with age, culture conditions, and genetic background).

Color

In males, the posterior segments of the abdomen (A5 and A6) are entirely dark and shiny; in females, the coloration of these segments varies from pale to almost entirely dark. Both sexes have a pattern of dark transverse stripes on the dorsal side of each abdominal segment.

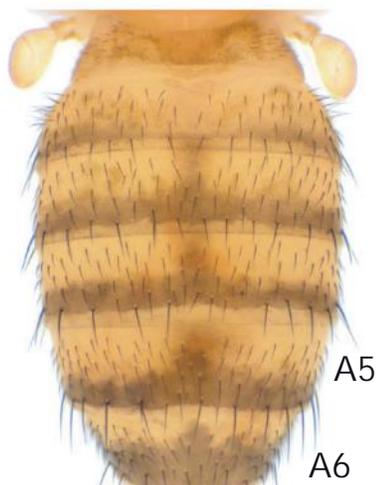
External morphology

- Females have an abdomen with a pointed tip while the male abdomen is rounded; additionally, the male abdomen tends to curl inwards.
- Male external genitalia (epandrium) are larger, more complex, and darker than the female external genitalia (genital plates and ovipositor).
- Forelegs of males *only* carry sex combs—rows of thick dark bristles on the first tarsal segment. This trait is easy to score and reliable, although affected by several mutations.

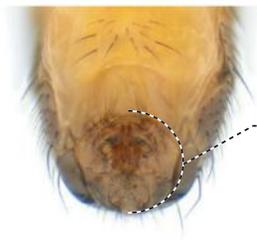


DORSAL ABDOMEN

SEX COMBS

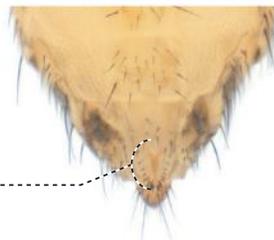


VENTRAL ABDOMEN



epandrium

ovipositor



Head

Adult *Drosophila* have a moveable head with sensory organs for vision (compound eyes and ocelli), olfaction (antennae, maxillary palps), gustation (proboscis), hearing (antennae), and touch (numerous mechanosensory bristles).

Compound eyes are the most prominent morphological structures located on the external head capsule. Each compound eye contains 750 units called ommatidia (commonly referred to as facets). Primary pigment cells of wild-type flies have reddish pigment, which absorbs excess blue light. Neighboring ommatidia are separated by short, erect, yellowish interommatidial bristles.

A darker area at the center of the eye, the pseudopupil, is visible in the wild-type, but may not be present in some mutants.

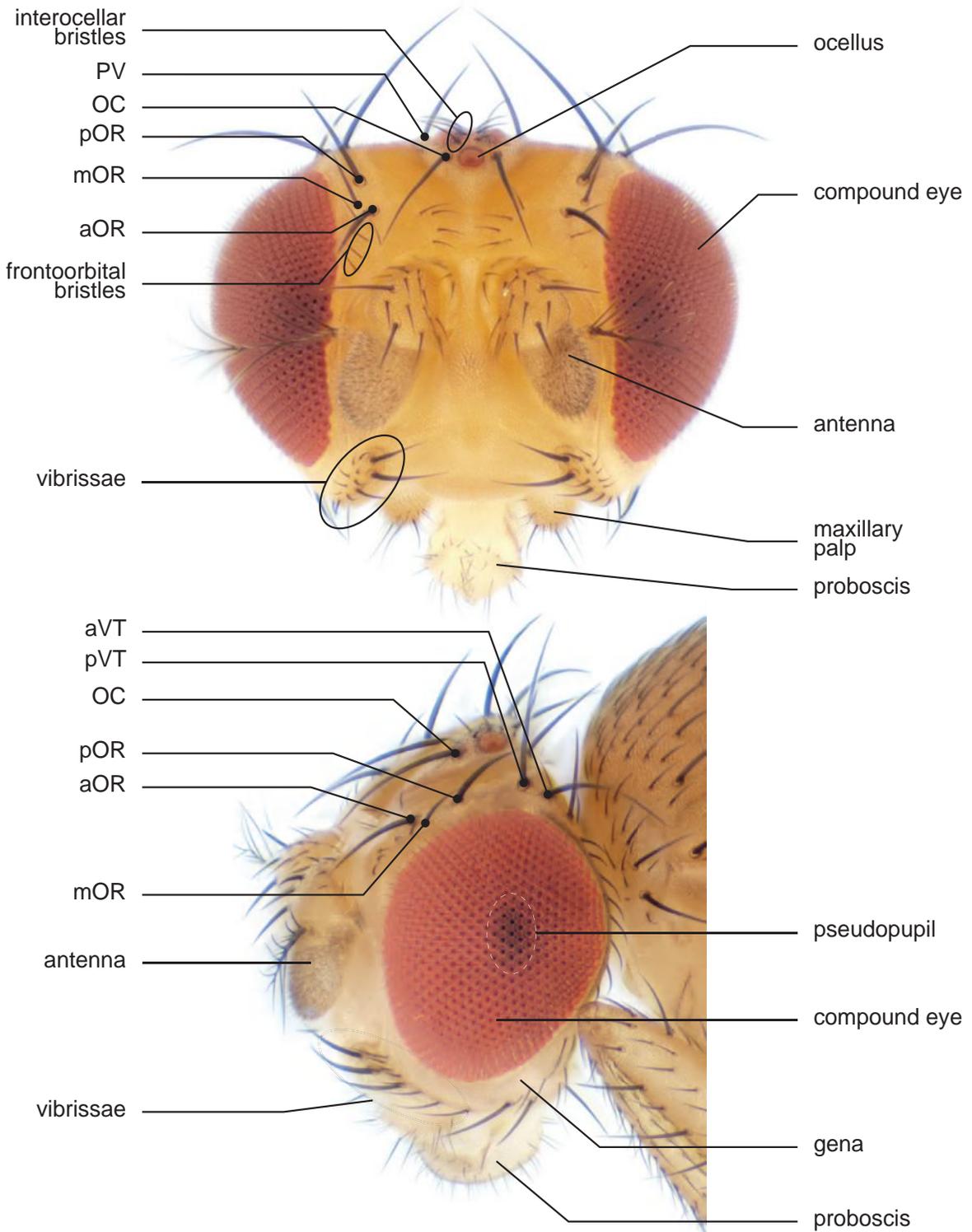
Compound eyes are surrounded by identified bristles, or group of bristles, placed at stereotypical positions: (anterior to posterior) vibrissae, fronto-orbital bristles, orbital (OR) bristles, anterior, middle, and posterior — (aOR, mOR, pOR), respectively.

Ocelli (*singular* ocellus) or simple eyes are found on the dorsal aspect of the head as a triplet: two lateral ocelli are directed to the left and right of the head, respectively, while a medial ocellus is directed frontally. Within the ocellar triangle, there are two rows of interocellar bristles.

The ocelli and the compound eyes provide fruit flies with two anatomically separate and functionally different visual pathways.

On either side of the central ocellus there are ocellar (OC) bristles. Posterior to the lateral ocelli are postvertical (PV) bristles, and further laterally there are two vertical (VT) bristles (anterior and posterior, aVT and pVT).

PV	postvertical bristles
OC	ocellar bristles
aOR, mOR, pOR	anterior, middle, and posterior orbital bristles
aVT, pVT	anterior and posterior vertical bristles



Head appendages

Antennae

Between the compound eyes but anterior to the ocelli are the antennae (*singular* antenna)—paired and movable sensory appendages composed of six segments or antennomeres: scape (1), pedicel (2), and flagellum (3), which connects to a branched arista via two further segments.

The pedicel contains Johnston's organ, a cluster of chordotonal neurons (stretch receptors) involved in sound, wind direction, and gravity detection.

Antennomere 3 houses about 400 multiporous olfactory sensilla housing approximately 1200 olfactory receptor neurons (ORNs).

Antennomere 3 also houses the sacculus, an invagination of the epithelium at the base of the flagellum containing thermoreceptors and hygrometers.

The most distal segment of antenna is an arista, an elongated bristle-like structure with numerous side branches.

Mouthparts

The secondary olfactory organs, paired maxillary palpal (*singular* palpus) are located ventral to the antennae and contain approximately 120 ORNs each, innervating multiporous sensilla.

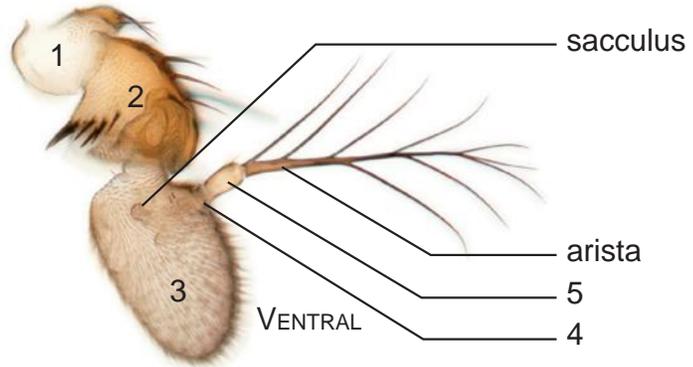
The proboscis, the adult fly's feeding appendage, is a structure resulting from the fusion of bilateral labella (*singular* labellum). It is directly involved in food detection and food intake. The proboscis is an articulated appendage and can be extended or retracted. It contains within the labrum a food canal through which liquids are pumped into the gut.

The fly can sense food quality through various gustatory sensilla containing both taste and mechanosensory neurons.

ANTENNAE

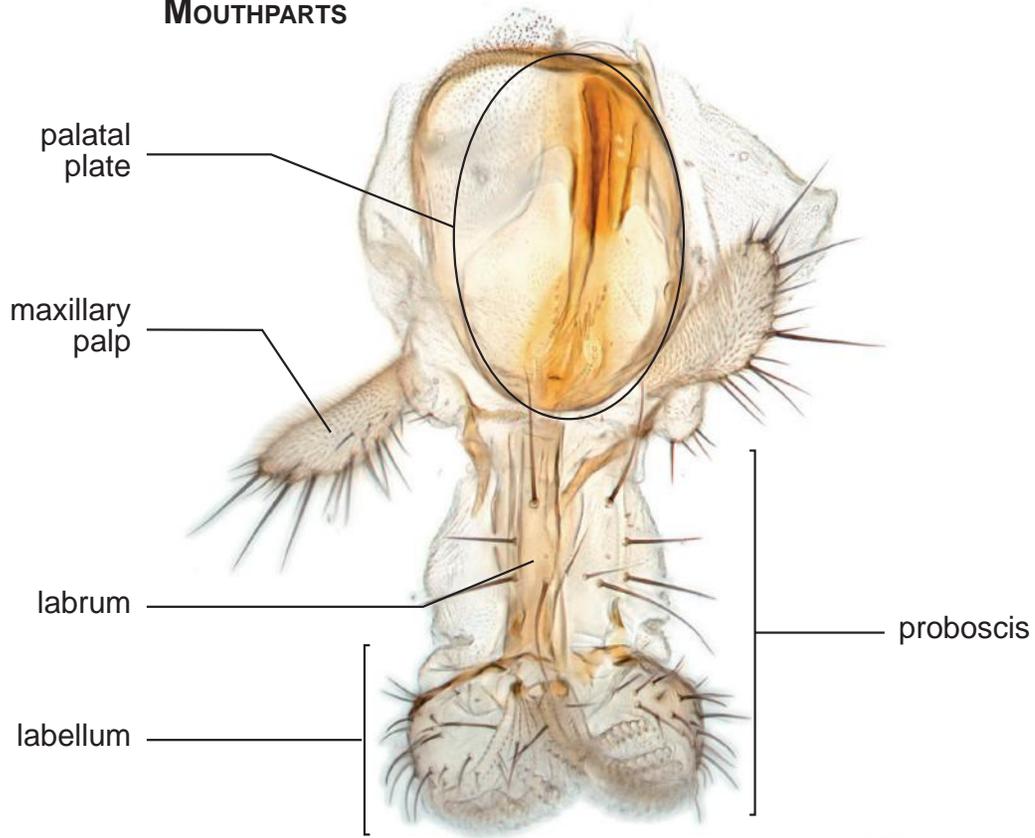


DORSAL



VENTRAL

MOUTHPARTS



Thorax (dorsal view)

The notum is composed of two main parts: anterior scutum and posterior scutellum separated by the scutoscutellar suture.

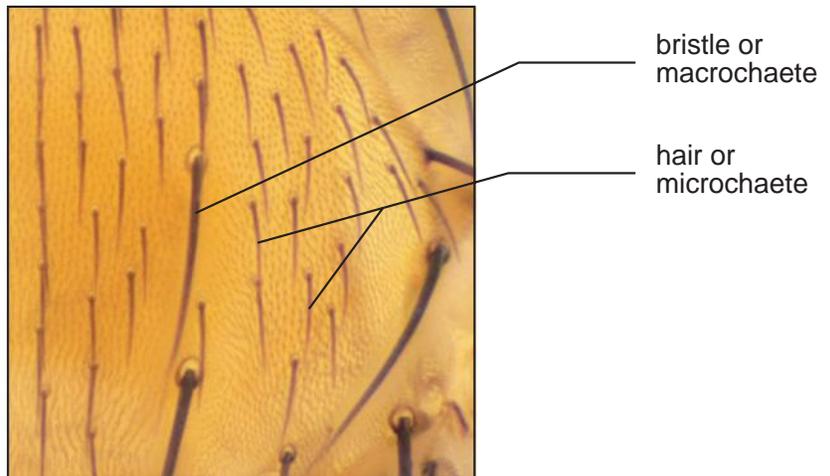
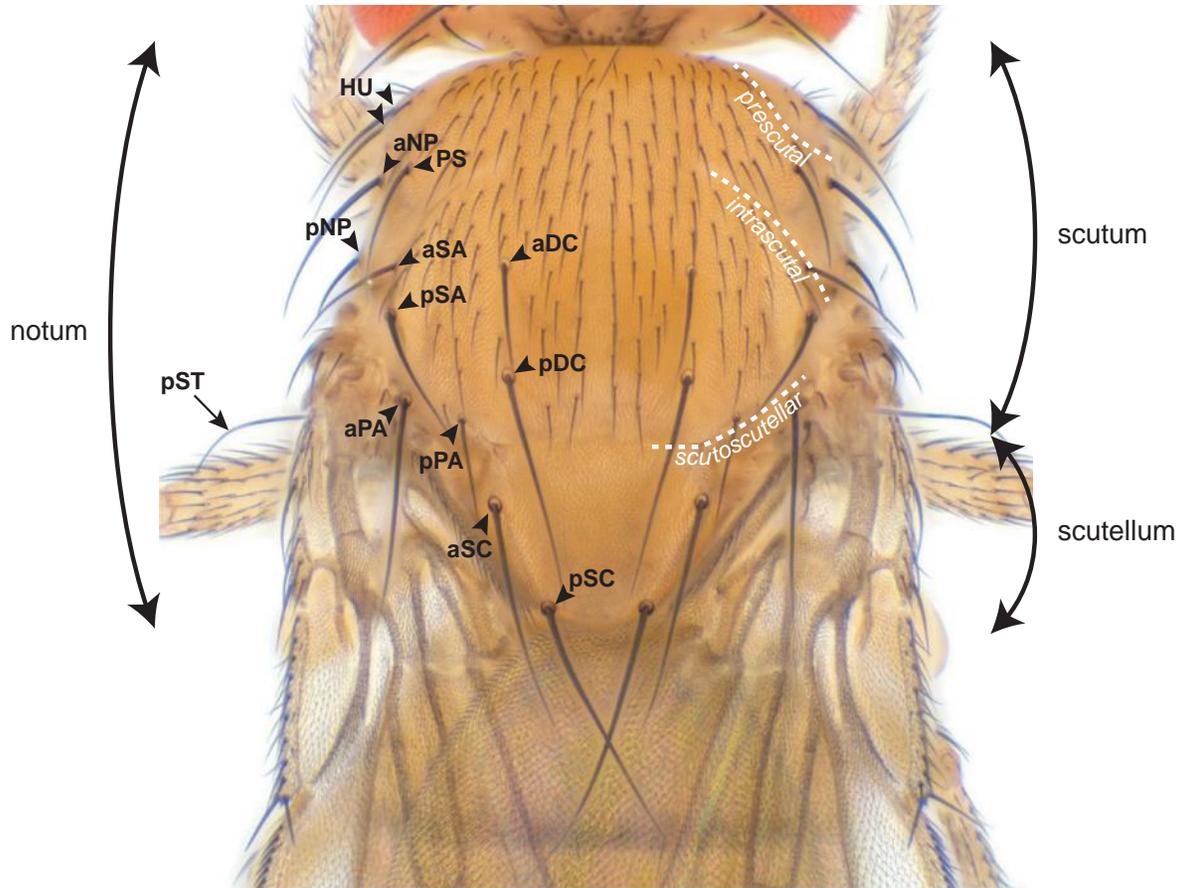
Scutum

HU	humeral
aNP, pNP	anterior and posterior notopleural
aSA, pSA	anterior and posterior supra-alar
aPA, pPA	anterior and posterior post-alar
PS	presutural
aDC, pDC	anterior and posterior dorso-central

Scutellum

aSC, pSC	anterior and posterior scutellar
----------	----------------------------------

Macrochaetae and microchaetae are cuticular structures found on all body parts of an adult and are most commonly referred to as bristles and hairs, respectively. Note that the term 'hair' is often used to denote both sensory (microchaetes) and non sensory cuticular structures; the latter are much smaller than the microchaetae and should more correctly be referred to as 'trichomes'.



Thorax (lateral view)

Scutum

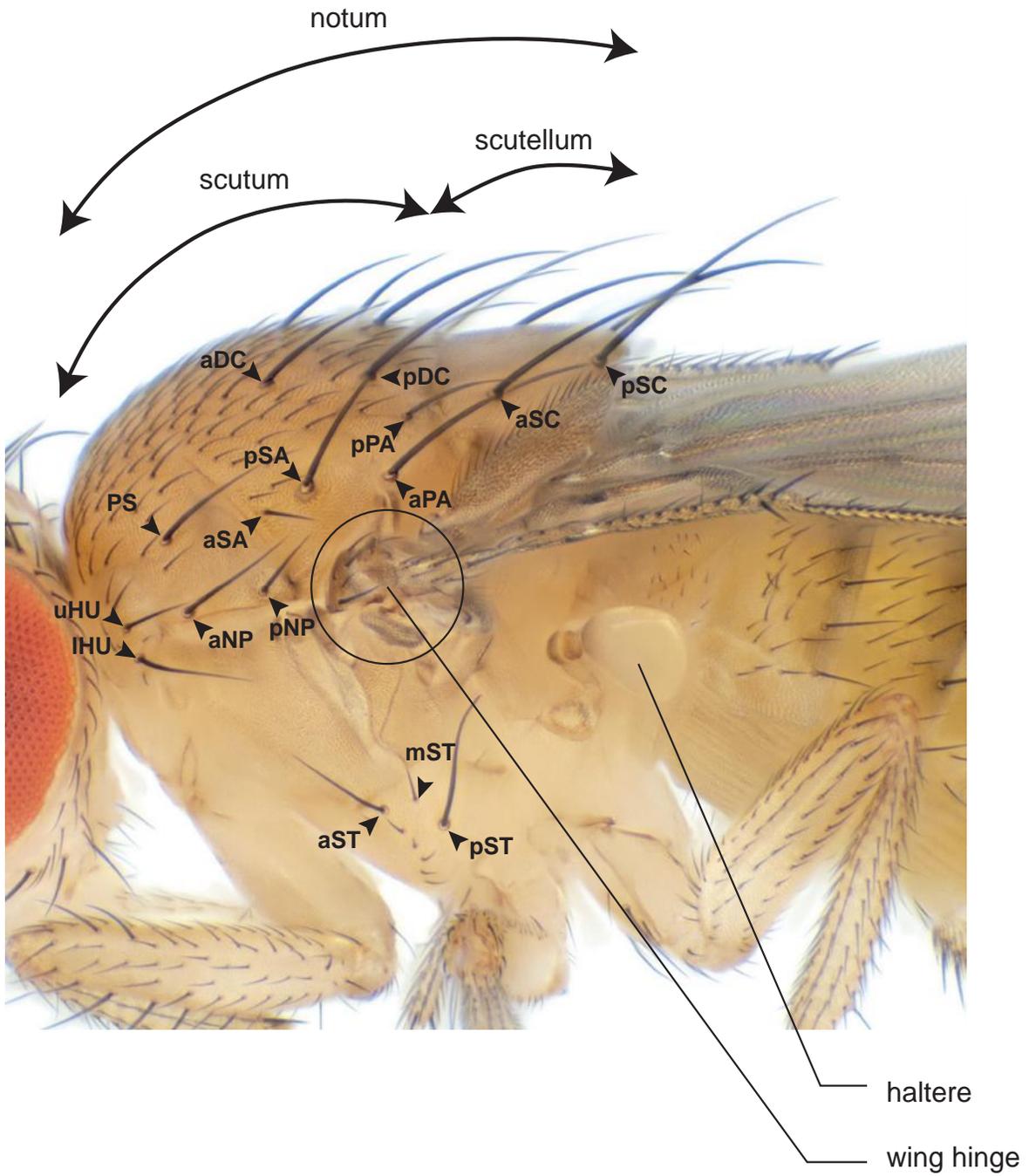
uHU, lHU	upper and lower humeral
aNP, pNP	anterior and posterior notopleural
aSA, pSA	anterior and posterior supra-alar
aPA, pPA	anterior and posterior post-alar
PS	presutural
aDC, pDC	anterior and posterior dorso-central

Scutellum

aSC, pSC	anterior and posterior scutellar
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Sternopleurum

aST, mST, pST	anterior, middle and posterior sternopleural
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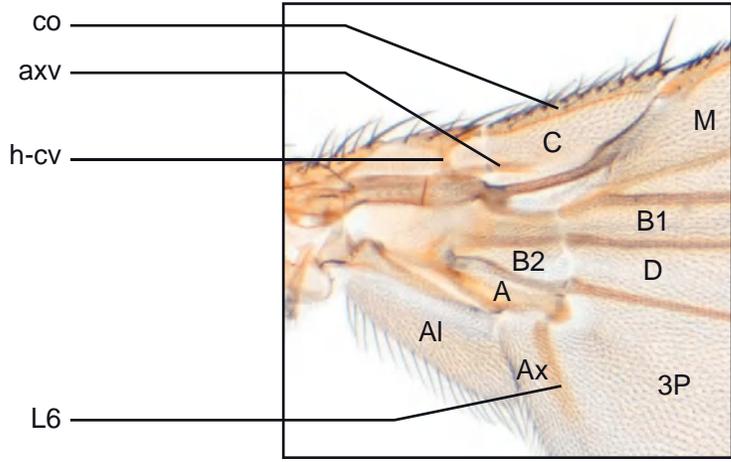
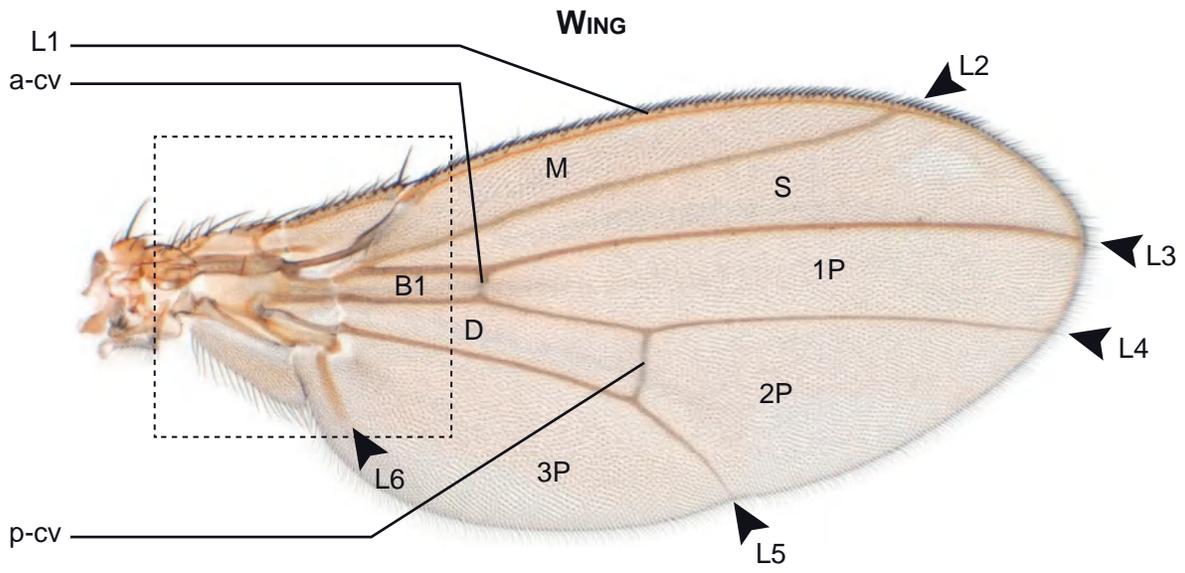
Wings and halteres

Wing cells

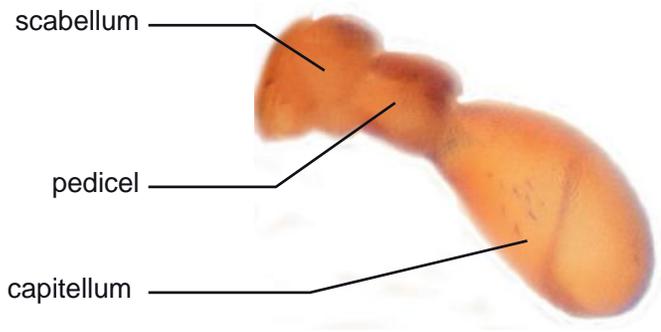
C	Costal cell
M	Marginal cell
S	Submarginal cell
B1	Basal cell 1
1P	1st posterior cell
B2	Basal cell 2
D	Discal cell
2P	2nd posterior cell
A	Anal cell
3P	3rd posterior cell
Al	Alula
Ax	Axillary cell

Wing veins

L1	vein L1
L2	radial vein
L3	medial vein
L4	cubital vein
L5	distal vein
L6	vein L6
co	costal vein
axv	axillary vein
h-cv	humeral cross-vein
a-cv	anterior cross-vein
p-cv	posterior cross-vein



HALTERE



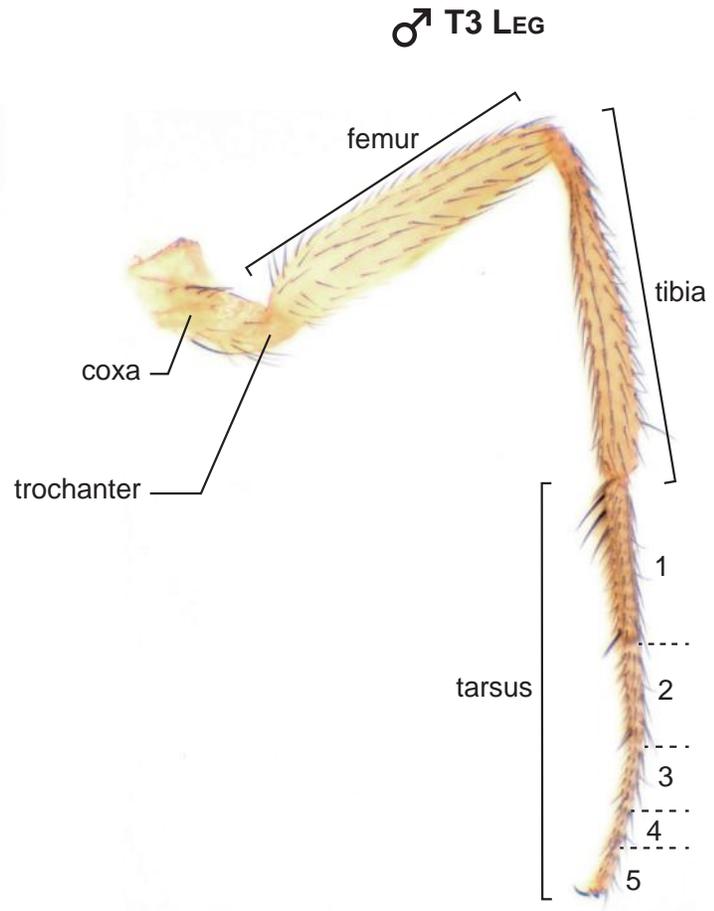
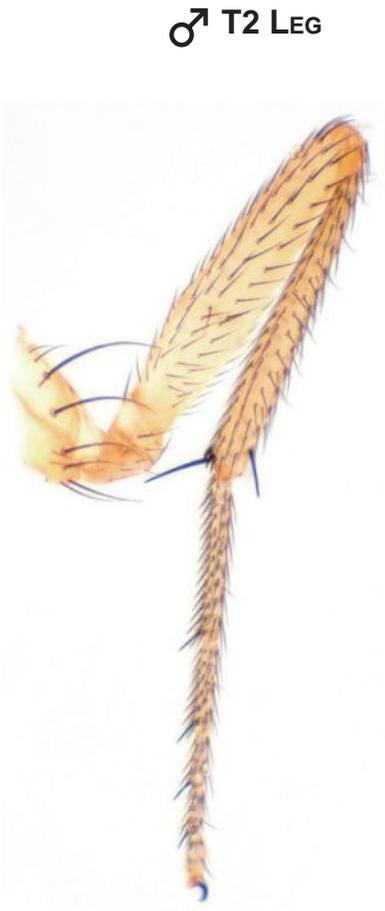
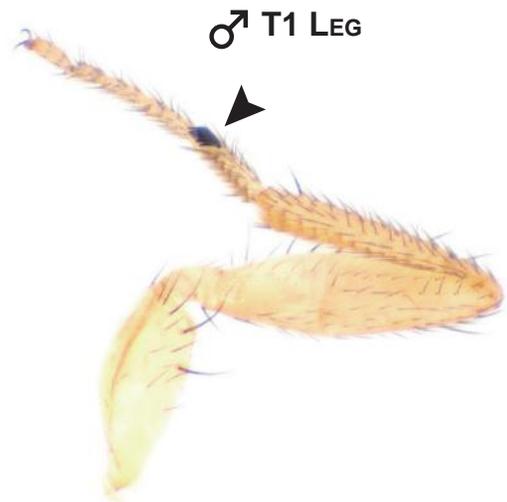
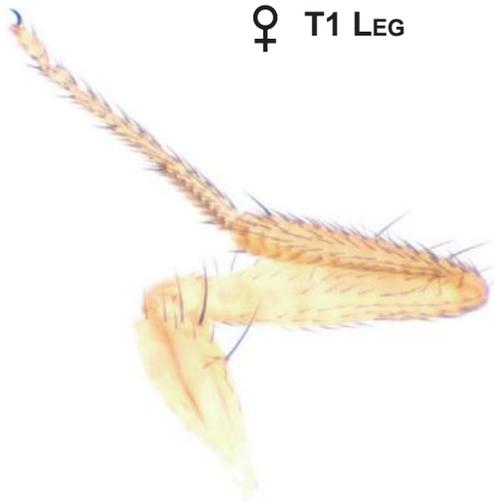
Legs

The three pairs of legs, each associated with a corresponding thoracic segment, have a similar structure but differ in their relative size, i.e., they become progressively larger from anterior to posterior.

Male and female legs do not differ with the exception of the prothoracic legs: *only* forelegs of males carry sex combs, rows of thick dark bristles on the first tarsal segment.

Each leg is composed of five parts, from proximal to distal: coxa, trochanter, femur, tibia, and tarsus. Each tarsus (*plural tarsi*) is composed of five tarsomeres.

- T1 prothoracic leg
- T2 mesothoracic leg
- T3 metathoracic leg



Life stages: third instar larva and pupa

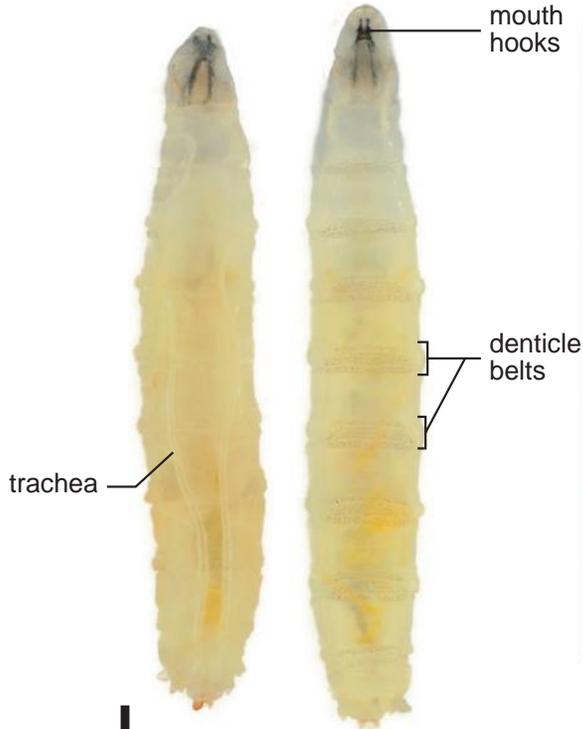
Drosophila melanogaster completes its life cycle over about 10 days at 25°C. The embryo develops over 24h. There are three larval stages: L1 and L2 (~1 day each) followed by L3 (~3 days), a pupal stage (4 days), and an imago stage. Adult flies reach sexual maturity after 2–4 days, and fertilized females then start to lay eggs. The developmental timing can vary considerably (by several days) with environmental conditions (temperature, crowding, food quality) and genetic background.

Third instar larvae can be sexed, as the male and female gonads, visible without the need for dissection, differ in size. Gonads are visible in side view, against a dark background and ideally with back-illumination. Gonads are located on each side (black arrowheads), in the posterior third of the larva, slightly below the dorsal trachea. The males gonads are about five times bigger than the female gonads. They can be distinguished from the fat body in both sexes as they are translucent, while the fat body is milky.

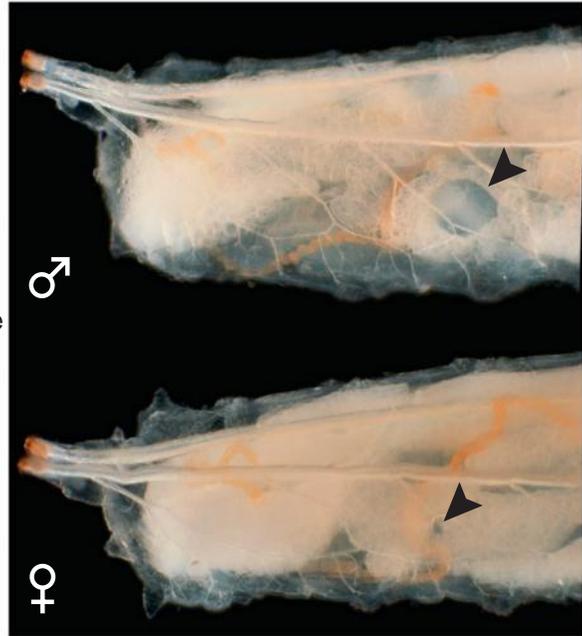
Pupae can be sexed on the last day of the pupal stage, when the cuticular structures become pigmented and the sex combs become visible on the ventral face of the male pupa (white arrowheads).

THIRD INSTAR LARVA

DORSAL VENTRAL



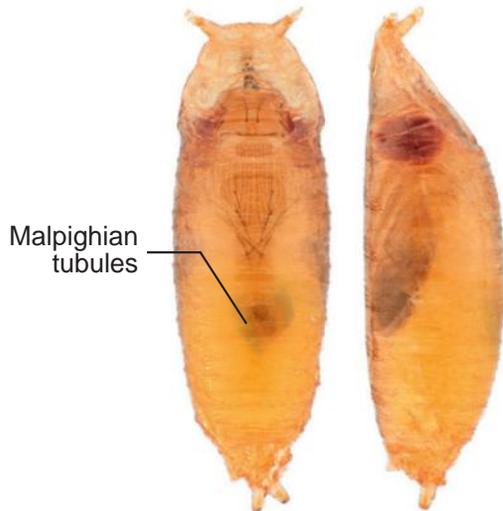
THIRD INSTAR LARVA GONADS



1 mm

PUPA

DORSAL LATERAL



SEX COMBS IN PUPAE

♂ ♀



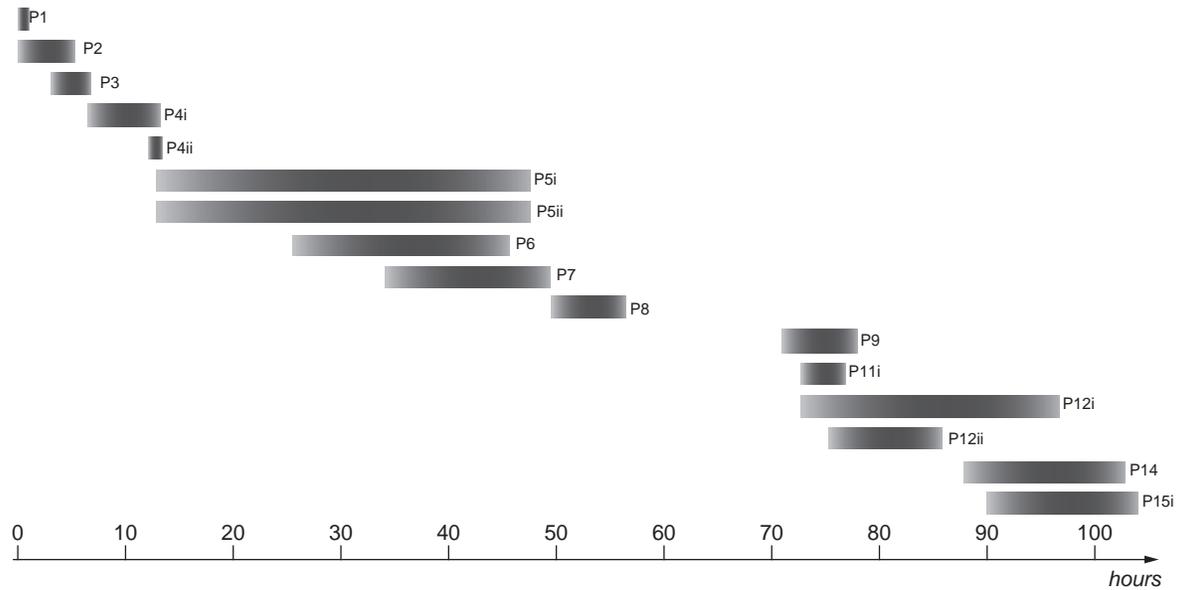
Pupal development

The images on this plate are stills from a time-lapse movie of the pupal development of a wild-type fly from pupariation to adult eclosion (4 days at 25°C). Each image is assigned two values: a “P stage” from Bainbridge and Bownes (1981), and the percentage of completed pupal development.

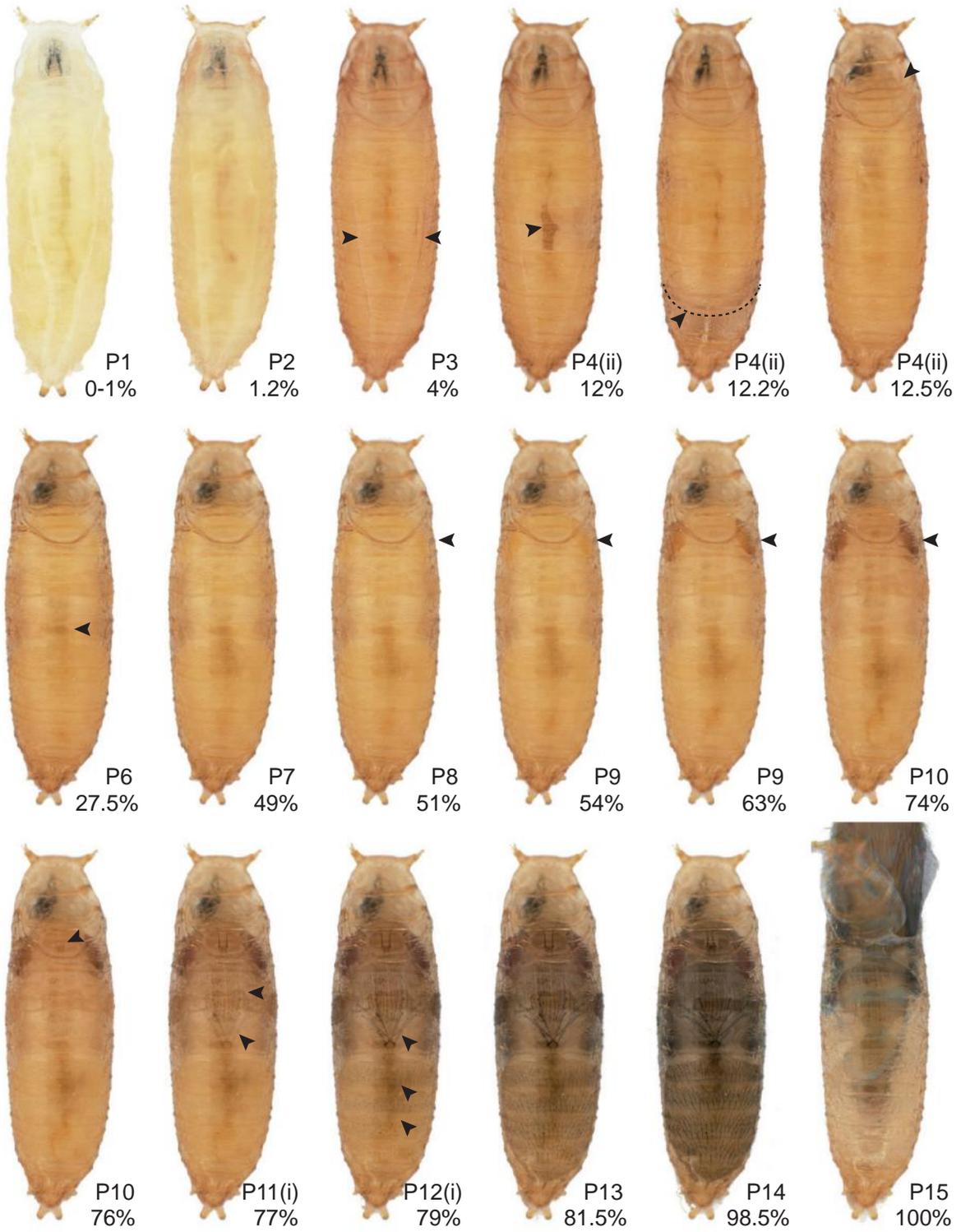
A summary of the stages by Bainbridge and Bownes (1981) is presented below as a diagram. We also show the correspondence between P stages and percentage of completed pupal development.

Note the considerable variation in start, duration, and end for most P stages. In addition, the different characters used for staging are not synchronous between pupae, making it difficult to have an absolute reference of developmental timing.

P1	0–1%	Pupariation	P8	51%	Onset of eye pigmentation
P2	1.2%	White prepupa	P9	54%	Eyes yellow
P3	4%	Dorsal trachea still visible	P9	63%	Eyes darken to amber
P4(i)	12%	Bubble forms	P10	74%	Eyes and ocelli red
P4(ii)	12.2%	Pupation (animal detaches from case)	P10	76%	Head bristles become visible
P4(ii)	12.5%	Head everts	P11(i)	77%	Thorax bristles become visible
P6	27.5%	“Yellow body” appears (arrowhead)	P12(i)	79%	Wings gray
P7	49%	Pharate adult	P13	81.5%	Wings black
			P14	98.5%	Meconium appears
			P15	100%	Eclosion



Bainbridge, S. P., and Bownes, M. (1981). Staging the metamorphosis of *Drosophila melanogaster*. *Journal of embryology and experimental morphology*, 66, 57–80.



Eclosion and virgins

Newly enclosed flies, both males and females, are strikingly pale in appearance. Their pigmentation darkens progressively over the next few hours following emergence.

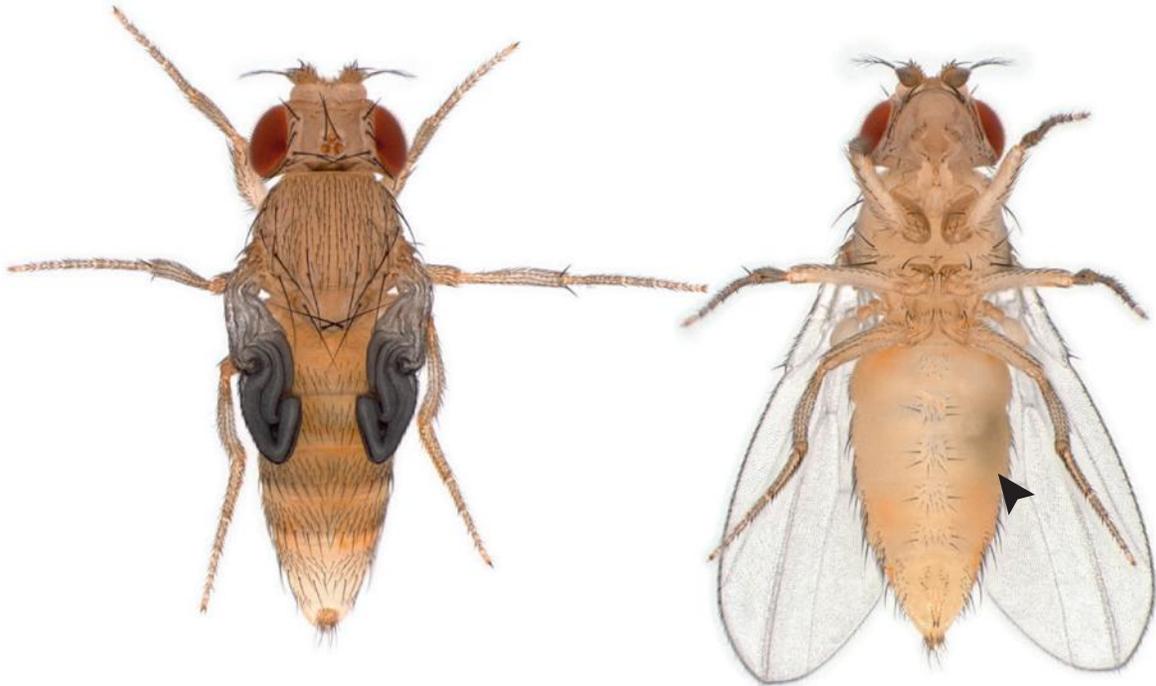
Upon eclosion the fly wings are neatly folded and are gray in wild-type flies.

In the next 30 min, the wings unfold.

For the next 2 h, the wings remain fragile and are held at a slight angle away from the body.

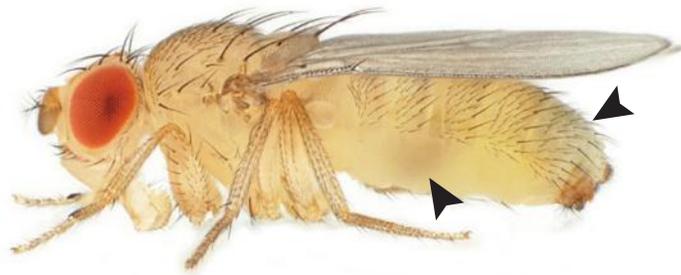
The abdomen becomes distended and a dark spot is visible on its left ventral side (meconium, waste products of pupal metabolism). This spot persists for up to 6 h, although its intensity fades. Females with visible meconium can be assumed to be virgins.

Within a few hours, the cuticle darkens and the pigmentation pattern of abdominal stripes appears.



♀ <math>< 30 \text{ min}</math>

♀ <math>< 2 \text{ h}</math>



♂ <math>< 2 \text{ h}</math>

Bristle markers



Bristle

Bl



Flybase ID: FBgn0000193

Chromosome: 2L

Cytogenetic location: 38B5-9

Recombination map: 2-54.8

Sequence location: N/A

Description

Head and thoracic bristles shorter than normal (half to two thirds of WT), thicker with a blunt end

Hairs unaffected

Allele information

*Bl*¹ shown, homozygous lethal

Temperature dependence

Overlaps WT when reared at temperatures below 20°C

Age dependence

None

Penetrance

100%

Expressivity variation

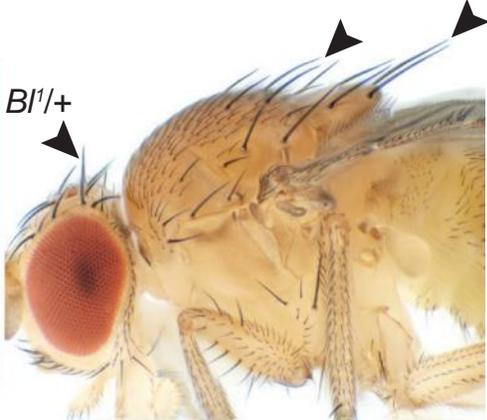
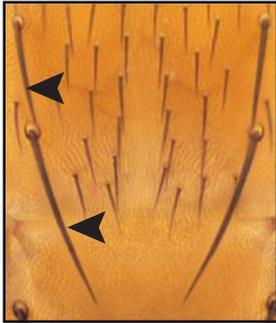
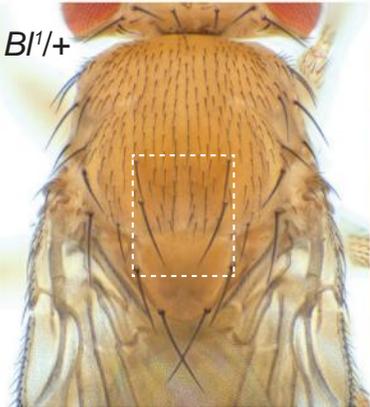
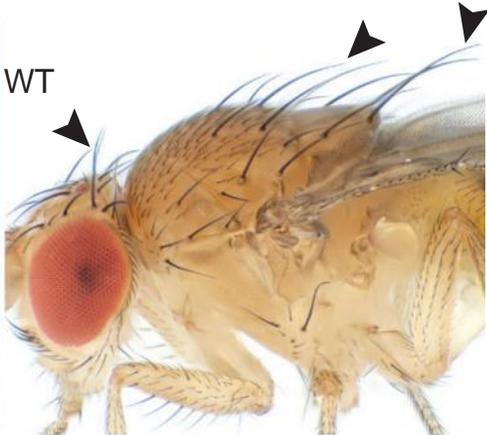
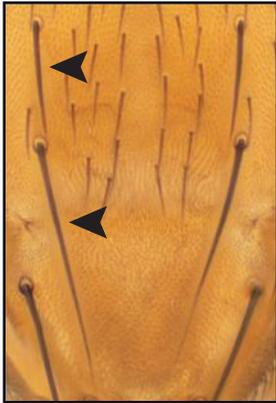
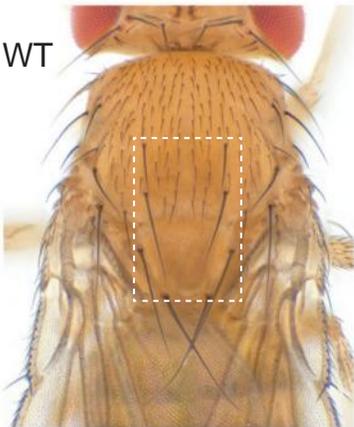
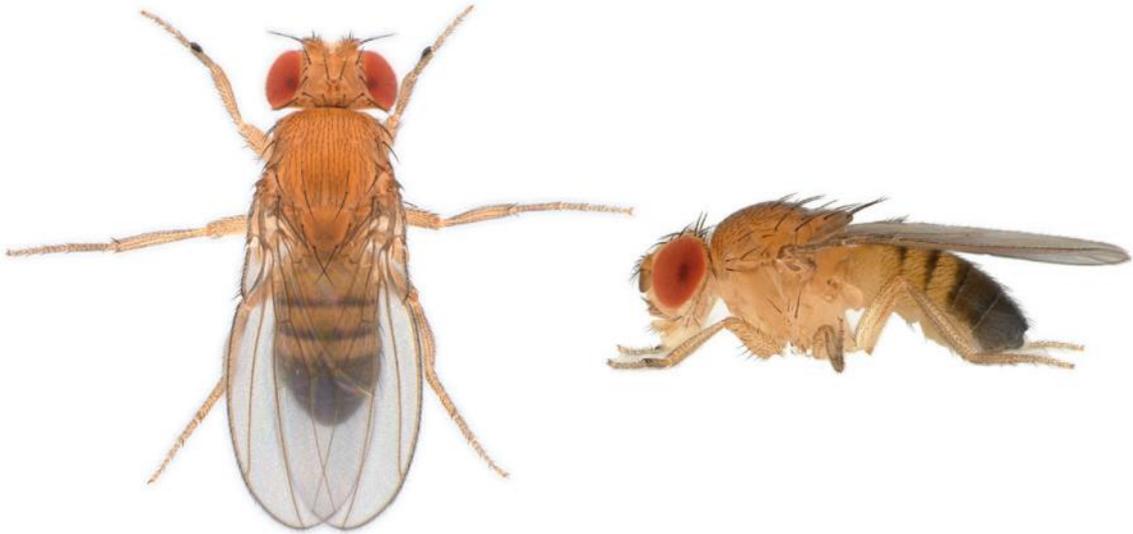


Similarity

WT at low temperatures (<20°C)

Pin: at higher temperatures has even shorter bristles sometimes discolored at their tip (*Pin*^{Yt})

Stubble: has short, stout, and even blunter bristles



diminutive

dm



Flybase ID: FBgn0262656

Chromosome: X

Cytogenetic location: 3D1-3D2

Recombination map: 1-4.0

Sequence location: X:3,267,192..3,285,730 [+]

Description

Head and thoracic bristles very slender

Overall body size reduced

Allele information

*dm*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

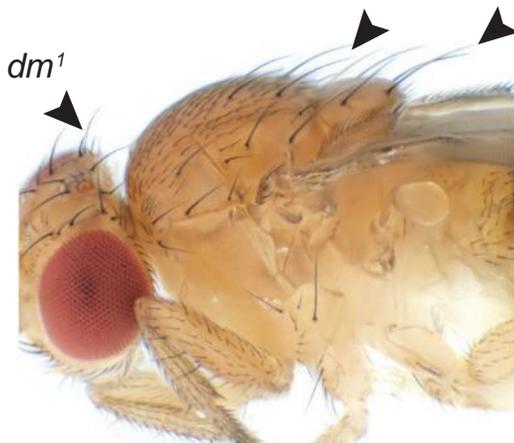
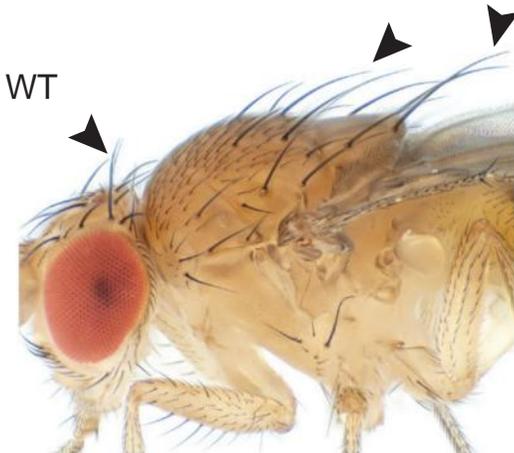
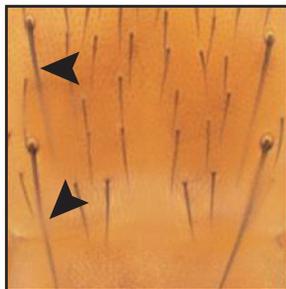
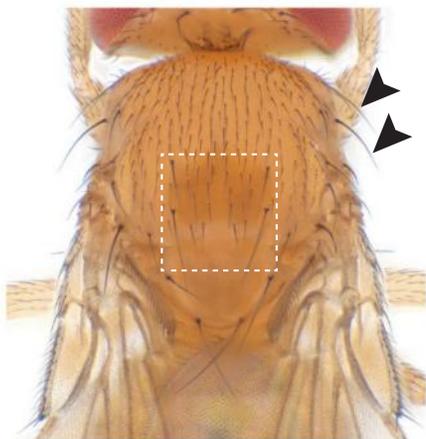
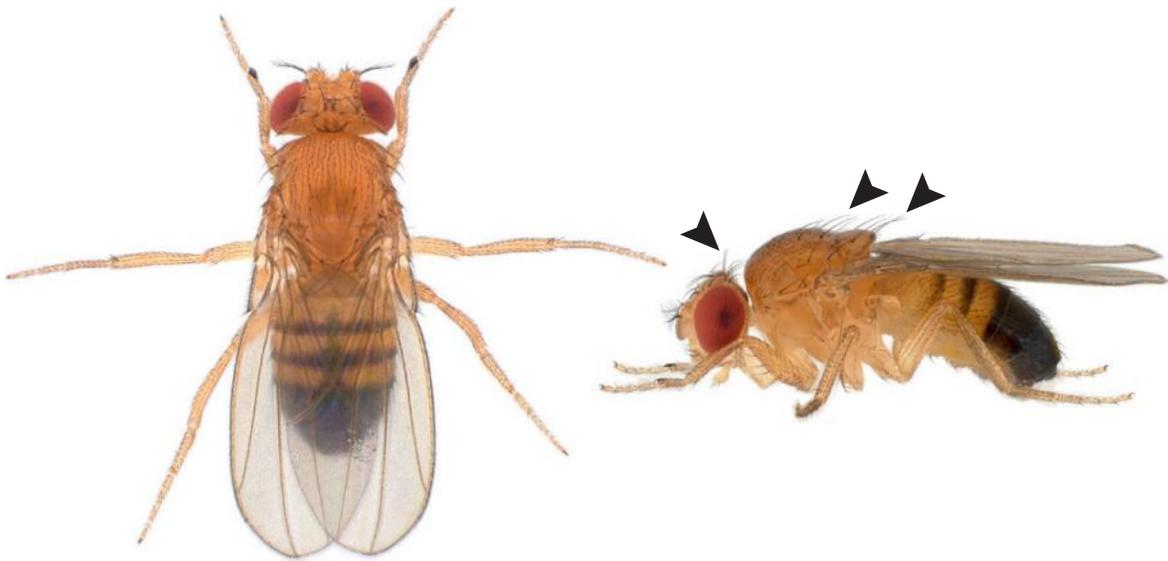
100%

Expressivity variation



Similarity

Minute: bristles similar but body size unaffected



extra macrochaetae

emc



Flybase ID: FBgn0000575

Chromosome: 3L

Cytogenetic location: 61C9

Recombination map: 3-0.0

Sequence location: 3L:749,400...753,492 [+]

Description

Additional thoracic (notum) bristles, most commonly DC, less common are additional PS or SA bristles

Additional thoracic (notum) hairs, usually shorter

Allele information

*emc*¹ recessive marker on TM2

emc^{E6} shown

Temperature dependence

None

Age dependence

None

Penetrance

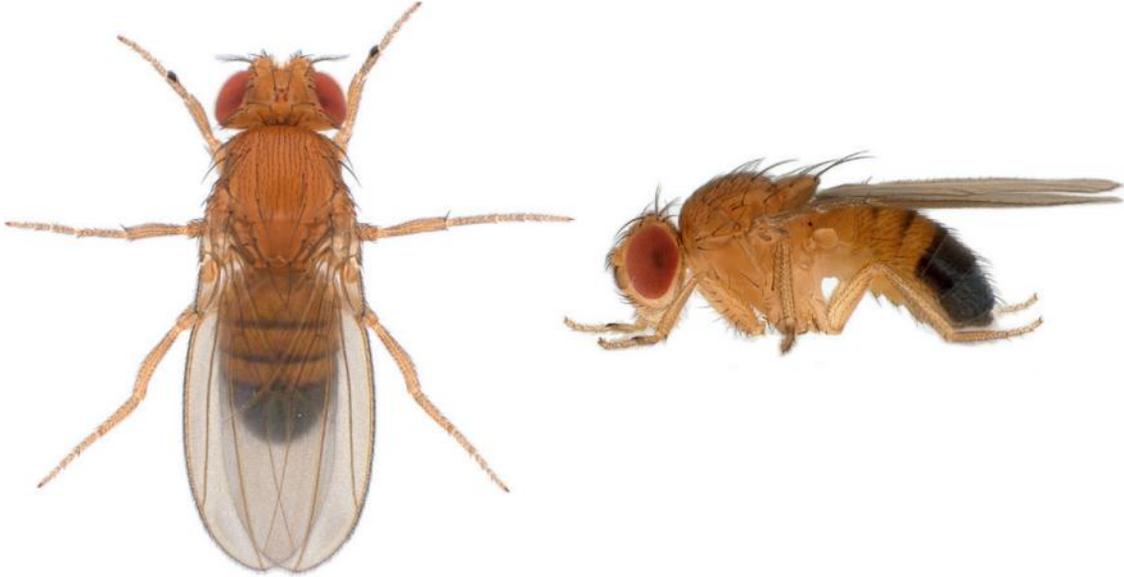
100%

Expressivity variation



Similarity

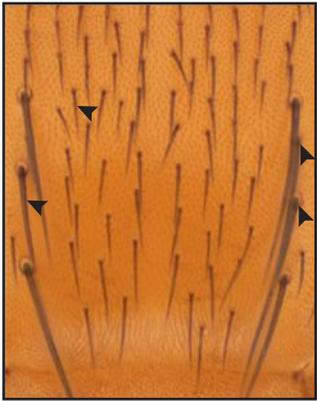
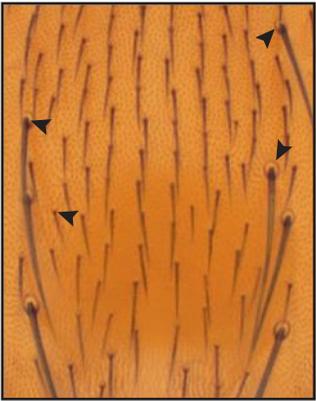
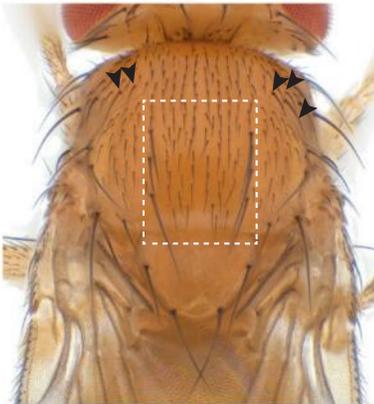
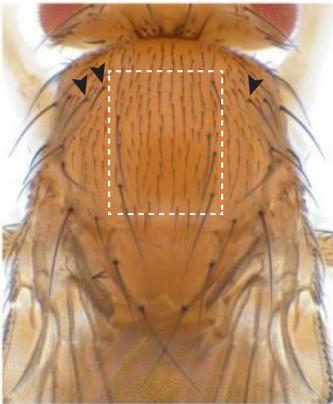
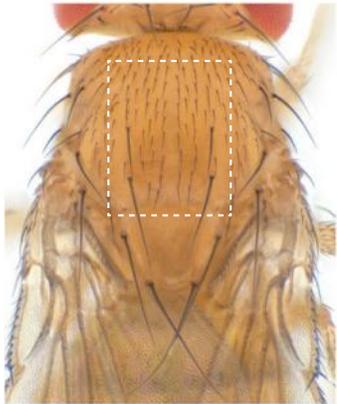
Easy to score



WT

emc^{E6}

emc^{E6}



forked

f



Flybase ID: FBgn0262111

Chromosome: X

Cytogenetic location: 15F4-7

Recombination map: 1-56.7

Sequence location: X:17,126,975..17,174,997 [+]

Description

Some thoracic bristles, mainly SC and ST, kinked, flattened, and branched

Regular row arrangement of thoracic hairs unaffected

Allele information

*f*¹ shown

*f*⁵ detail shown, affects more bristles than *f*¹

Temperature dependence

None

Age dependence

None

Penetrance

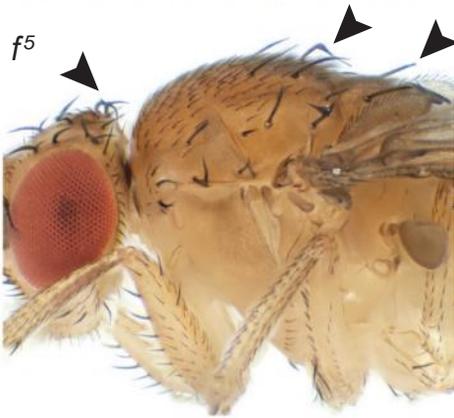
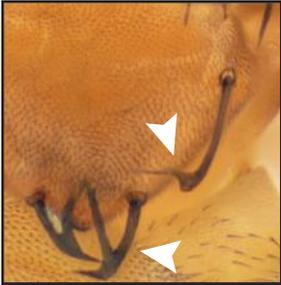
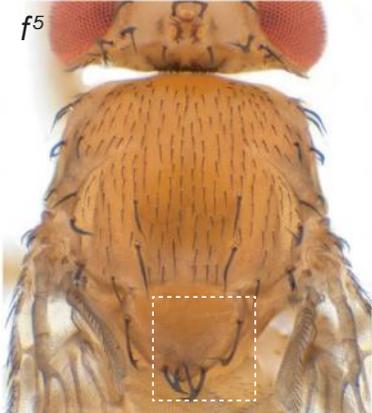
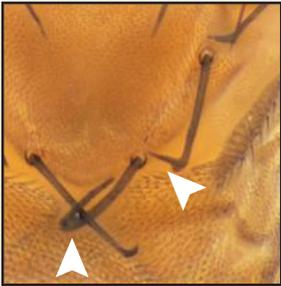
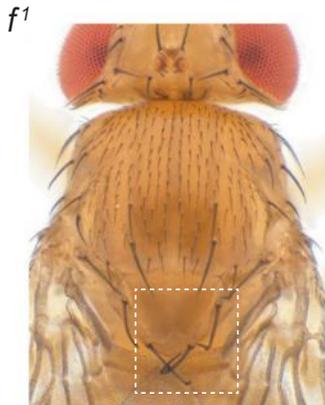
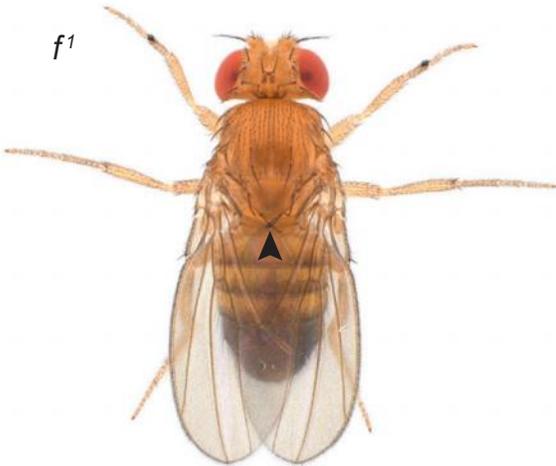
100%

Expressivity variation



Similarity

singed: bristles and hairs extremely deformed, not branched



hairy

h



Flybase ID: FBgn0001168

Chromosome: 3L

Cytogenetic location: 66D10

Recombination map: 3-26.5

Sequence location: 3L:8,668,859..8,672,353 [+]

Description

Numerous ectopic hairs present on head and thorax
Normally hairless scutellum has hairs amid SC bristles
Conspicuous hairs on wing blade and veins

Allele information

*h*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

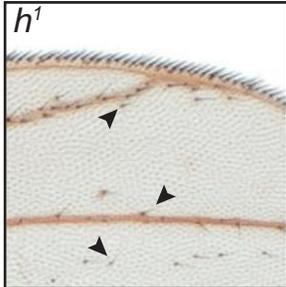
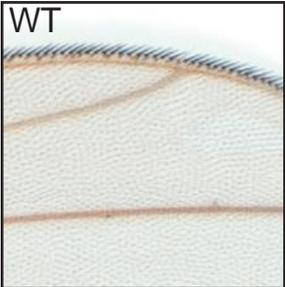
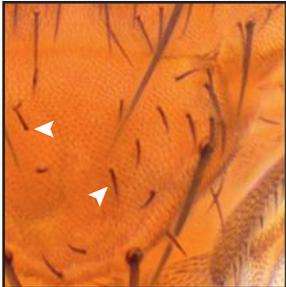
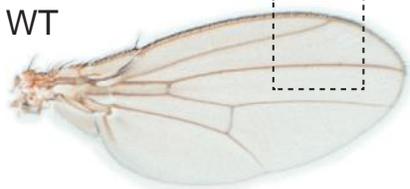
100%

Expressivity variation



Similarity

Easy to score



Humeral

Hu(*Antp*^{*Hu*})



Flybase ID: FBgn0260642

Chromosome: 3R

Cytogenetic location: 84A6-B2

Recombination map: 3-47.5

Sequence location: 3R:2,721,975..2,824,950 [-]

Description

Additional (3–6) HU bristles, some slightly shorter than normal

Allele information

Hu shown, unique allele, dominant marker on TM6B

Temperature dependence

None

Age dependence

None

Penetrance

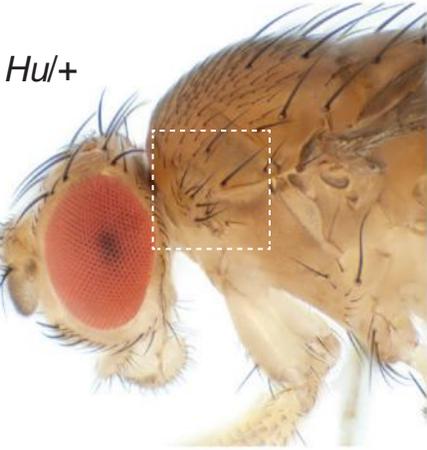
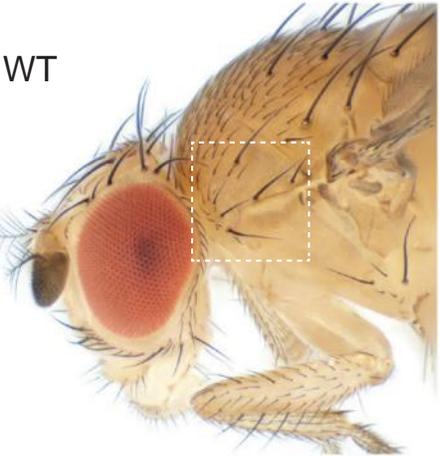
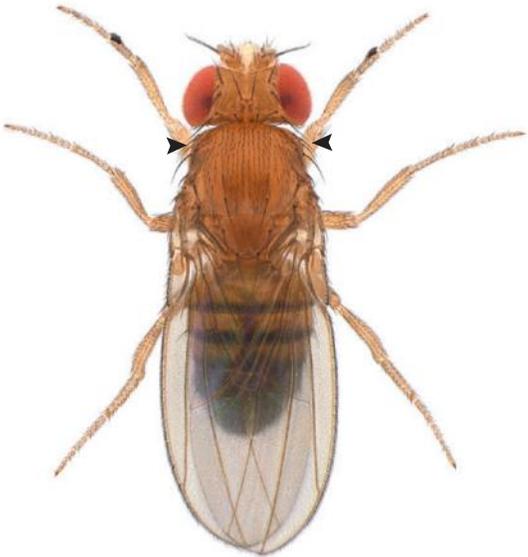
100%

Expressivity variation



Similarity

Easy to score



javelin

ju



Flybase ID: FBgn0263973

Chromosome: 3L

Cytogenetic location: 65A5-B5

Recombination map: 3-19.2

Sequence location: 3L:6,556,297...6,582,579 [-]

Description

Head and thorax bristles and hairs slightly shorter than WT, not tapered

Allele information

*ju*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

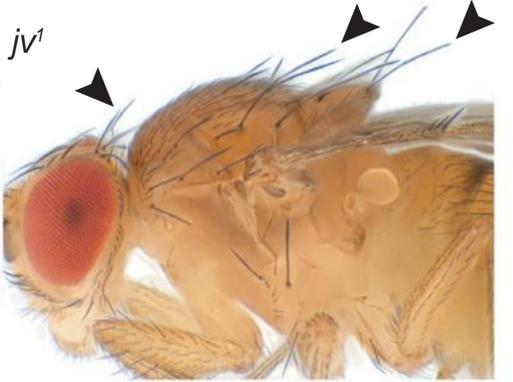
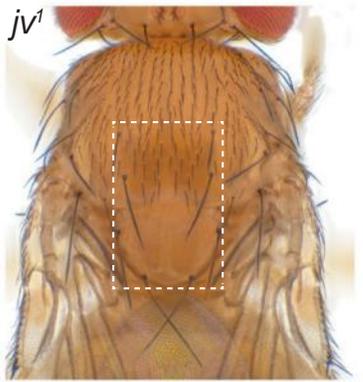
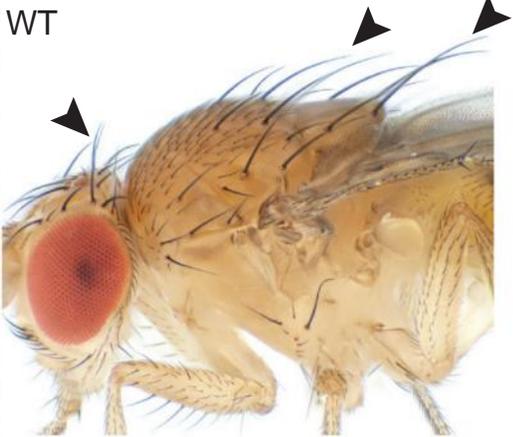
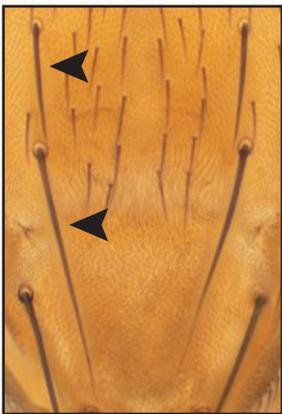
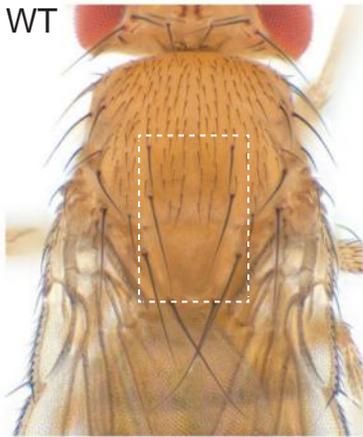
100%

Expressivity variation



Similarity

Easy to score



Minute

M

**Flybase ID:** FBgn0017579 (*RpL14*)**Chromosome:** 3L**Cytogenetic location:** 66D8**Recombination map:** 3-[46]**Sequence location:** 3L:8,594,106..8,595,492 [+]

Description

Bristles, thin and short, particularly on dorsal thorax and head.

Hairs unaffected

Delayed development

Minute is a unique case: it refers strictly to a phenotype, not to the mutation of a single gene. This phenotype of reduced bristles is produced by mutants of various ribosomal protein genes

Allele information

*RpL14*¹ shown, strong allele, recessive lethal*M(3)76A* very weak allele, marker on MKR and MKRS balancers, phenotype hardly visible

Temperature dependence

Overlaps WT when reared at temperatures below 20°C

Age dependence

None

Penetrance

*RpL14*¹: 100%

Expressivity variation

*RpL14*¹:  *M(3)76A*: 

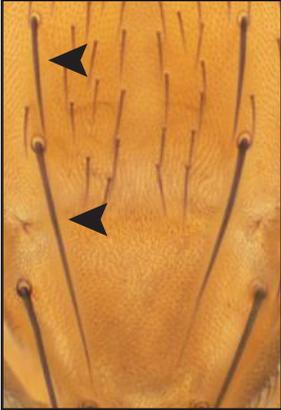
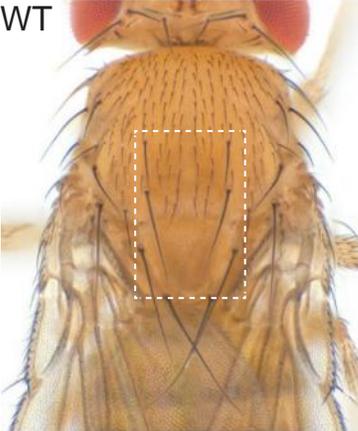
Similarity

Weak alleles overlap WT and are difficult to score

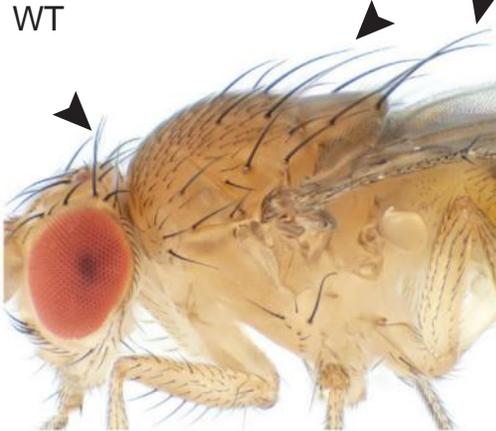
diminutive: bristles similar but body smaller in size*spineless*: thicker bristles, particularly pSC



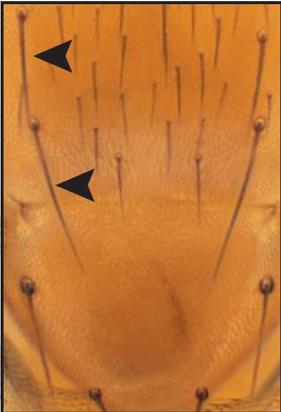
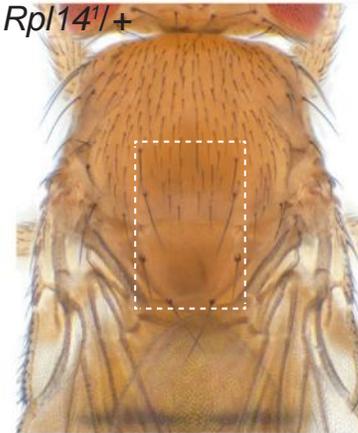
WT



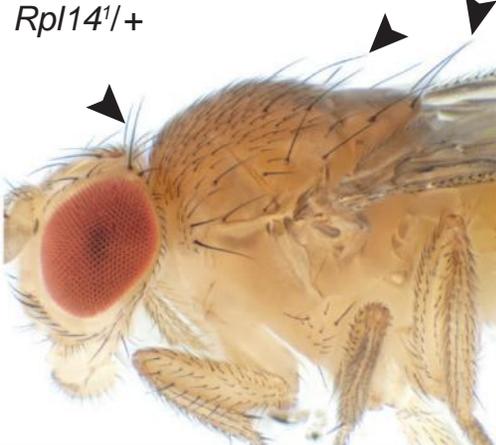
WT



Rpl14^{1/+}



Rpl14^{1/+}



Pin

Pin



Flybase ID: FBgn0003088

Chromosome: 2R

Cytogenetic location: 60C6-D1

Recombination map: 2-107.3

Sequence location: N/A

Description

Head and thorax bristles much shorter than WT, straight and erect

Allele information

*Pin*¹ shown

Pin^{Yt} bristles have yellowish tips, lethal in combination with any *Pin* allele

Temperature dependence

None

Age dependence

None

Penetrance

100%

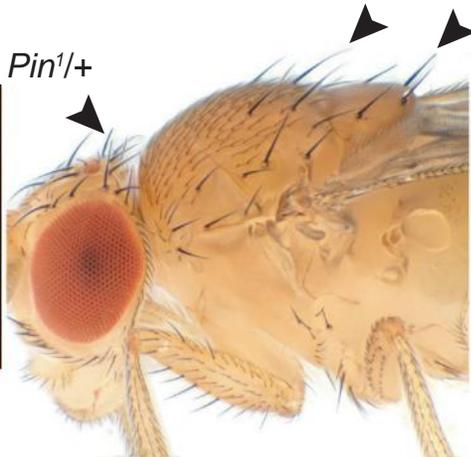
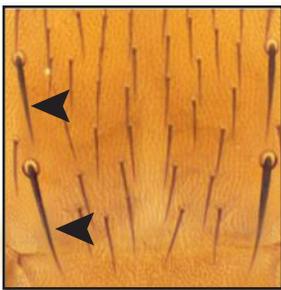
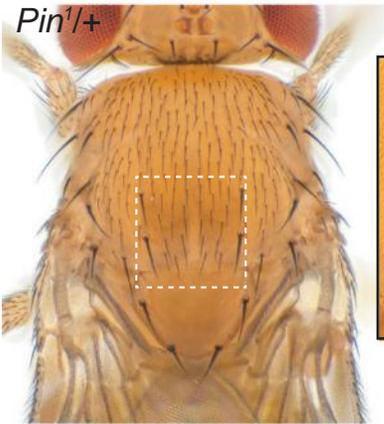
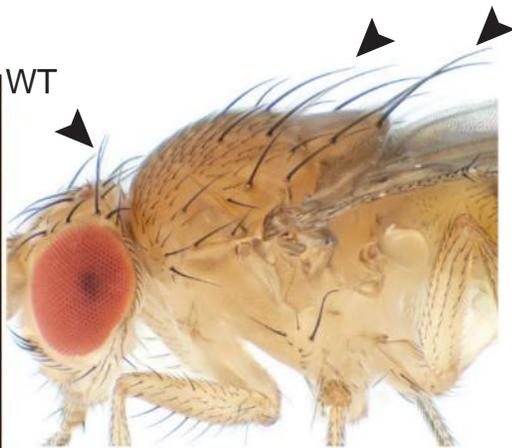
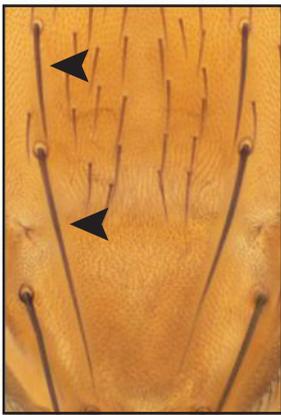
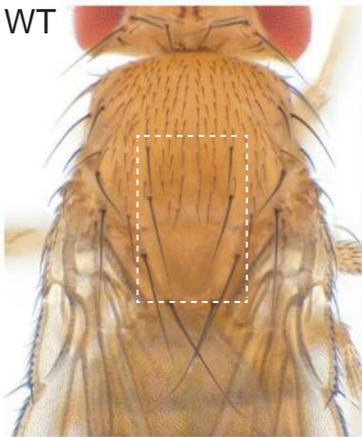
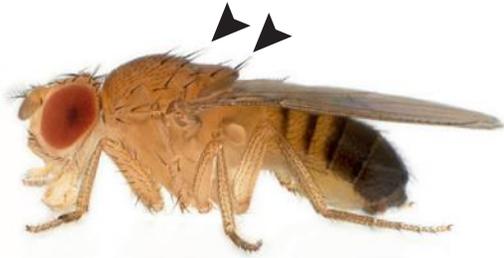
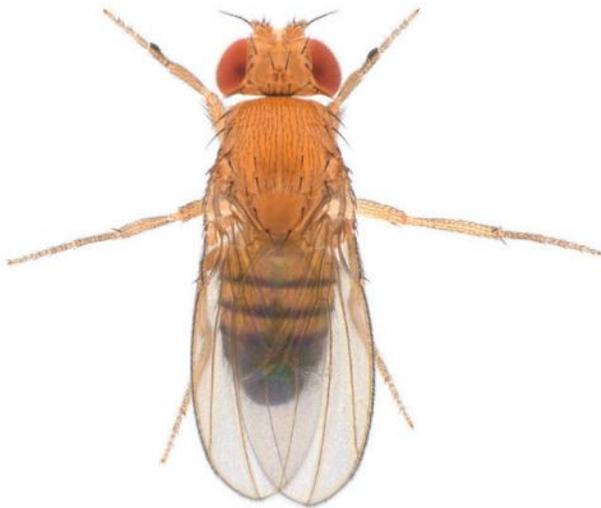
Expressivity variation



Similarity

spineless: bristles even shorter, usually curved; only pSC are erect

Bristle: bristles longer, thicker, and with a blunt end



scute

SC



Flybase ID: FBgn0004170
Chromosome: X
Cytogenetic location: 1A8
Recombination map: 1-0.0
Sequence location: X:290,093..291,530 [+]

Description

Loss of bristles, or reduction in number, in particular SC

Allele information

*sc*¹ shown

*sc*⁸ recessive marker on FM6, FM7a, FM7c, FM7d, and FM7i

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation



Similarity

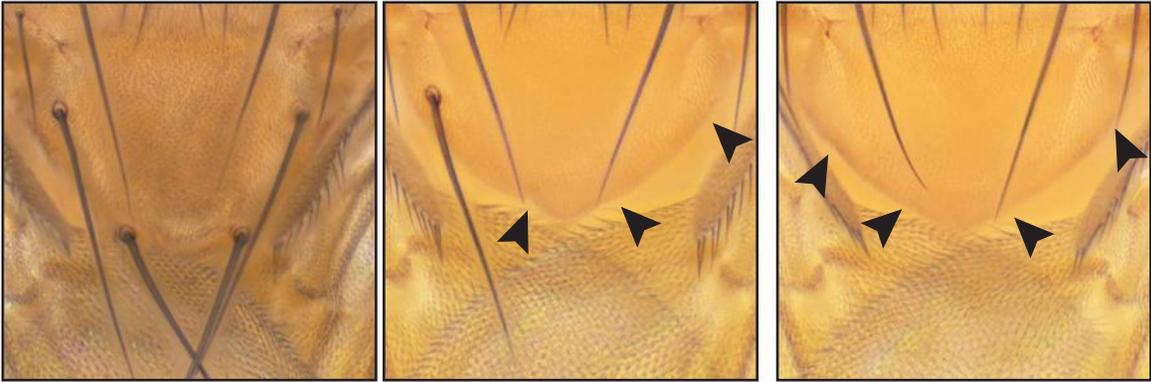
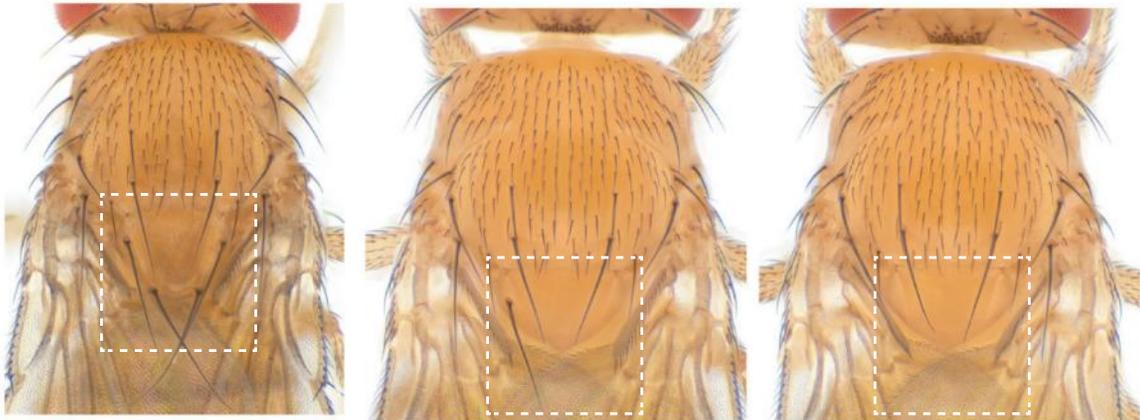
Scutoid: dominant marker



WT

*sc*¹

*sc*¹



Scutoid

Sco(sna^{Sco})



Flybase ID: FBgn0003448

Chromosome: 2L

Cytogenetic location: 35D2

Recombination map: 2-51.0

Sequence location: 2L:15,476,593..15,478,269 [-]

Description

Many thoracic bristles missing, most commonly SC, NP, HU, and PA

Allele information

Sco shown, unique allele

Temperature dependence

None

Age dependence

None

Penetrance

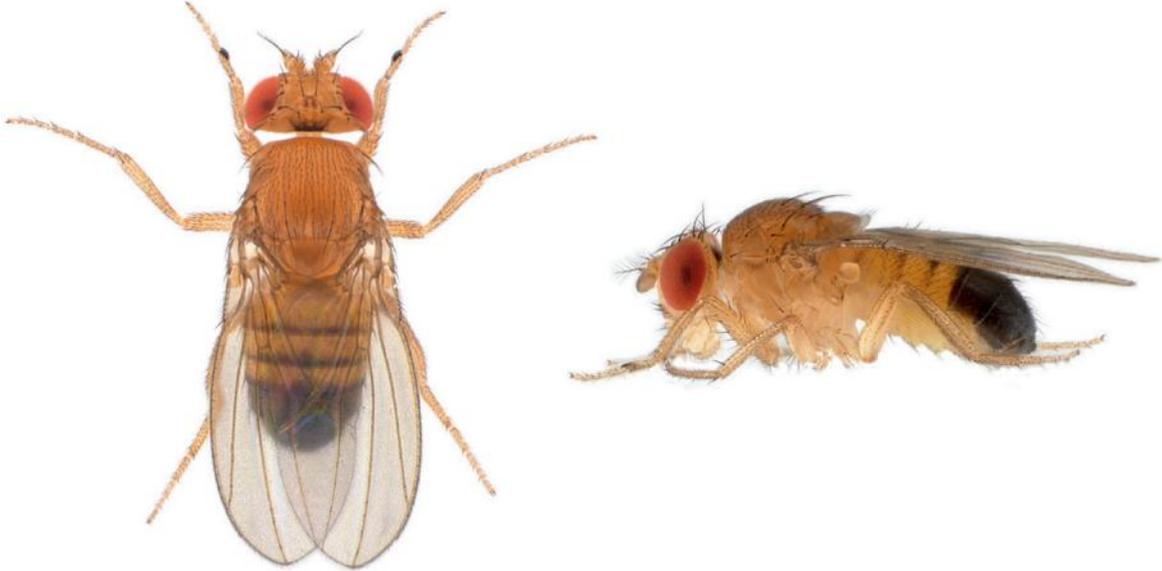
100%

Expressivity variation



Similarity

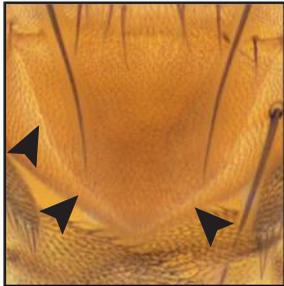
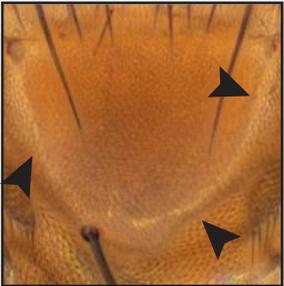
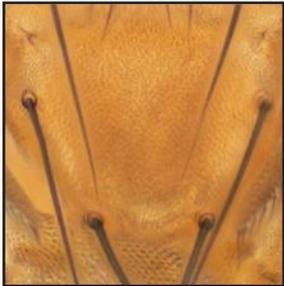
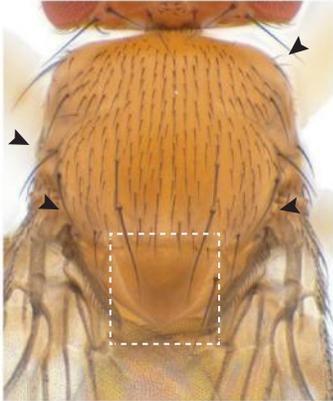
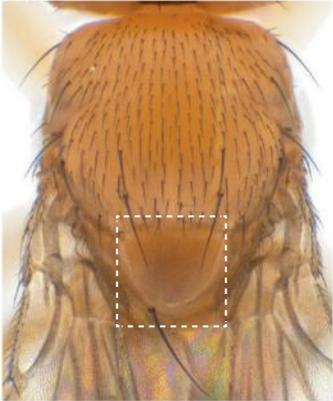
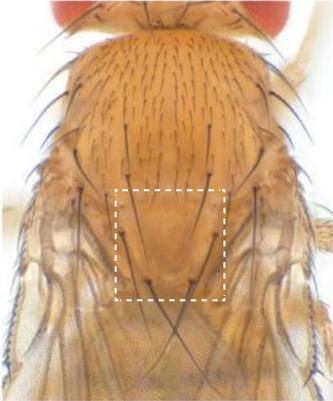
scute: recessive marker



WT

Sco/+

Sco/+



singed

sn



Flybase ID: FBgn0003447

Chromosome: X

Cytogenetic location: 7D1-2

Recombination map: 1-21.0

Sequence location: X:7,858,057..7,880,118 [+]

Description

Bristles flattened with one or more kinks, adhere to the body

Hairs less affected, mostly bent

Homozygous females sterile

Allele information

*sn*³ shown

sn^{X2} recessive marker on FM7c

Temperature dependence

None

Age dependence

None

Penetrance

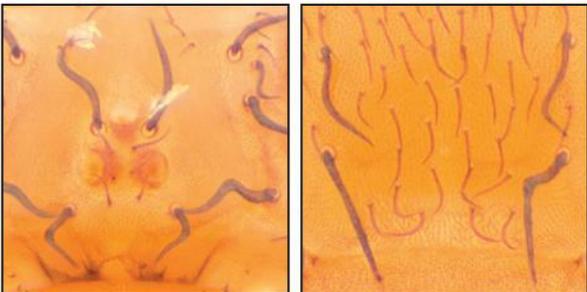
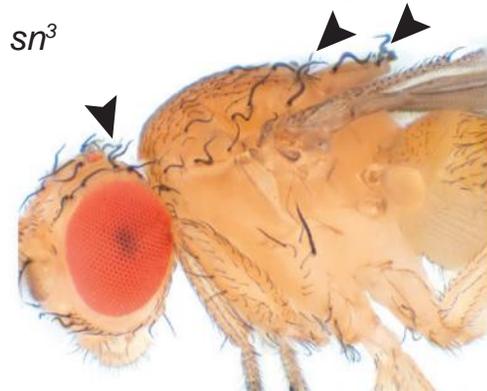
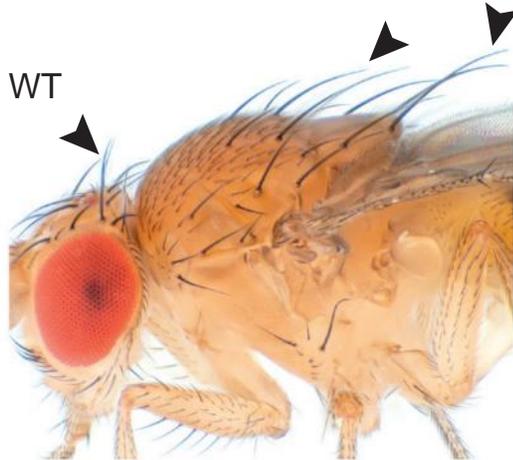
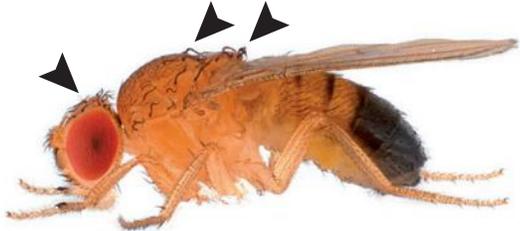
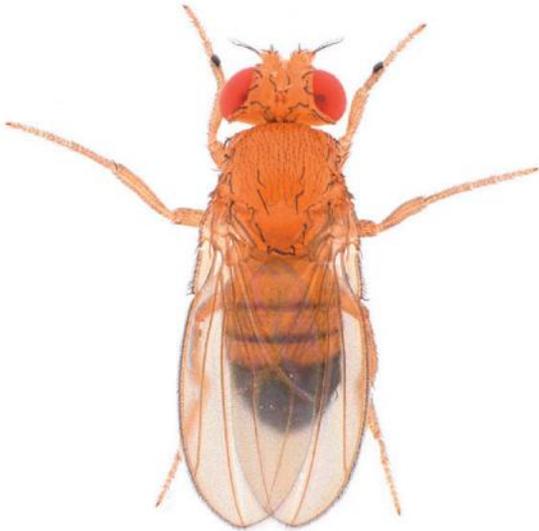
100%

Expressivity variation



Similarity

forked: bristles branched at the tip, hairs unaffected



Sternopleural

Sp(wg^{Sp-1})



Flybase ID: FBgn0004009

Chromosome: 2L

Cytogenetic location: 27F1

Recombination map: 2-21.9

Sequence location: 2L:7,307,161..7,316,265 [+]

Description

Extra bristles and hairs on the sternopleurite

Allele information

Sp shown, unique allele, homozygous lethal

Temperature dependence

WT at 18°C, overlaps WT at 25°C, requires 28–30°C to fully express

Age dependence

None

Penetrance

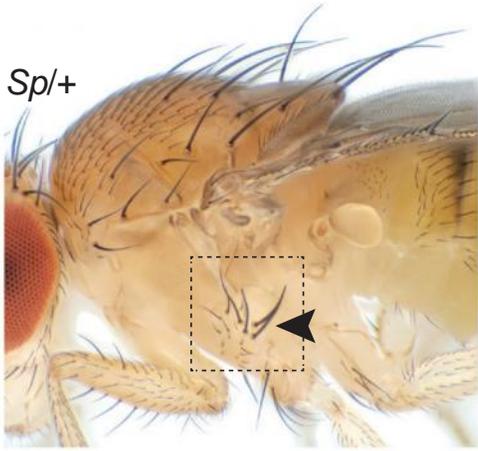
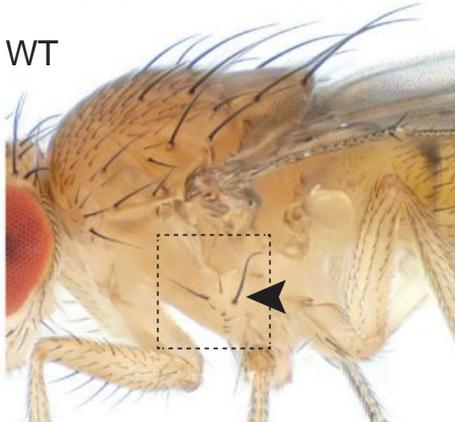
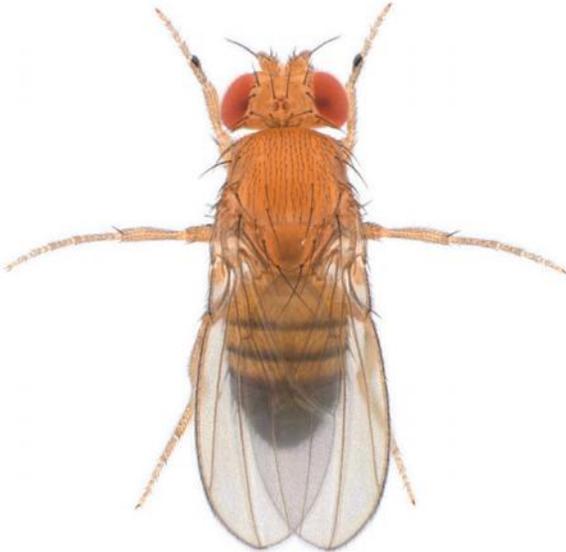
100%

Expressivity variation



Similarity

Easy to score



spineless

SS



Flybase ID: FBgn0003513

Chromosome: 3R

Cytogenetic location: 89B14-15

Recombination map: 3-58.5

Sequence location: 3R:12,200,148..12,229,412 [-]

Description

Head and thorax bristles shortened, some only slightly longer than hairs

SC strongly affected, erect; pDC least affected

Allele information

*ss*¹ shown

ss^{aP88} recessive marker on TM6

Temperature dependence

None

Age dependence

None

Penetrance

100%

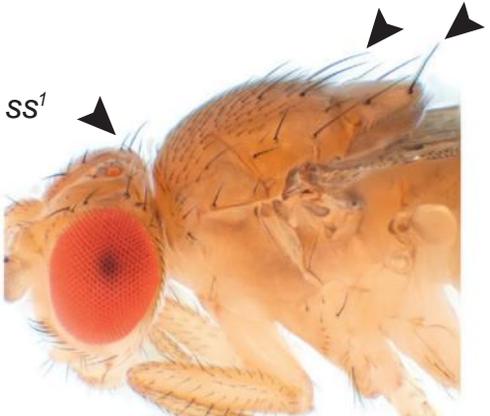
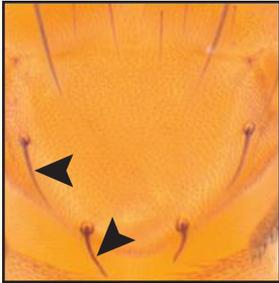
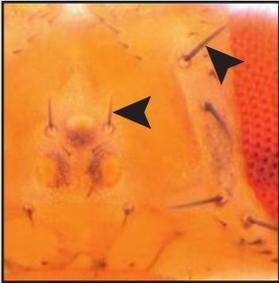
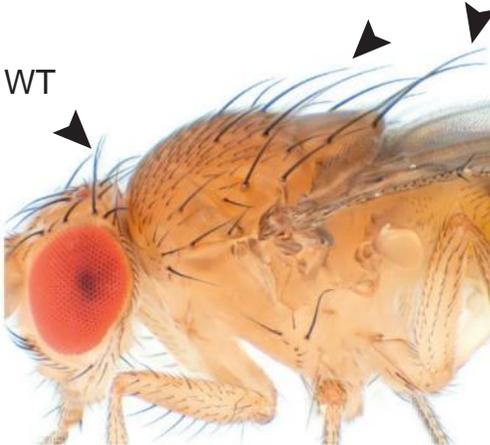
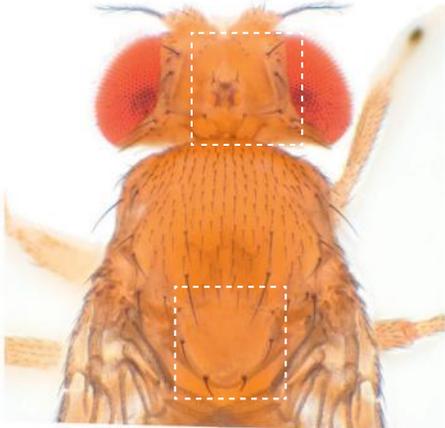
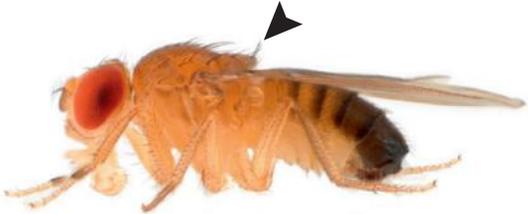
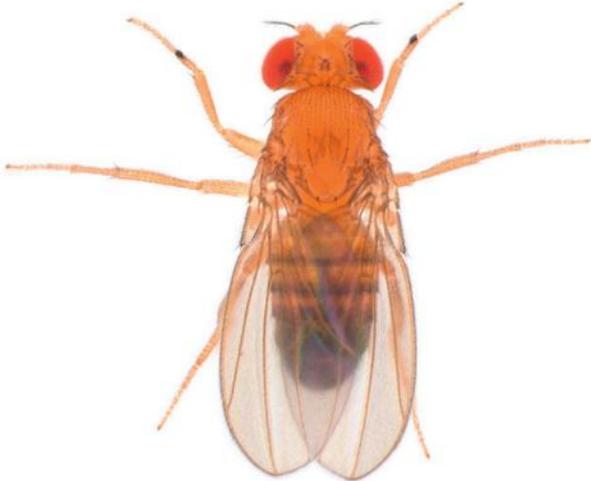
Expressivity variation



Similarity

Pin: at higher temperatures has even shorter bristles sometimes discolored at their tip (*Pin*^{Y^t})

Minute: pSC longer



Stubble

Sb



Flybase ID: FBgn0003319

Chromosome: 3R

Cytogenetic location: 89B4-6

Recombination map: 3-58.2

Sequence location: 3R:11,954,451..11,971,006 [+]

Description

Bristles stout and short, some no more than half the normal size
Hairs unaffected

Allele information

*Sb*¹ shown, dominant marker on some variants of TM3 and TM6B
Sb^{*sbd-1*} recessive marker on TM1

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation

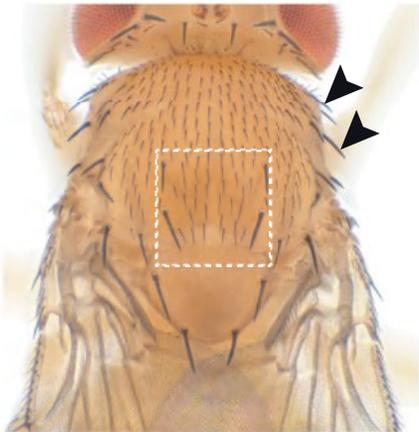
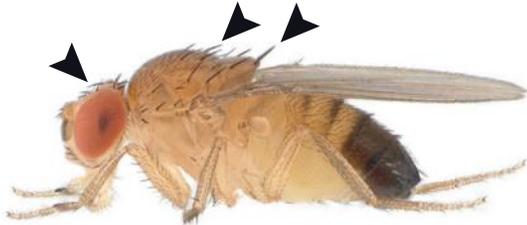


Similarity

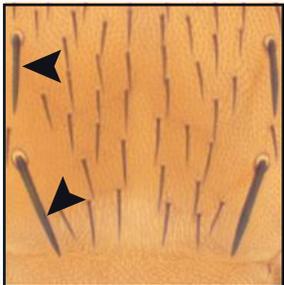
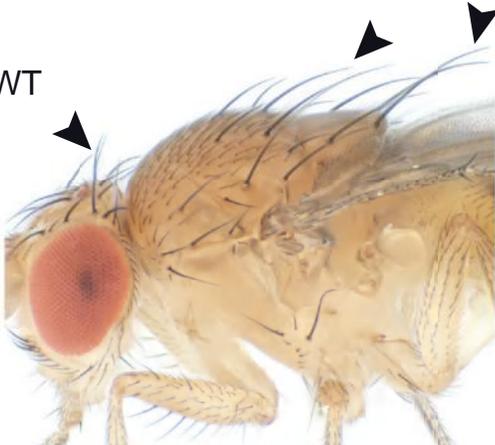
Easy to score



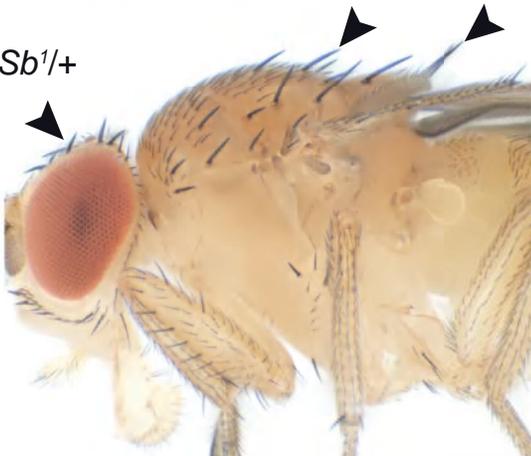
Sb^{1/+}



WT



Sb^{1/+}

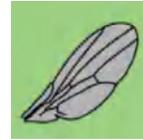


Wing markers



cubitus interruptus

ci



Flybase ID: FBgn0004859

Chromosome: 4

Cytogenetic location: 102A1-3

Recombination map: 4-0.0

Sequence location: 4:68,336..77,667 [-]

Description

L4 vein shows gaps which are more common distal to the posterior cross-vein

L5 vein thinning toward the wing edge

Allele information

ci¹ shown

ci^D details shown

Temperature dependence

ci¹: vein pattern more disrupted at 18°C

Age dependence

None

Penetrance

100%

Expressivity variation

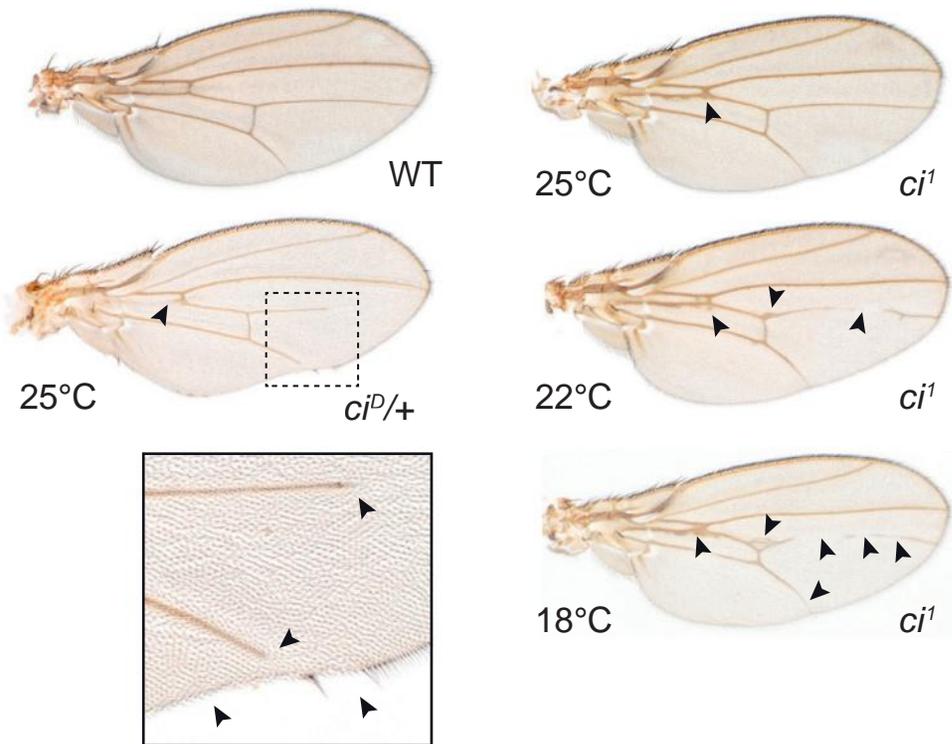
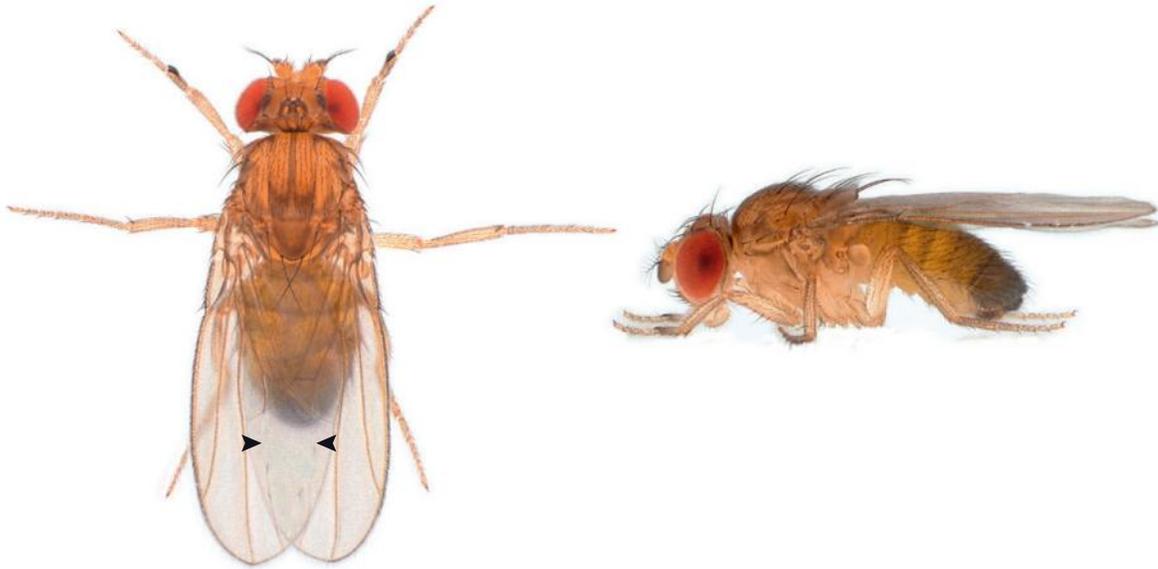


Similarity

ci¹ easy to score at lower temperatures, WT above 25°C

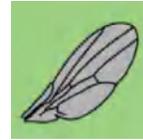
radius incompletus: only L2 vein interrupted

veinlet: most veins incomplete



cut

ct



Flybase ID: FBgn0004198

Chromosome: X

Cytogenetic location: 7B4-6

Recombination map: 1-20.0

Sequence location: X:7,503,181..7,572,892 [+]

Description

Wings smaller and narrower, wing margins severely disrupted

Anterior wing margin has missing bristles

Vein pattern normal but L4 and L5 appear shorter due to notches in ventral wing margin

Allele information

*ct*⁶ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

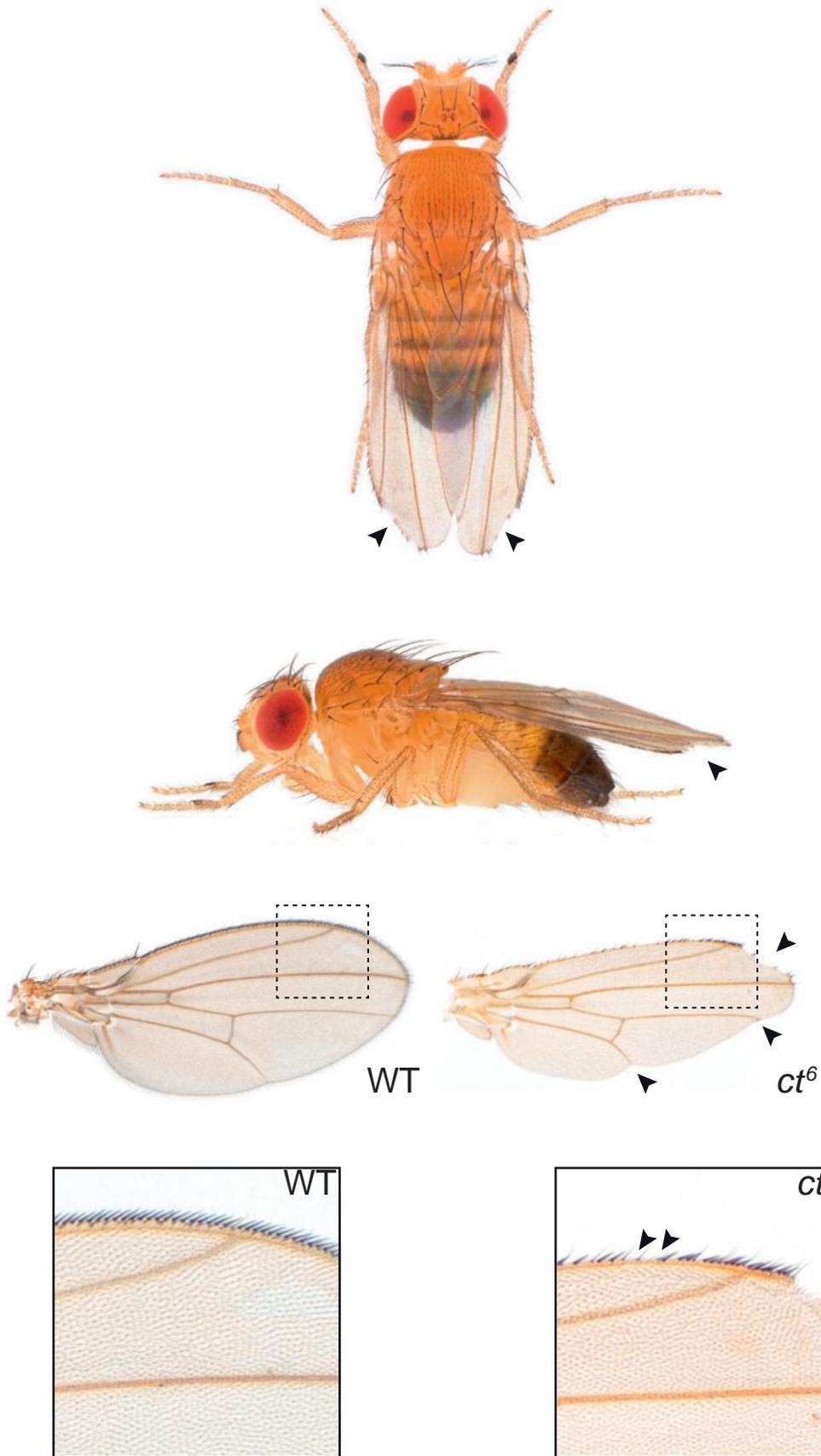
Expressivity variation



Similarity

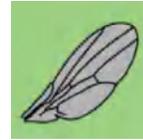
Notch: wings larger with thickened veins

Serrate: wings larger with severe notching shortening L4 vein



curled

cu



Flybase ID: FBgn0261808

Chromosome: 3R

Cytogenetic location: 86D7

Recombination map: 3-50.0

Sequence location: 3R:7,026,138..7,034,357 [+]

Description

Wings bowing away from the body upward but parallel to the body axis

pSC erect and crossed

Allele information

*cu*¹ shown

Temperature dependence

Overlaps WT at 18°C

Note: the darker pigmentation at 18°C may be due to other mutations expressed at this temperature in this stock

Age dependence

None

Penetrance

100%

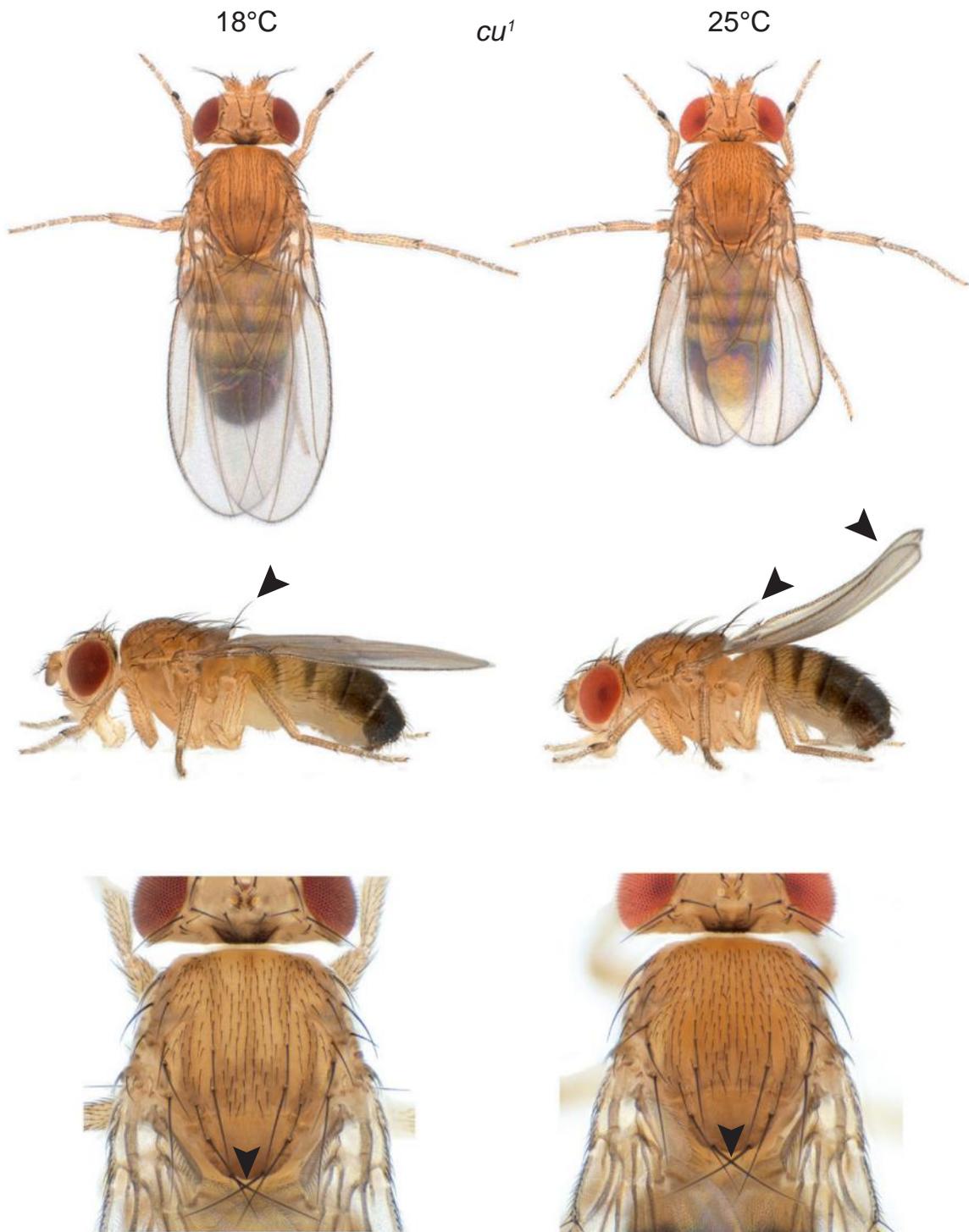
Expressivity variation



Similarity

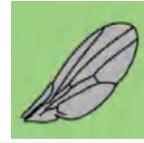
Curly: dominant marker, *Cy*/+ wings markedly more up-turned and extended away from the body axis; temperature-dependent

WT at 18°C



Curly

Cy



Flybase ID: FBgn000403

Chromosome: 2L

Cytogenetic location: 23A4-23B2

Recombination map: 2-6.1

Sequence location: N/A

Description

Wings curled upward and outward

Allele information

Cy¹ shown, dominant marker on CyO, SM1, SM5, SM6a, SM6b, and T(2;3)CyO-TM9

Temperature dependence

Overlaps WT at 18°C, expressivity increases with temperature

Age dependence

None

Penetrance

100%

Expressivity variation



Similarity

curled: recessive marker, wings less up-turned and parallel to body axis

WT below 20°C

Cy¹/+



25°C



25°C



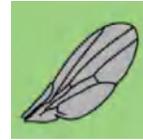
22°C



18°C

Dichaete

D



Flybase ID: FBgn0000411

Chromosome: 3L

Cytogenetic location: 70D3

Recombination map: 3-40.7

Sequence location: 3L:14,168,710..14,171,720 [-]

Description

Wings held at 45° angle in relation to the body axis

Missing allulae

Missing some bristles, in particular DC

Allele information

*D*¹ shown, homozygous lethal

*D*³ less extreme than *D*¹ and not affected by temperature, present on some variants of TM6B

Temperature dependence

*D*¹ overlaps WT at 18°C

Age dependence

None

Penetrance

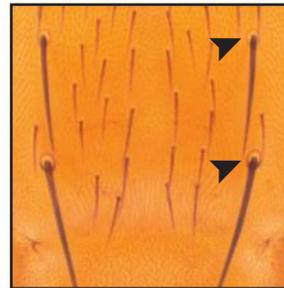
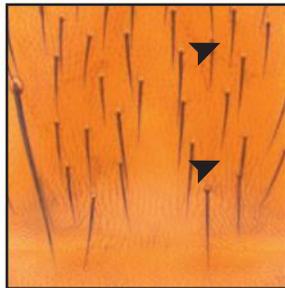
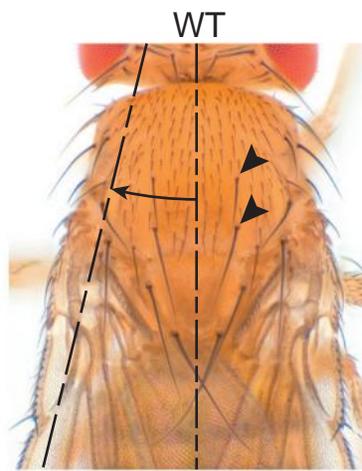
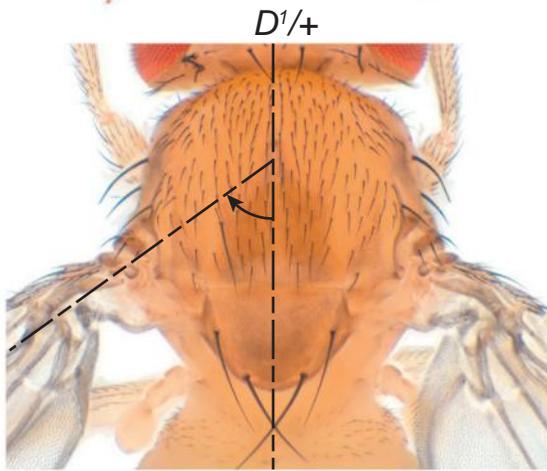
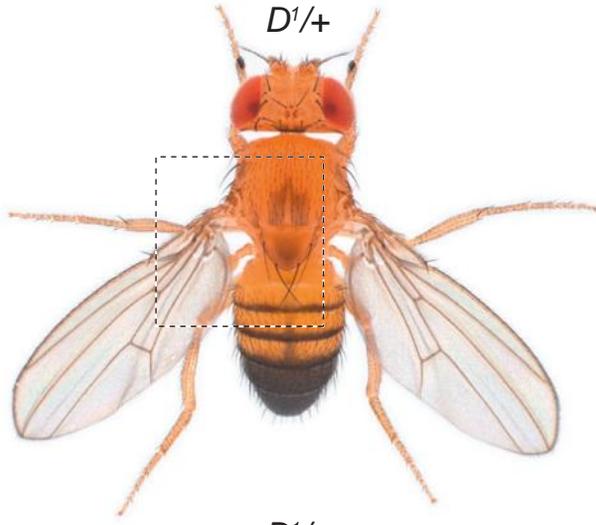
100%

Expressivity variation

*D*¹:  *D*³: 

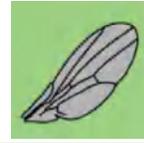
Similarity

Easy to score



dumpy

dp



Flybase ID: FBgn0053196

Chromosome: 2L

Cytogenetic location: 24F4-25A1

Recombination map: 2-13.0

Sequence location: 2L:4,477,462..4,595,054 [-]

Description

Wings much shorter and truncated distally

Wings notched in the distal area but bristle pattern unaffected

L3 vein has a kink distally toward L5 vein

DC bristles pointing toward medial groove in thorax (vortex phenotype)

Allele information

dp^{ov1} shown

dp^{lv1} recessive lethal marker in CyO and SM6 balancers

Temperature dependence

Vortex phenotype on thorax generally seen at elevated temperatures (29°C), which further reduces the wing size

Age dependence

None

Penetrance

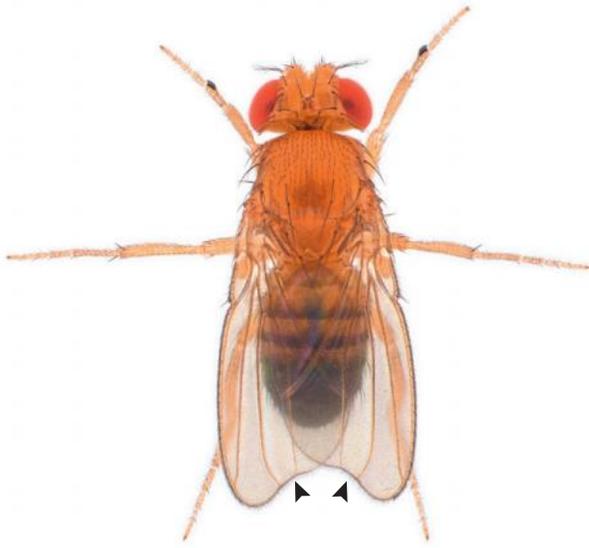
100%

Expressivity variation



Similarity

Easy to score



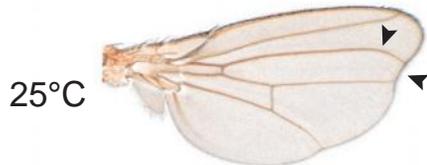
25°C



29°C



WT



25°C



29°C

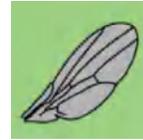
dp^{ov1}



29°C

Lyra

Ly



Flybase ID: FBgn0002573

Chromosome: 3L

Cytogenetic location: 70A8

Recombination map: 3-40.5

Sequence location: 3L:13,389,328..13,394,225 [-]

Description

Dorsal and lateral wing margins missing

Wings have characteristic narrow rectangular appearance

Allele information

*Ly*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

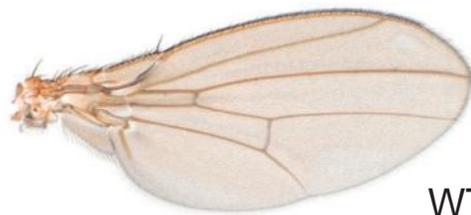
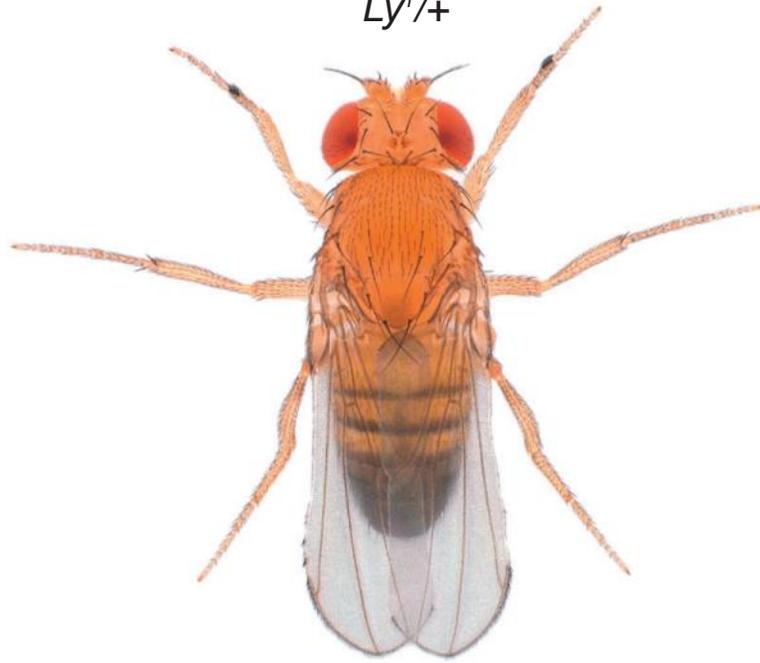
Expressivity variation



Similarity

Easy to score

*Ly*¹/+



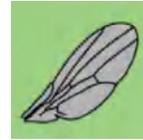
WT



*Ly*¹/+

miniature

m



Flybase ID: FBgn0002577

Chromosome: X

Cytogenetic location: 10E1-2

Recombination map: 1-36.2

Sequence location: X:11,648,306..11,663,541 [+]

Description

Wings scaled down to about two-thirds of the WT wing size

Wings darker and opaque

Allele information

*m*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

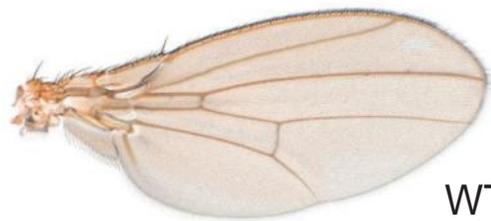
100%

Expressivity variation



Similarity

Easy to score



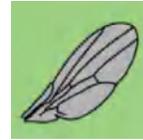
WT



m^1

Notch

N



Flybase ID: FBgn0004647

Chromosome: X

Cytogenetic location: 3C7-9

Recombination map: 1-3.0

Sequence location: X:3,028,905..3,066,295 [+]

Description

Wings have incisions of variable pattern and extent

Parts of wing margin may be missing

L3 and L5 veins thickened

Allele information

N^{nd-1} shown

Temperature dependence

Weak phenotype at low temperature: at 18°C thickened veins only, notches require 25°C

Age dependence

None

Penetrance

100%

Expressivity variation

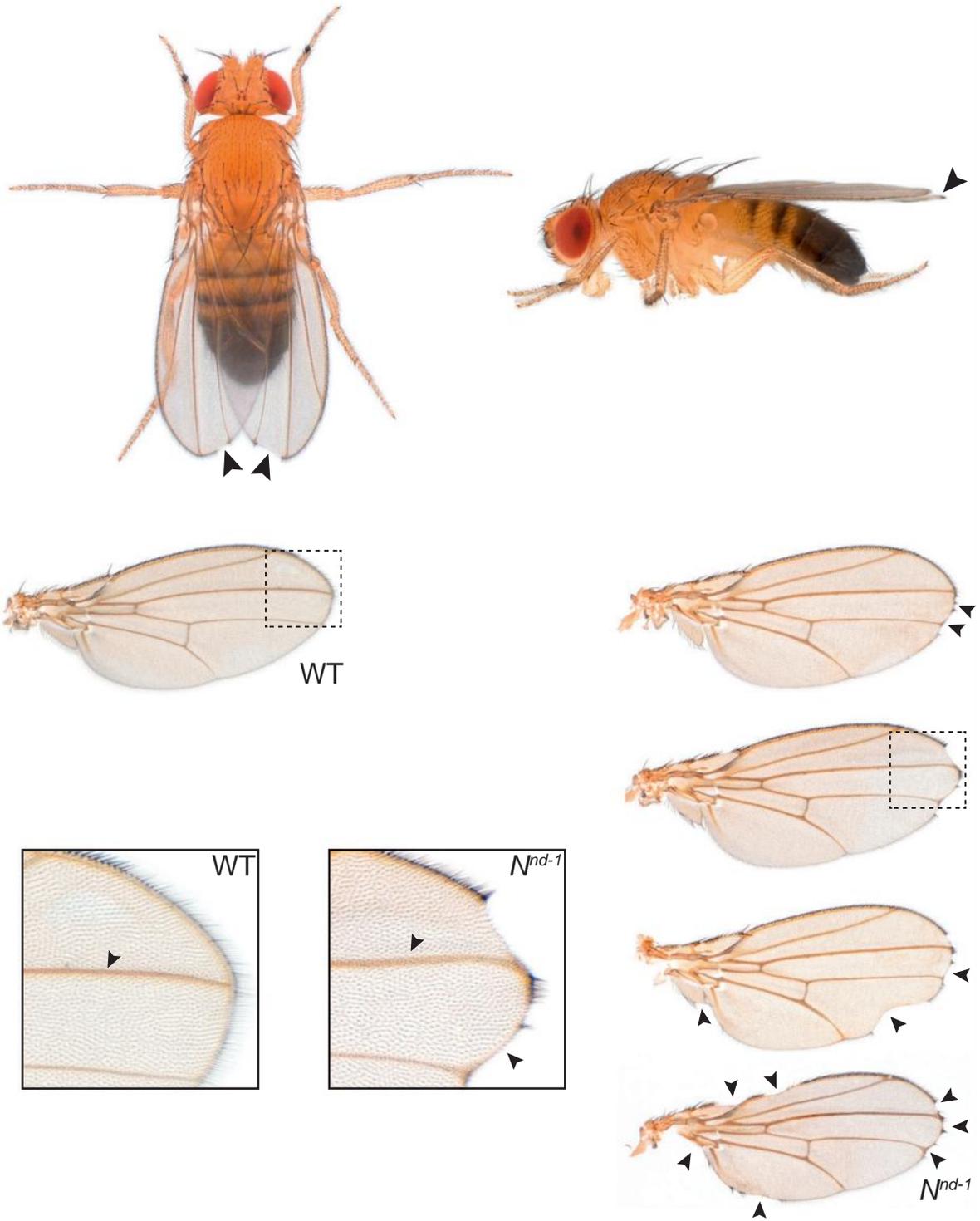


variable at all temperatures

Similarity

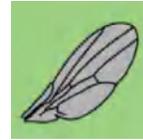
cut: wings much smaller in size, shortened veins (L5 in particular)

Serrate: severe notch shortening L4 vein



radius incompletus

ri(kni^{ri-1})



Flybase ID: FBgn0001320

Chromosome: 3L

Cytogenetic location: 77E3

Recombination map: 3-47

Sequence location: 3L:20,685,430..20,688,463 [-]

Description

L2 vein ends abruptly and its distal part is missing

Allele information

ri¹ shown, a recessive marker on TM3

Temperature dependence

None

Age dependence

None

Penetrance

100%

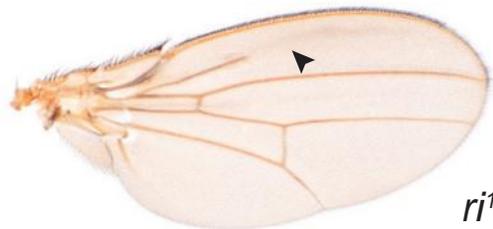
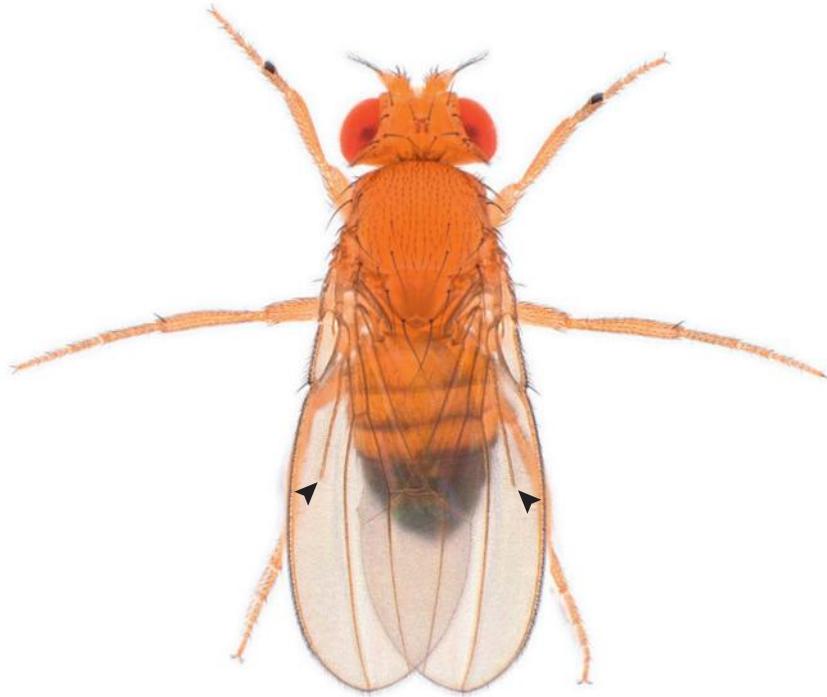
Expressivity variation



Similarity

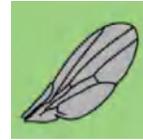
cubitus interruptus: L4 vein affected

veinlet: most veins incomplete



Serrate

Ser



Flybase ID: FBgn0004197

Chromosome: 3R

Cytogenetic location: 97E6-8

Recombination map: 3-92.5

Sequence location: 3R:22,997,818..23,019,716 [-]

Description

Wings with multiple notches

The most severe notch shortens the L4 vein, reducing the size of the second posterior cell; smaller notches on either side of L3 vein affecting submarginal cell and first posterior cell

Reduced allula

Homozygous viable

Allele information

*Ser*¹ shown, common dominant marker of TM3 (along with *Sb*¹)

Temperature dependence

None

Age dependence

None

Penetrance

Often \ll 100%, extremely variable with genetic background

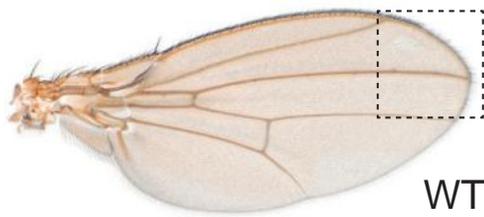
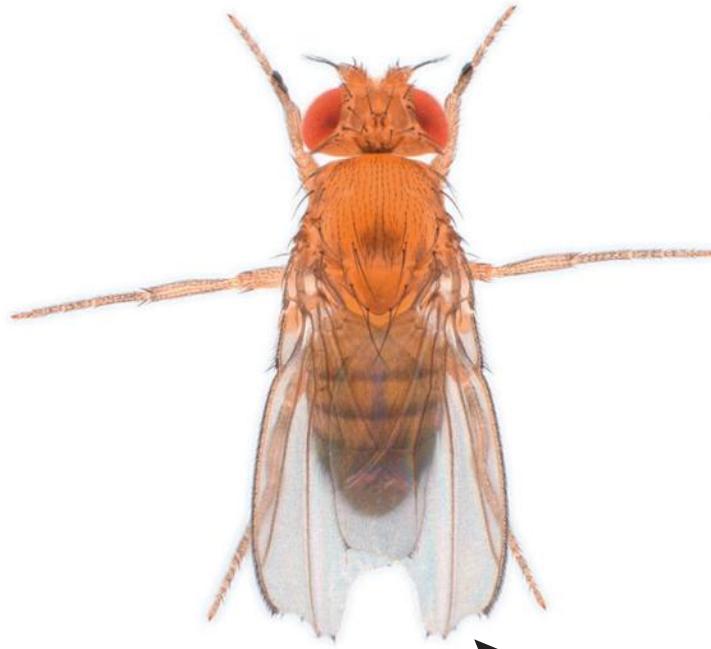
Expressivity variation



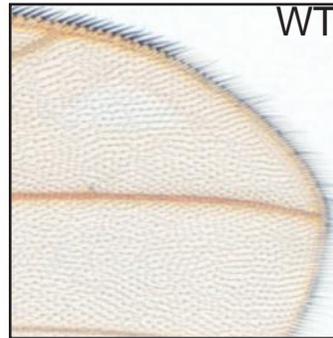
Similarity

cut: smaller size wings, with small notches

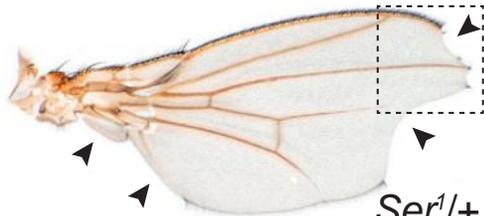
Notch: similar size wings but small notches



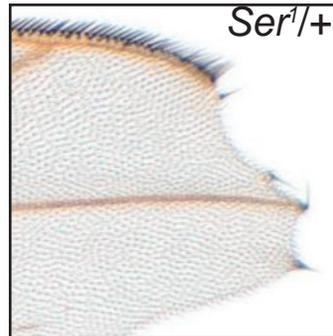
WT



WT



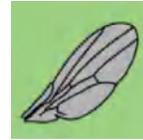
Ser^{1/+}



Ser^{1/+}

veinlet

ve(rho^{ve-1})



Flybase ID: FBgn0004635

Chromosome: 3L

Cytogenetic location: 62A2

Recombination map: 3-0.2

Sequence location: 3L:1,463,811..1,468,944 [+]

Description

Wing veins incomplete: disrupted or ending abruptly

L2 has a gap at its tip while L3–L5 do not reach the wing margin

Cross-veins unaffected

Allele information

*ve*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

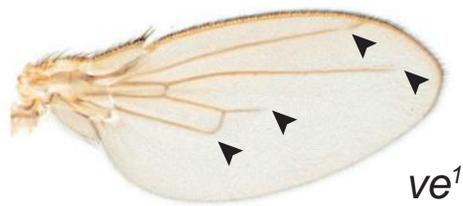
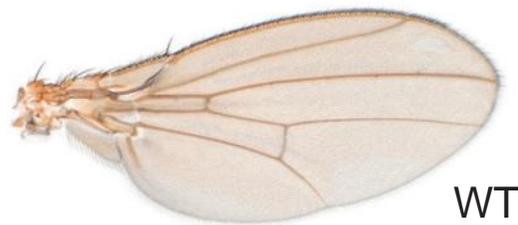
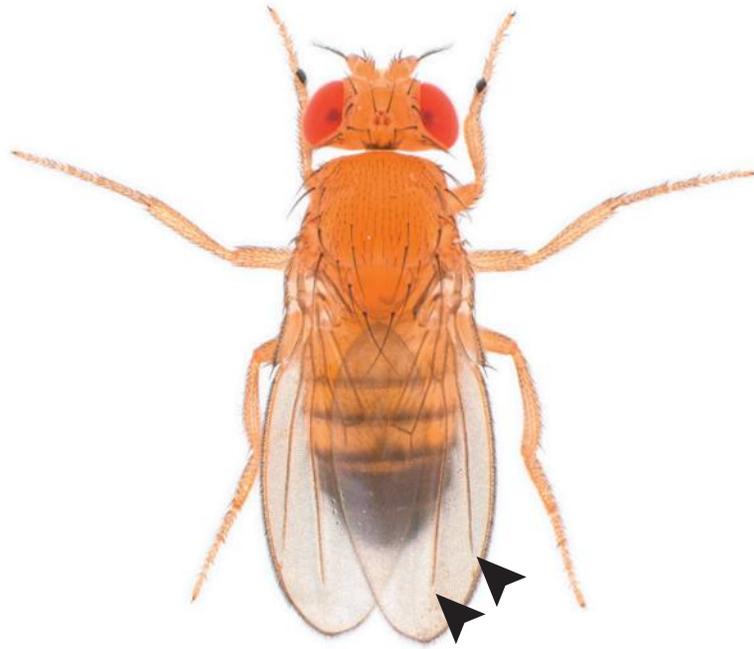
Expressivity variation



Similarity

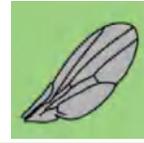
radius incompletus: only affects L2

cubitus interruptus: affects cross-veins and L4 vein



vestigial

vg



Flybase ID: FBgn0003975

Chromosome: 2R

Cytogenetic location: 49E1

Recombination map: 2-67.0

Sequence location: 2R:8,771,706..8,786,899 [+]

Description

Wings and halteres atrophied, vein pattern on residual wing similar to WT

pSC erect and crossed

Allele information

*vg*¹ shown

Temperature dependence

Wing size decreases with temperature; a highly modifiable phenotype

Age dependence

None

Penetrance

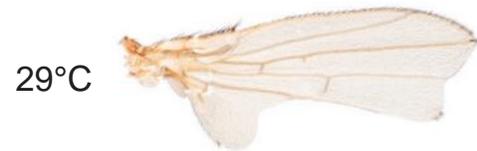
100%

Expressivity variation

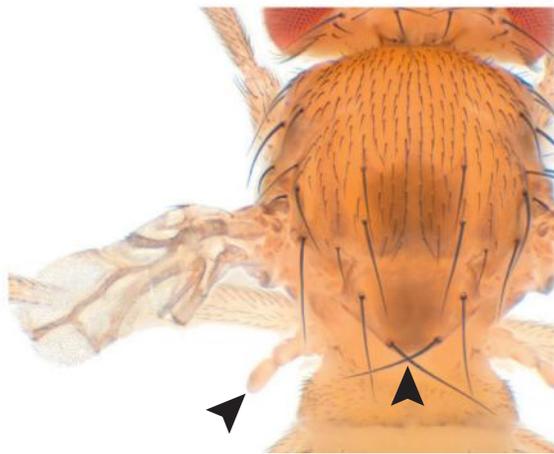


Similarity

Easy to score

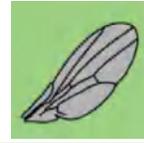


*vg*¹



wingless

wg



Flybase ID: FBgn0004009

Chromosome: 2L

Cytogenetic location: 27F1

Recombination map: 2-21.9

Sequence location: 2L:7,307,161..7,316,265 [+]

Description

One or occasionally both wings missing and transformed into thoracic tissue; thorax enlarged, with a double-hump appearance in lateral view

Compound eyes slightly smaller than WT, with a posterior-ventral dimple

Allele information

wg¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

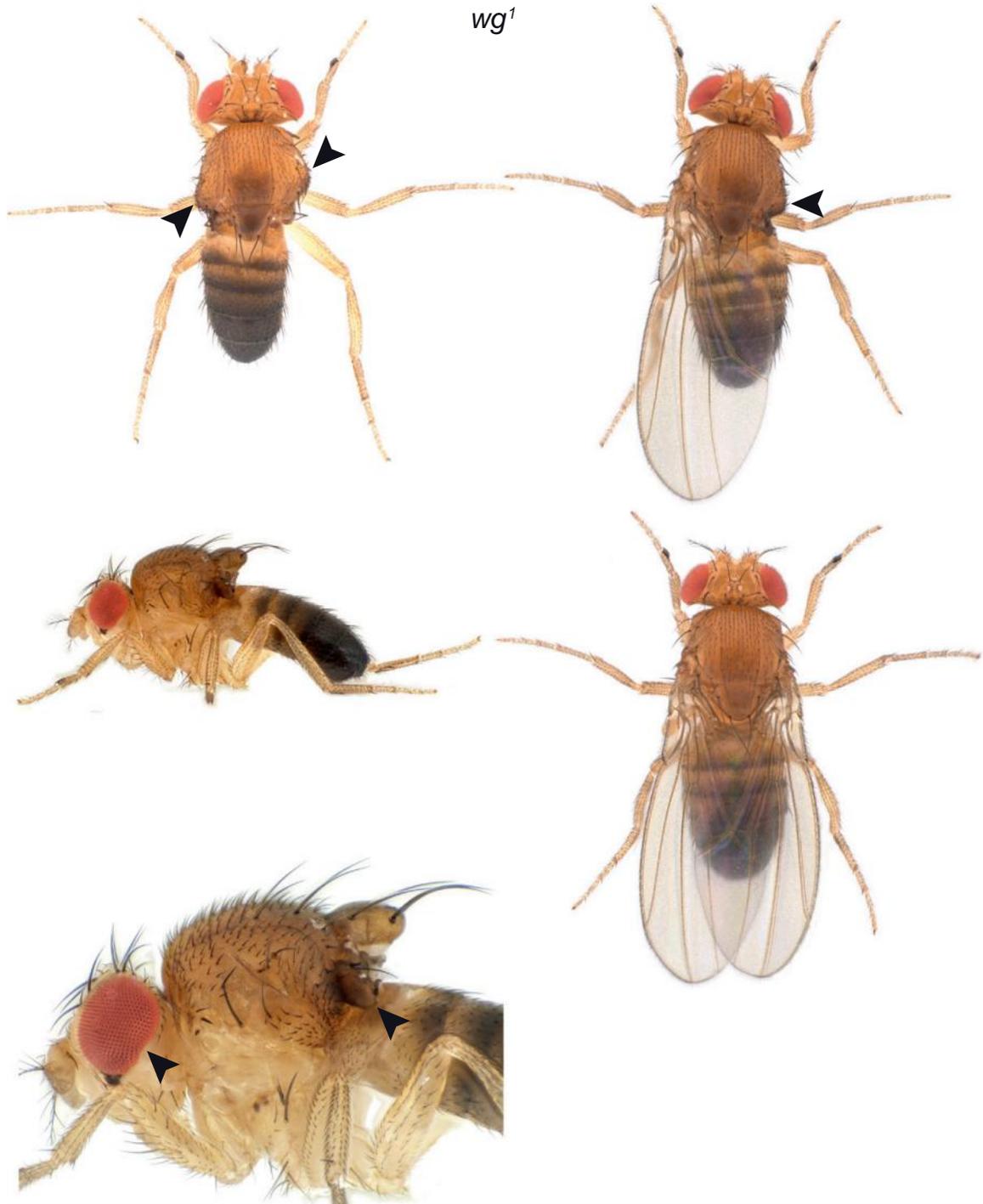
<100%

Expressivity variation



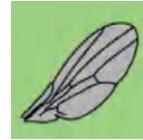
Similarity

Easy to score



Xasta

Xa(ap^{Xa})



Flybase ID: FBgn0000099

Chromosome: 2R

Cytogenetic location: 41F8

Recombination map: 2-55.2

Sequence location: 2R:1,593,707..1,614,335 [-]

Description

Wings smaller than WT and severely notched giving them a mitten-shaped appearance

Notching affects L3 vein and to a lesser degree L2 and L4 veins

Homozygous lethal, rare escapers

Allele information

Xa shown

Temperature dependence

None

Age dependence

None

Penetrance

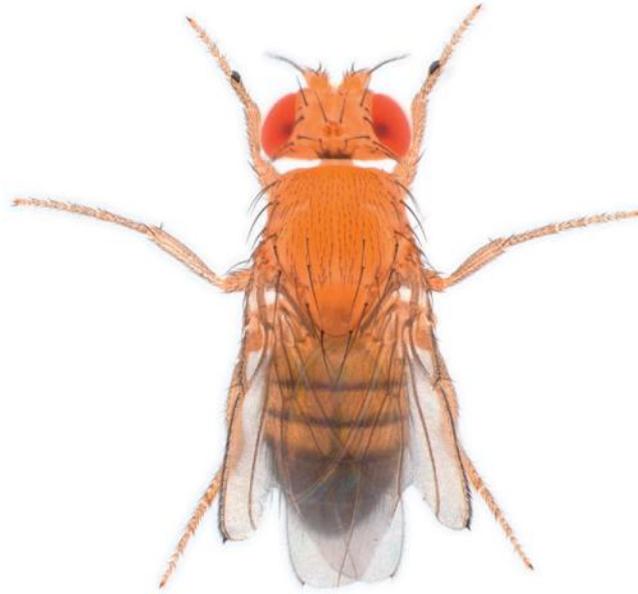
100%

Expressivity variation



Similarity

Easy to score



WT



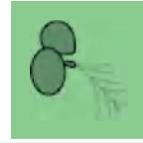
$Xa/+$

Markers of other appendages



aristaless

al



Flybase ID: FBgn0000061

Chromosome: 2L

Cytogenetic location: 21C1

Recombination map: 2-0.4

Sequence location: 2L:378,112..387,439 [+]

Description

Arista significantly reduced in size

Shortened scutellum with erect and usually divergent pSC

Allele information

*al*¹ shown

*al*² recessive marker on SM1, SM5, SM6a, and SM6b

Temperature dependence

Undetermined

Age dependence

None

Penetrance

100%

Expressivity variation

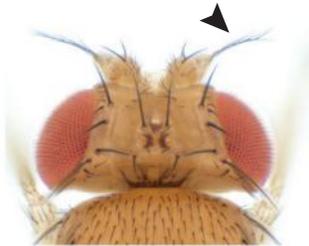
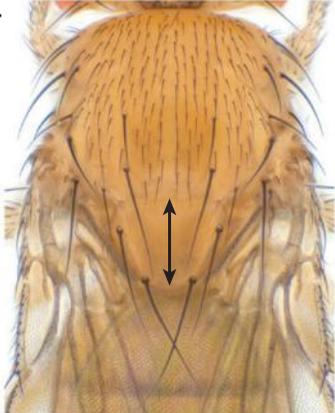


Similarity

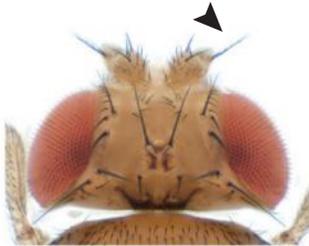
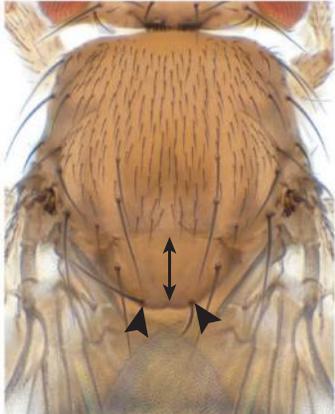
thread: affects the size of arista branches



WT

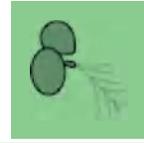


al¹



Antennapedia

Antp



Flybase ID: FBgn0260642

Chromosome: 3R

Cytogenetic location: 84A6-B2

Recombination map: 3-47.5

Sequence location: 3R:2,721,975..2,824,950 [-]

Description

Antenna partially transformed into a leg

Allele information

Antp^{Wu} shown (arrowhead indicates remaining arista)

Antp^{Ns} detail shown

Temperature dependence

None

Age dependence

None

Penetrance

Antp^{Wu}: 100%

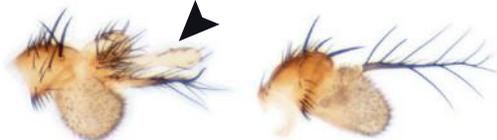
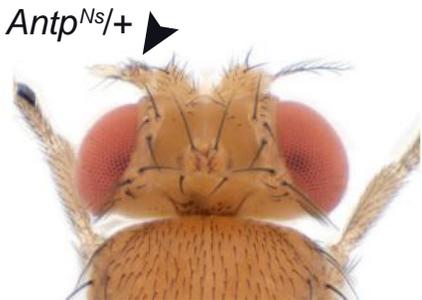
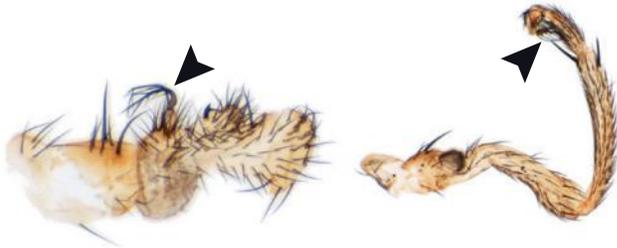
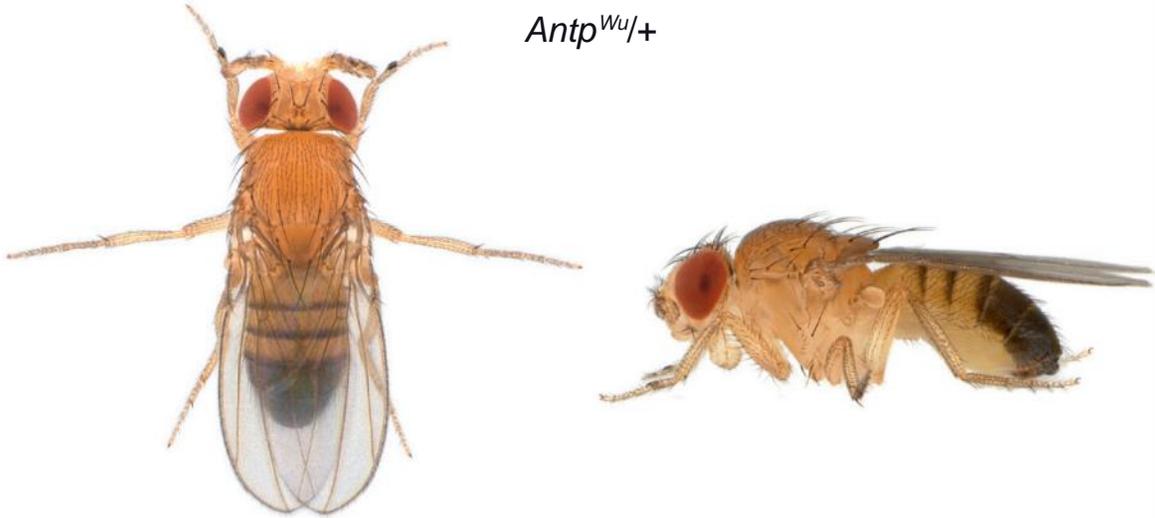
Antp^{Ns}: \ll 100%

Expressivity variation

Antp^{Wu}:  *Antp^{Ns}*: 

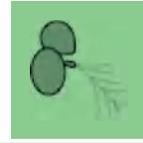
Similarity

Distal-less: affects not only antennae but also maxillary palpaes and proboscis



Distal-less

Dll



Flybase ID: FBgn0000157

Chromosome: 2R

Cytogenetic location: 60E2

Recombination map: 2-107.8

Sequence location: 2R:20,702,353..20,722,686 [+]

Description

Arista reduced in size or modified to a mesothoracic leg

Maxillary palpa and labellum have also been reported to be affected (not shown)

Allele information

*Dll*⁵ shown

Temperature dependence

Undetermined

Age dependence

None

Penetrance

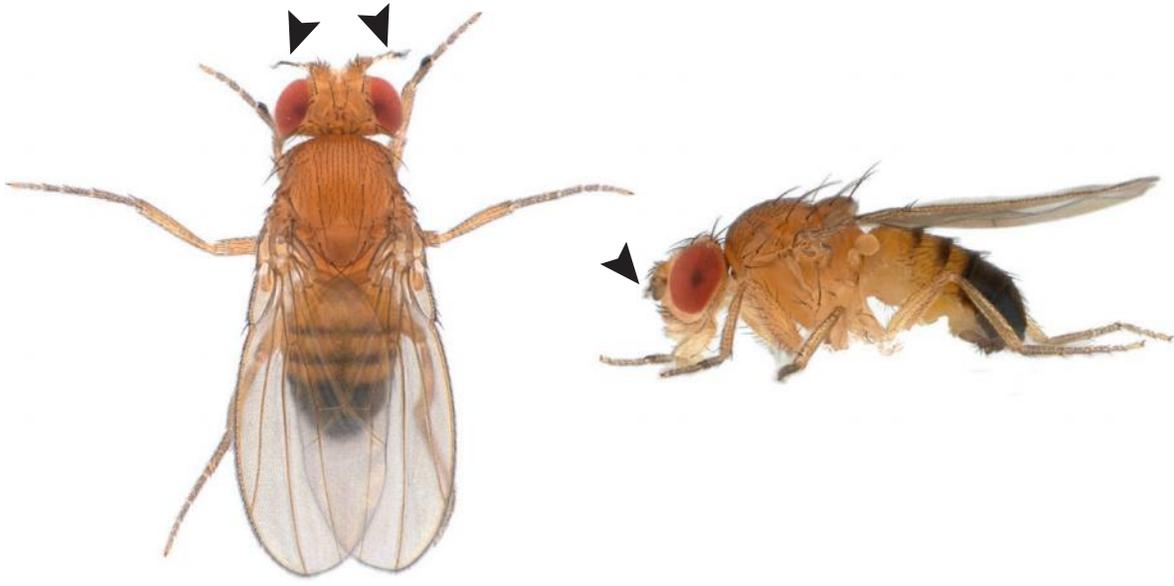
<100%

Expressivity variation



Similarity

Antennapedia: affects only the antennae

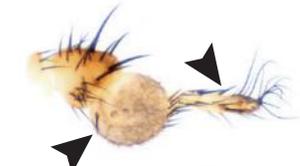


WT



WT

Dll^{5/+}



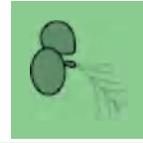
Dll^{5/+}



Dll^{5/+}

Sex combs reduced

Scr



Flybase ID: FBgn0003339

Chromosome: 3R

Cytogenetic location: 84A5

Recombination map: 3-47.5

Sequence location: 3R:2,648,842..2,675,703 [-]

Description

Male-specific

Sex combs have fewer, short, and straight “teeth” (thick bristles)

Allele information

*Scr*¹ shown

*Scr*², *Scr*⁶ and *Scr*⁸ homozygous lethal

Temperature dependence

*Scr*⁶ and *Scr*⁸ cold sensitive

Age dependence

None

Penetrance

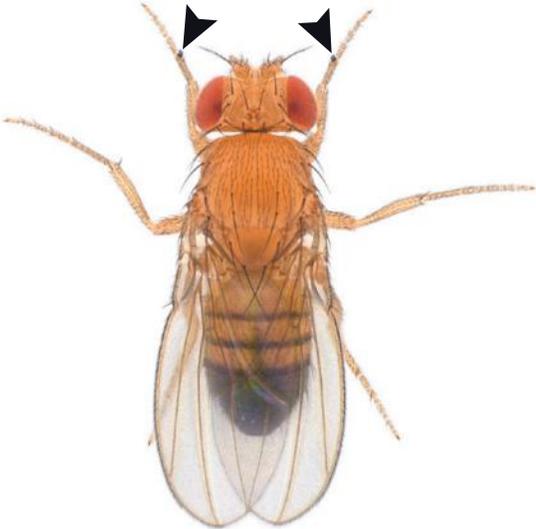
*Scr*¹: 100% Other alleles: undetermined

Expressivity variation



Similarity

None



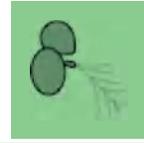
WT

Scr1/+



thread

th



Flybase ID: FBgn0260635

Chromosome: 3L

Cytogenetic location: 72C1-D1

Recombination map: 3-43.2

Sequence location: 3L:16,031,510..16,044,134 [-]

Description

Arista reduced to a thread

In extreme cases all side branches may be missing

Allele information

*th*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

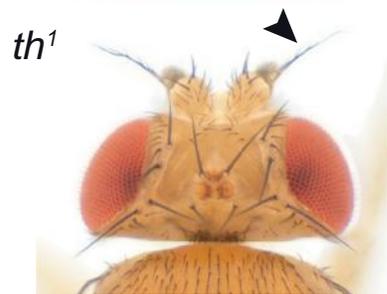
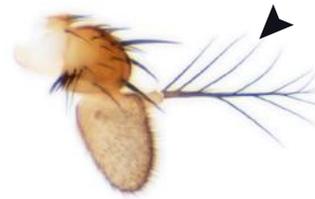
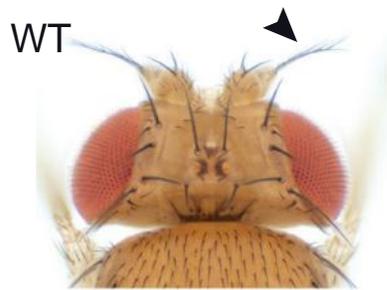
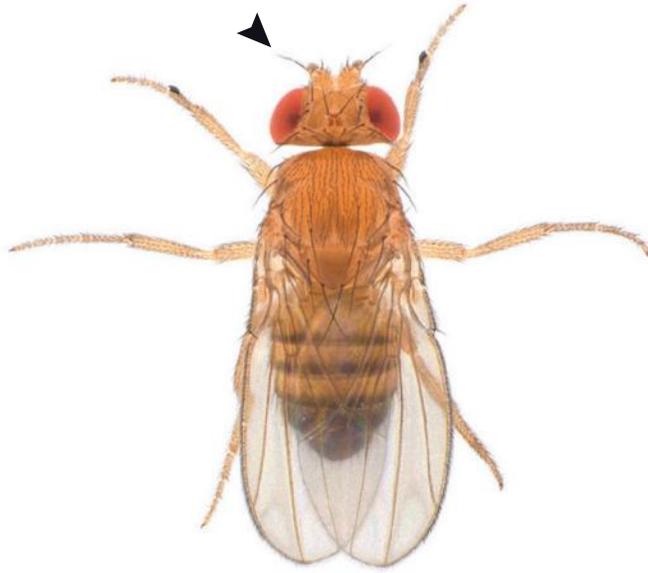
100%

Expressivity variation



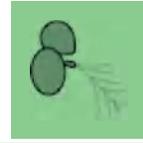
Similarity

aristaless: smaller arista, shorter scutellum with pSC erect



Ultrabithorax

Ubx



Flybase ID: FBgn0003944

Chromosome: 3R

Cytogenetic location: 89D6-9

Recombination map: 3-58.8

Sequence location: 3R:12,482,345..12,560,348 [-]

Description

Enlarged halteres showing various extent of transformation into wings, from an enlarged swollen capitellum, to a flattened, winglet-like haltere (not shown)

Drooping haltere

One or more bristles on the pedicel and capitellum

Allele information

*Ubx*¹⁰¹ shown, sometimes referred to as *bx*¹⁰¹

*Ubx*¹³⁰ detail shown, dominant marker on TM2

Ubx^{bx-34e} recessive marker on TM3 and TM6

Ubx^{P15} dominant marker on TM6

Temperature dependence

Higher temperatures enhance expressivity of some alleles

Age dependence

None

Penetrance

<100%

Expressivity variation

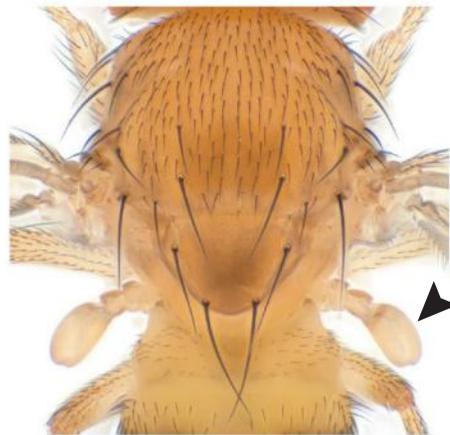


Similarity

None



WT



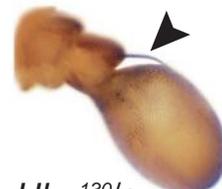
Ubx^{101/+}



WT



Ubx^{101/+}



Ubx^{130/+}

Eye shape markers



Bar

B



Flybase ID: FBgn0000154
Chromosome: X
Cytogenetic location: 16A1
Recombination map: 1-57.0
Sequence location: N/A

Description

Compound eyes reduced in size to rectangular vertical bars in homozygous females and hemizygous males
Eye kidney-shaped with anterior dimple in heterozygous females

Allele information

*B*¹ shown, dominant marker of most FM balancers

Temperature dependence

None

Age dependence

None

Penetrance

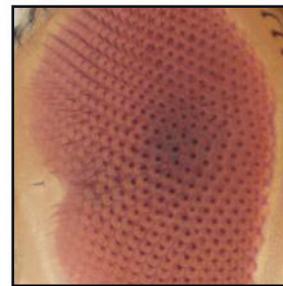
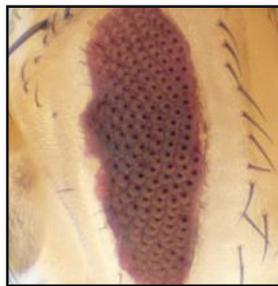
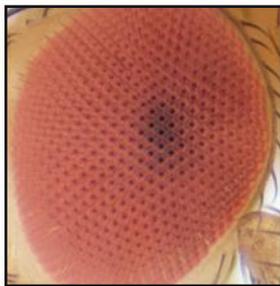
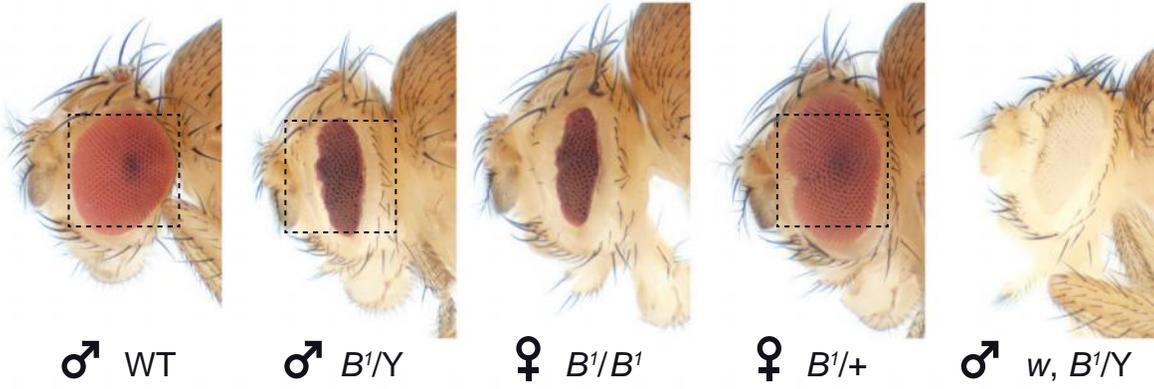
100%

Expressivity variation



Similarity

Easy to score



Deformed

Dfd



Flybase ID: FBgn0000439

Chromosome: 3R

Cytogenetic location: 84A5

Recombination map: 3-47.5

Sequence location: 3R:2,617,558..2,628,153 [+]

Description

Compound eye reduced in size on the ventral side

Two symmetrical dimples in lateral view give it the appearance of bulging toward proboscis

Allele information

Dfd^r shown, recessive allele

Temperature dependence

Overlaps with WT at 19°C

Age dependence

None

Penetrance

<100%

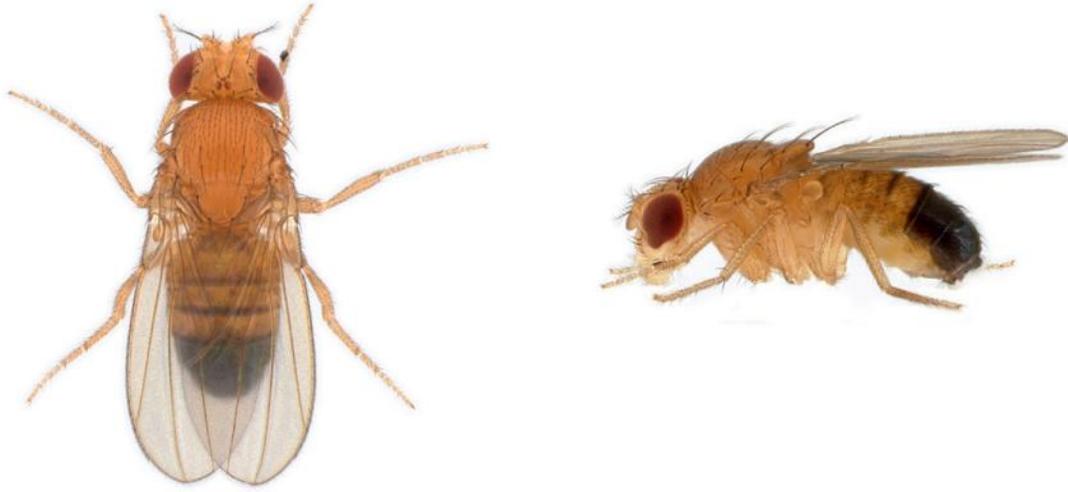
Expressivity variation



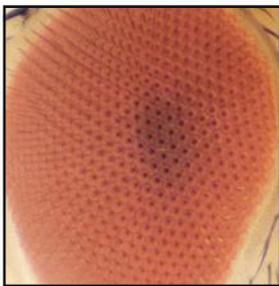
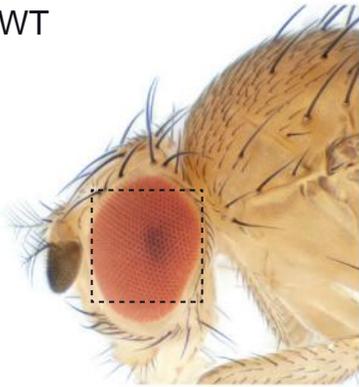
Similarity

WT at low temperature (<20°C)

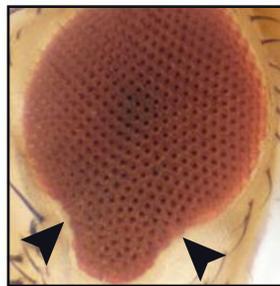
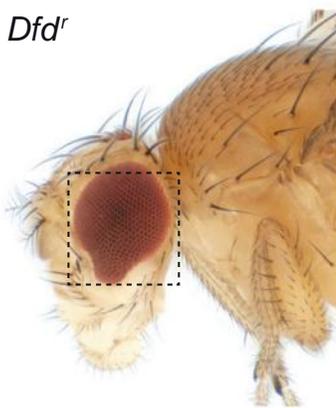
Dfd^r



WT



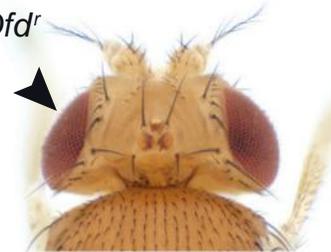
Dfd^r



WT



Dfd^r



Drop

Dr



Flybase ID: FBgn0000492

Chromosome: 3R

Cytogenetic location: 99B3

Recombination map: 3-99.2

Sequence location: 3R:25,382,109..25,391,007 [+]

Description

Compound eye reduced in size to about 15% of WT eye
Drop-like in appearance with dorsal and ventral pointed ends

Allele information

Dr¹ shown, homozygous lethal

Temperature dependence

None

Age dependence

None

Penetrance

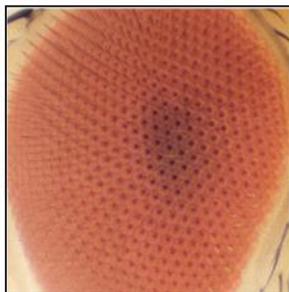
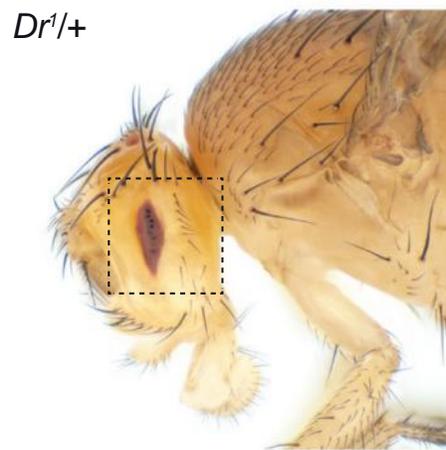
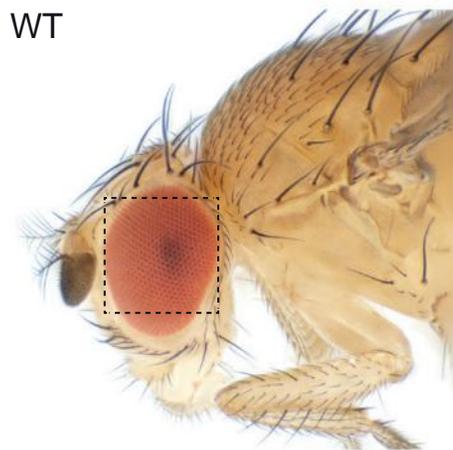
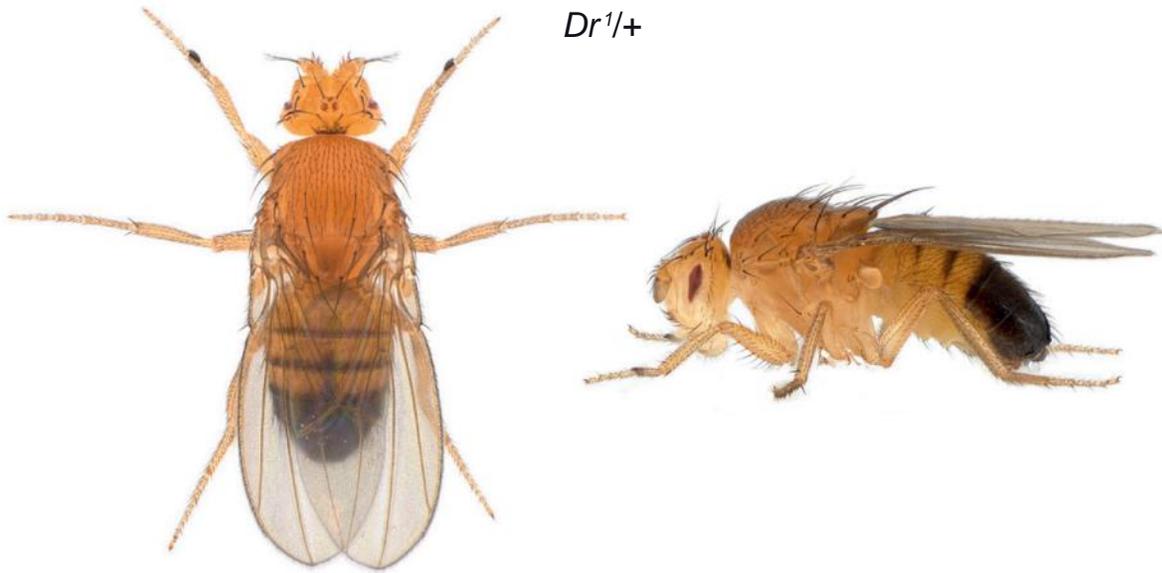
100%

Expressivity variation



Similarity

Bar: males and homozygous females with eyes bigger and rectangular in shape



eyeless-dominant

ey^D



Flybase ID: FBgn0005558

Chromosome: 4

Cytogenetic location: 102D4-5

Recombination map: 4-2.0

Sequence location: 4:718,315..741,787 [+]

Description

Eyes reduced in size to completely absent; effect not bilaterally symmetrical
Isolated facets sometimes present in the eye region (arrowheads)
Ocelli often altered or absent
Head deformed

Allele information

ey^D shown, homozygous lethal

Temperature dependence

None

Age dependence

None

Penetrance

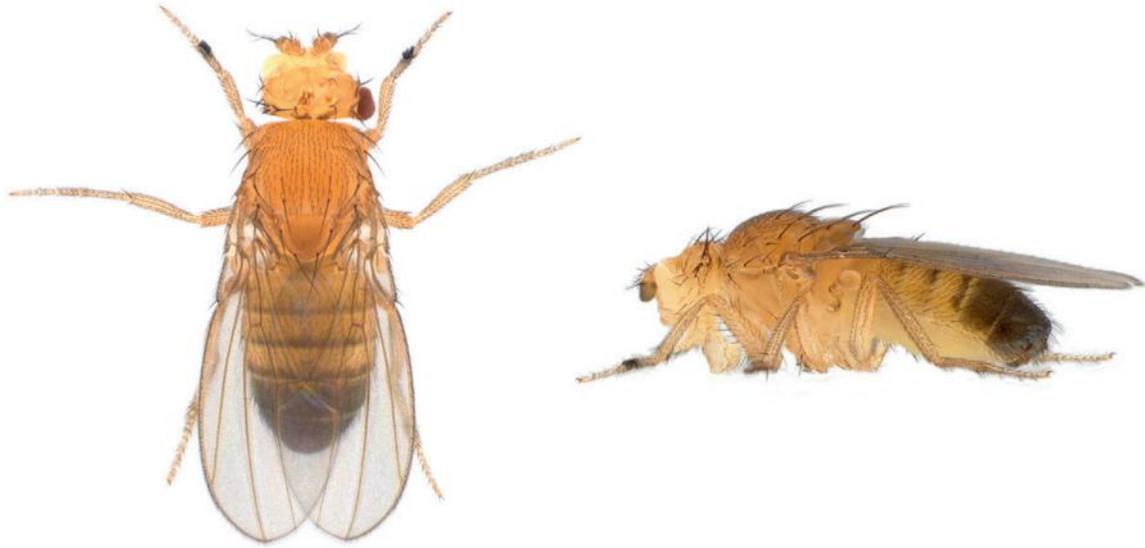
100%

Expressivity variation



Similarity

Lobe: both eyes show similar defect

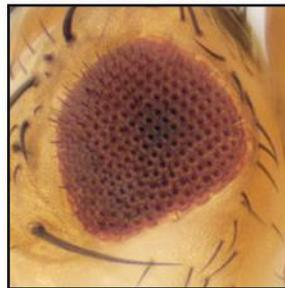
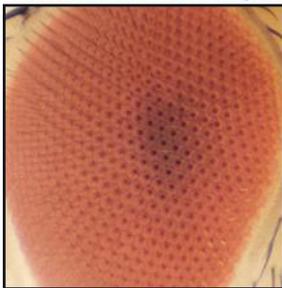
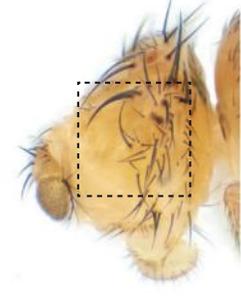
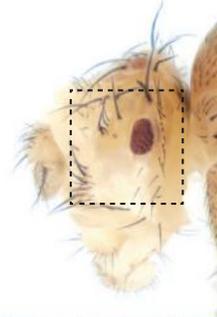
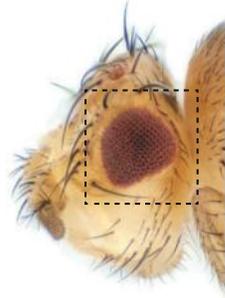
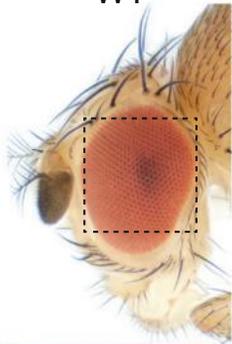


WT

ey^{D/+}

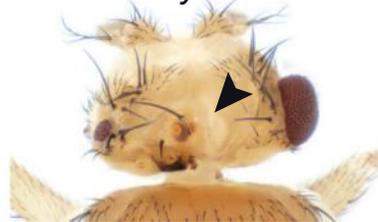
ey^{D/+}

ey^{D/+}



WT

ey^{D/+}



Glued

Gl



Flybase ID: FBgn0001108

Chromosome: 3L

Cytogenetic location: 70C5-6

Recombination map: 3-41.4

Sequence location: 3L:13,922,487...13,927,756 [+]

Description

Compound eyes reduced in size, oval in shape, and rough in appearance

Phenotype stronger in males with some facets fused

Allele information

Gl¹ shown, homozygous lethal

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation

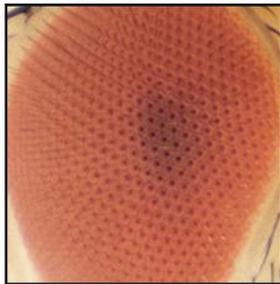
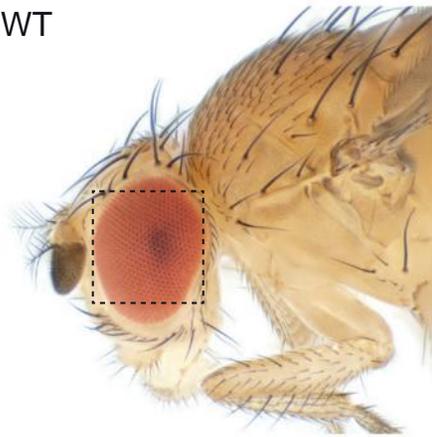


Similarity

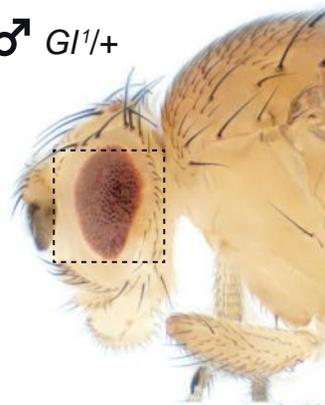
Difficult to distinguish from *rough*, *roughoid*, and *Rough eye*



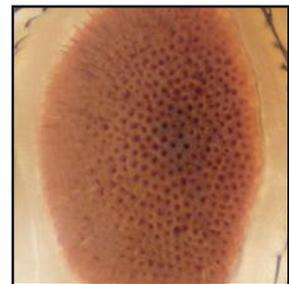
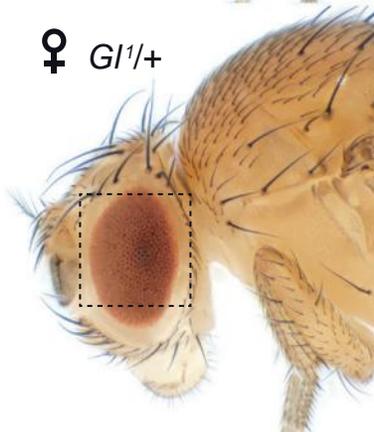
WT



♂ *Gl'1/+*



♀ *Gl'1/+*



glass

gl



Flybase ID: FBgn0004618

Chromosome: 3R

Cytogenetic location: 91A3

Recombination map: 3-63.1

Sequence location: 3R:14,193,649...14,198,460 [-]

Description

Compound eyes reduced in size, rough, paler than WT and glassy in texture

Ocelli colorless

Allele information

gl¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation



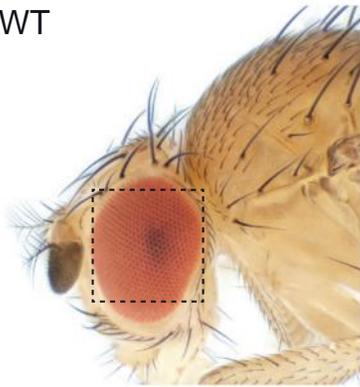
Similarity

Bar: males and homozygous females with eyes bigger and rectangular in shape

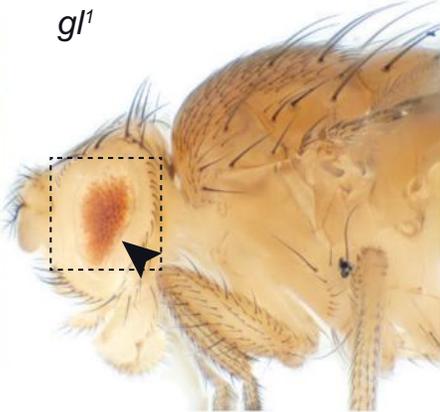
Drop: eyes slit-like and significantly darker, ocelli unaffected



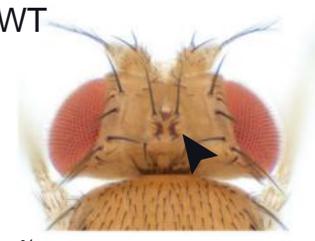
WT



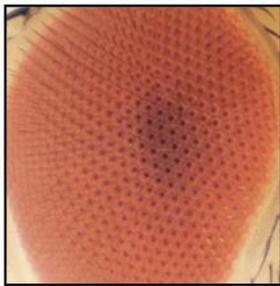
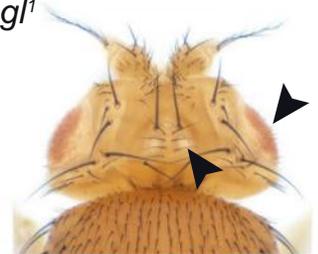
gl¹



WT



gl¹



Glazed

Gla(wg^{Gla})



Flybase ID: FBgn0004009

Chromosome: 2L

Cytogenetic location: 27F1

Recombination map: 2-21.9

Sequence location: 2L:7,307,161..7,316,265 [+]

Description

Eyes reduced in size, darker, flattened, and angular, pointy on their ventral side

Fused facets

Allele information

*Gla*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

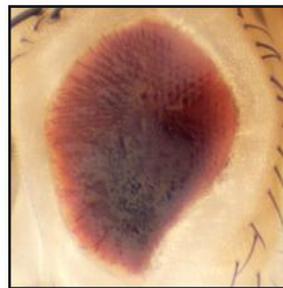
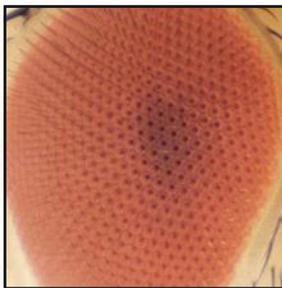
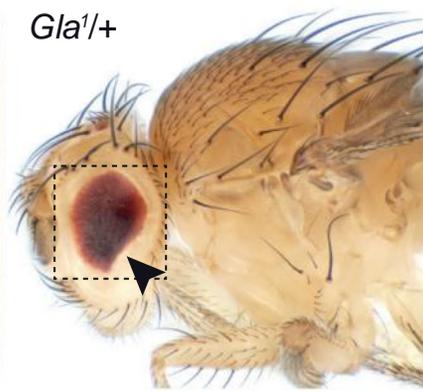
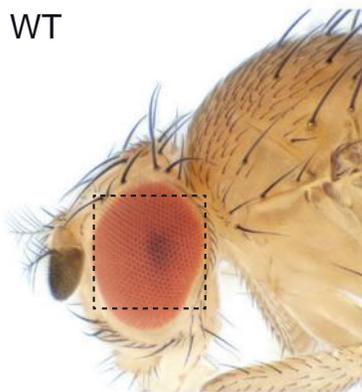
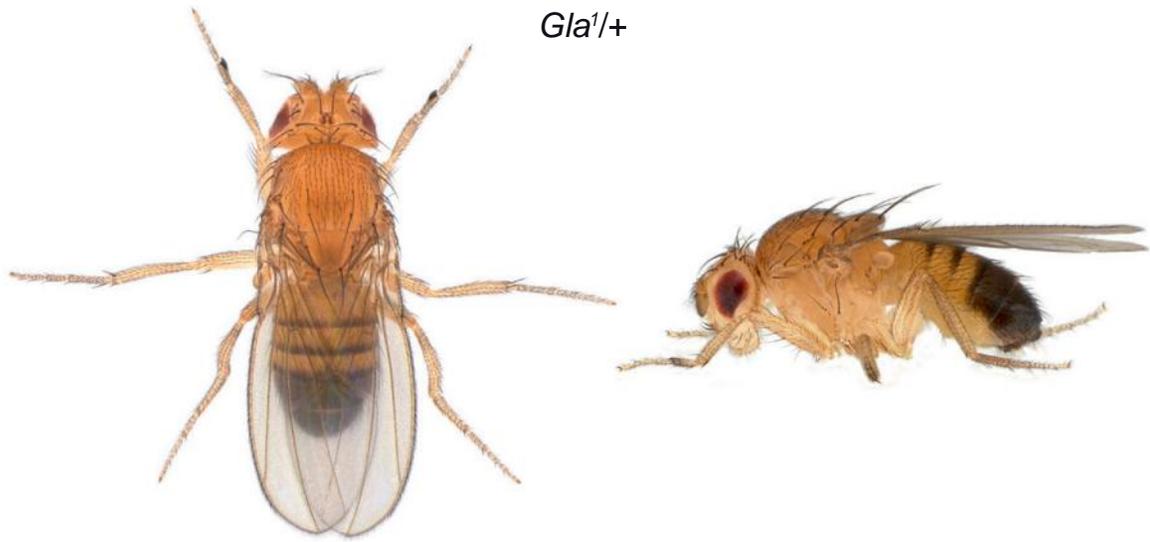
Expressivity variation



Similarity

Irregular facets: bigger elongated eyes, ommatidia (facets) arranged in patches

Drop: significantly smaller and slit-like in appearance



Irregular facets

If(Kr^{If-1})



Flybase ID: FBgn0001325

Chromosome: 2R

Cytogenetic location: 60F5

Recombination map: 2-107.6

Sequence location: 2R:21,114,134..21,118,917 [+]

Description

Compound eyes half the size of WT, oblong and narrow

Individual facets irregular in dorsal part of the eye, missing across the middle, and fused or absent in ventral part

Pattern of interommatidial bristles irregular

Allele information

*If*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation



Similarity

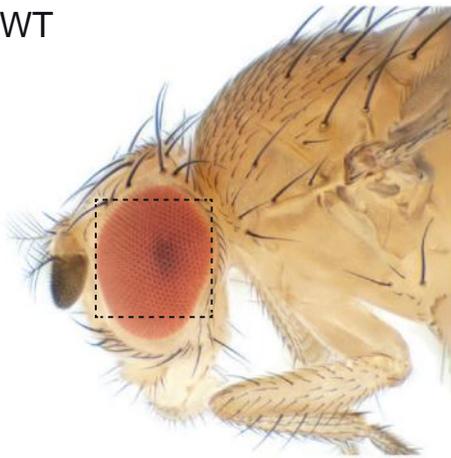
Glazed: smaller, angular eyes

Drop: eyes significantly smaller and slit-like in appearance

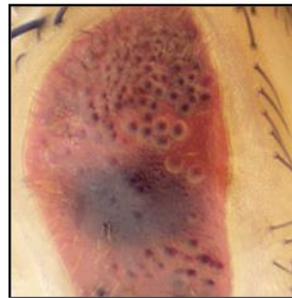
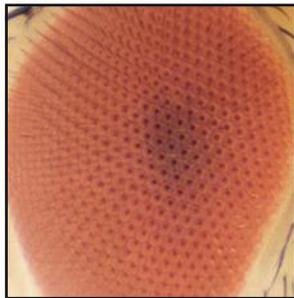
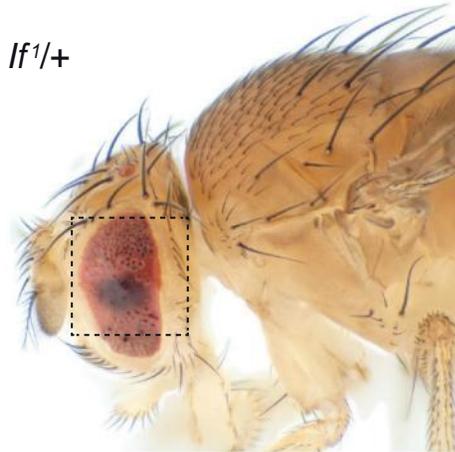
If¹/+



WT



If¹/+



Lobe

L



Flybase ID: FBgn0001325

Chromosome: 2R

Cytogenetic location: 51A4

Recombination map: 2-72.0

Sequence location: 2R:10,368,716..10,384,817 [+]

Description

Compound eyes smaller, almost perfectly round but for a missing ventral lobe

Depressed, showing dimples in dorsal view

Allele information

*L*¹ shown, homozygous viable

Temperature dependence

Penetrance is increased at higher temperatures

Age dependence

None

Penetrance

<100%

Expressivity variation

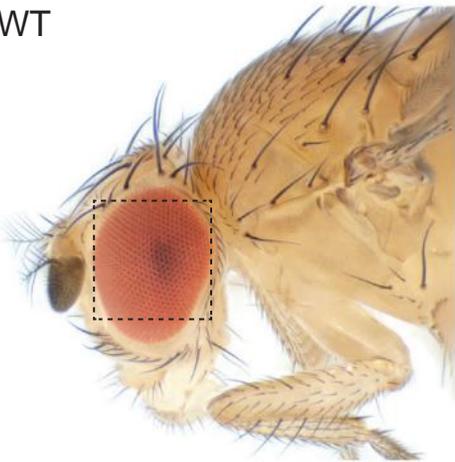


Similarity

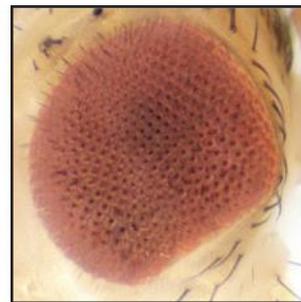
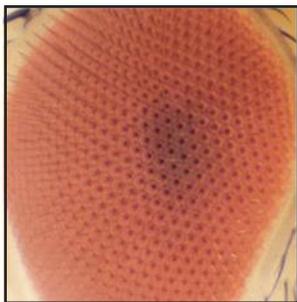
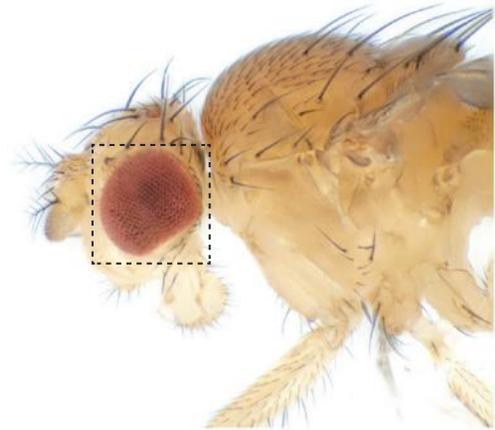
eyeless^D: eyes have pronounced bilateral asymmetry



WT



L^1



ocelliless

oc



Flybase ID: FBgn0004102

Chromosome: X

Cytogenetic location: 7F10-8A1

Recombination map: 1-23.1

Sequence location: X:8,524,192...8,544,714 [-]

Description

Ocelli absent and interocellar bristles missing
Additional hairs present in the ocellar area

Allele information

oc¹ shown, recessive marker on FM7i

Temperature dependence

None

Age dependence

None

Penetrance

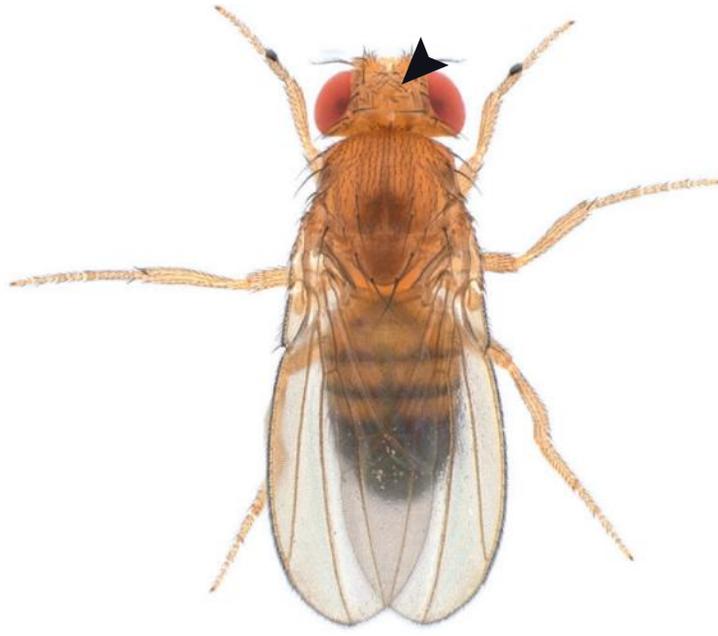
100%

Expressivity variation

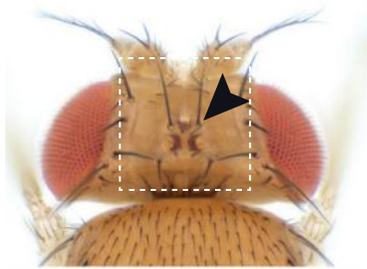


Similarity

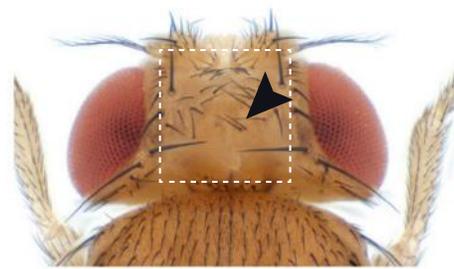
None



WT



oc¹/Y



rough

ro



Flybase ID: FBgn0003267

Chromosome: 3R

Cytogenetic location: 97D4-5

Recombination map: 3-91.1

Sequence location: 3L:22,702,493...22,706,893 [-]

Description

Compound eyes smaller, elliptical in shape, and rough in texture

Allele information

*ro*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation



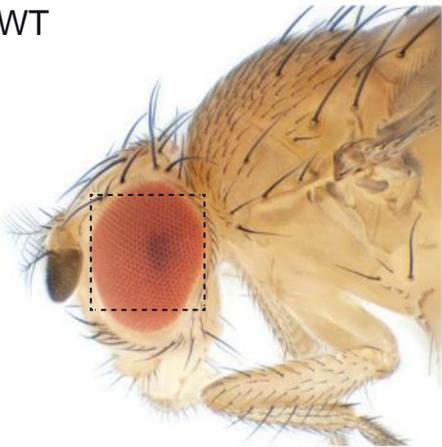
Similarity

Difficult to distinguish from *Glued* and *Rough eye*

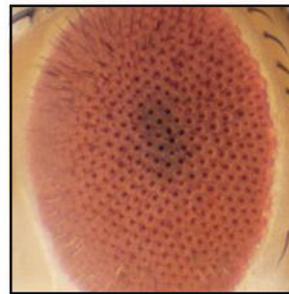
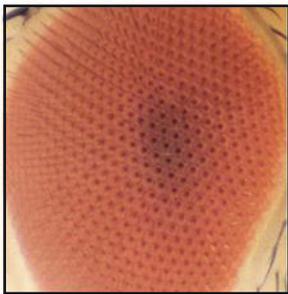
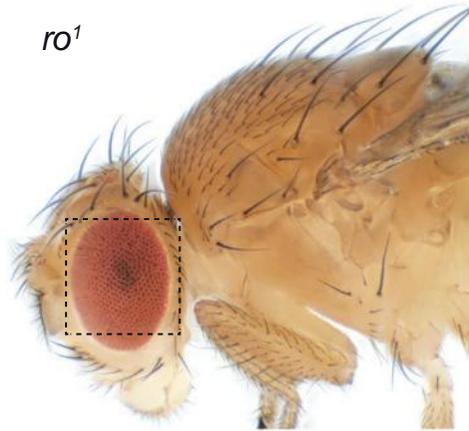
Roughoid: has colorless ocelli



WT



ro¹



Rough eye

Roi(amos^{Roi})



Flybase ID: FBgn0003270

Chromosome: 2L

Cytogenetic location: 36F6

Recombination map: 2-53.6

Sequence location: 2L:18,596,047..18,597,200 [-]

Description

Compound eyes rough in texture

Allele information

*Roi*¹ shown, homozygous lethal; dominant marker on SM6b (in addition to Cy)

Temperature dependence

None

Age dependence

None

Penetrance

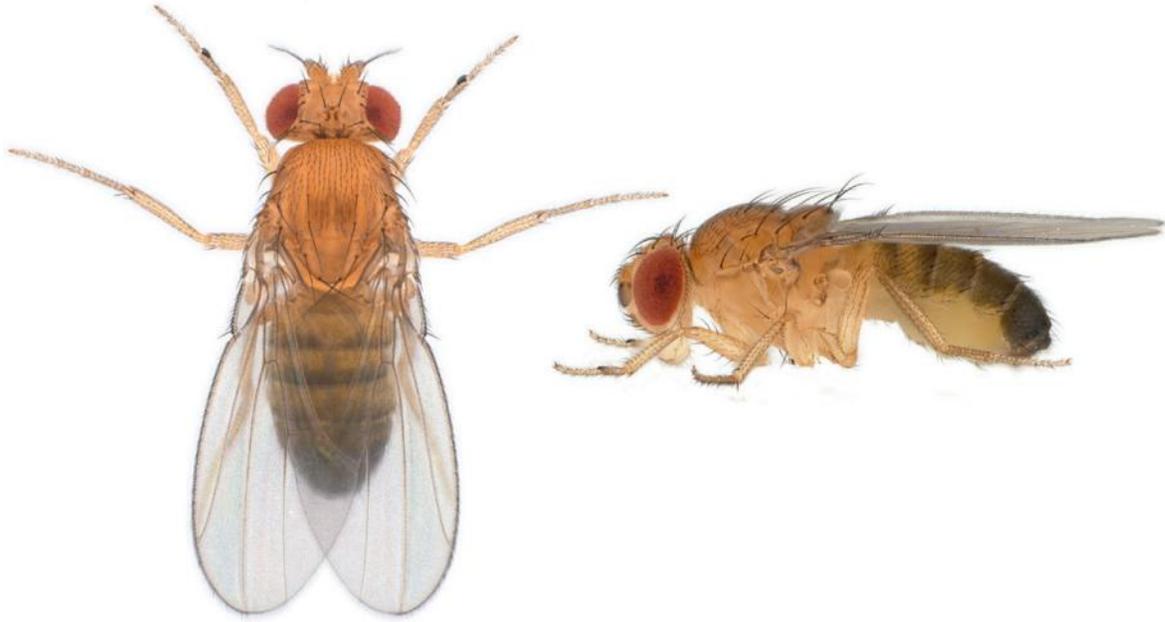
100%

Expressivity variation

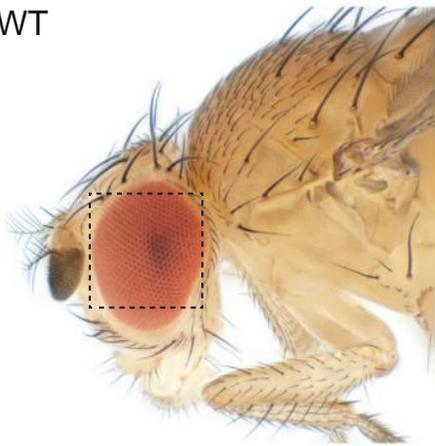


Similarity

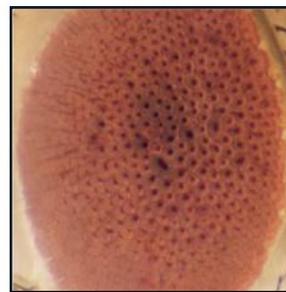
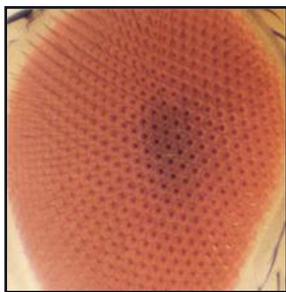
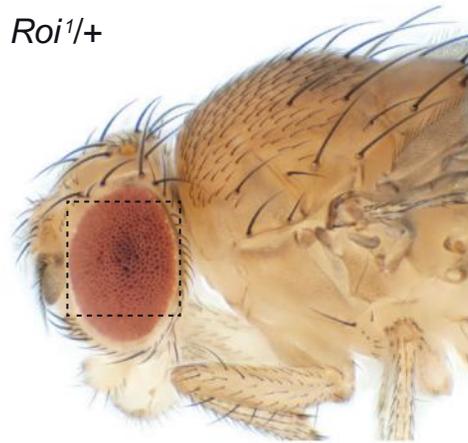
Difficult to distinguish from *Glued* and *rough*
roughoid: has colorless ocelli



WT



Roi1/+



roughoid

ru



Flybase ID: FBgn0003295

Chromosome: 3 L

Cytogenetic location: 61F8

Recombination map: 3-0.0

Sequence location: 3L:1,370,628..1,387,437 [+]

Description

Eyes smaller than WT, almost perfectly elliptical, darker in appearance

Irregular arrangement of facets

Ocelli colorless

Allele information

*ru*¹ shown

Temperature dependence

None

Age dependence

None

Penetrance

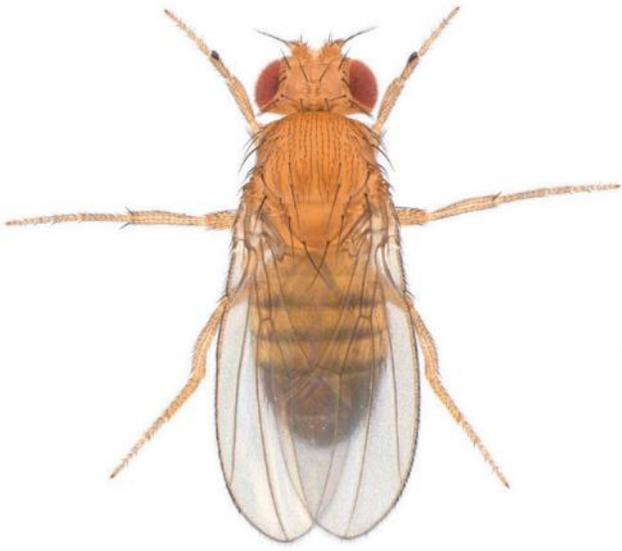
100%

Expressivity variation

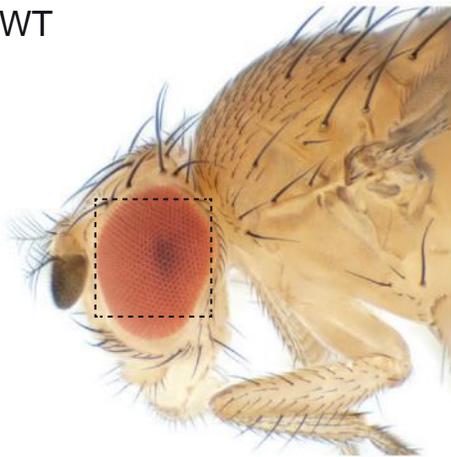


Similarity

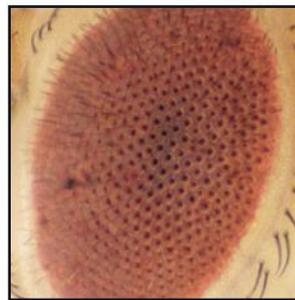
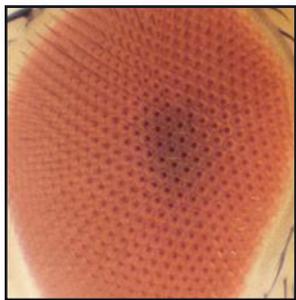
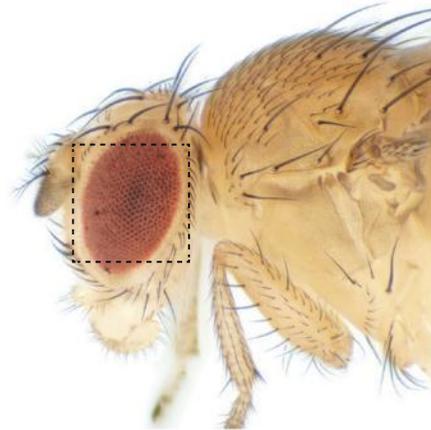
Glued, *rough*, and *Rough eye* have unaffected ocelli



WT



*ru*¹



Eye color markers



brown

bw



Flybase ID: FBgn0000241

Chromosome: 2R

Cytogenetic location: 59E2-3

Recombination map: 2-104.5

Sequence location: 2R:19,415,328..19,426,016 [-]

Description

Compound eyes light brown at eclosion and darken with age, lacking pseudopupil

Allele information

*bw*¹ shown

*bw*² darker and redder than *bw*¹

bw^D dominant allele with *bw*¹ phenotype

Temperature dependence

None

Age dependence

Darkens with age

Penetrance

100%

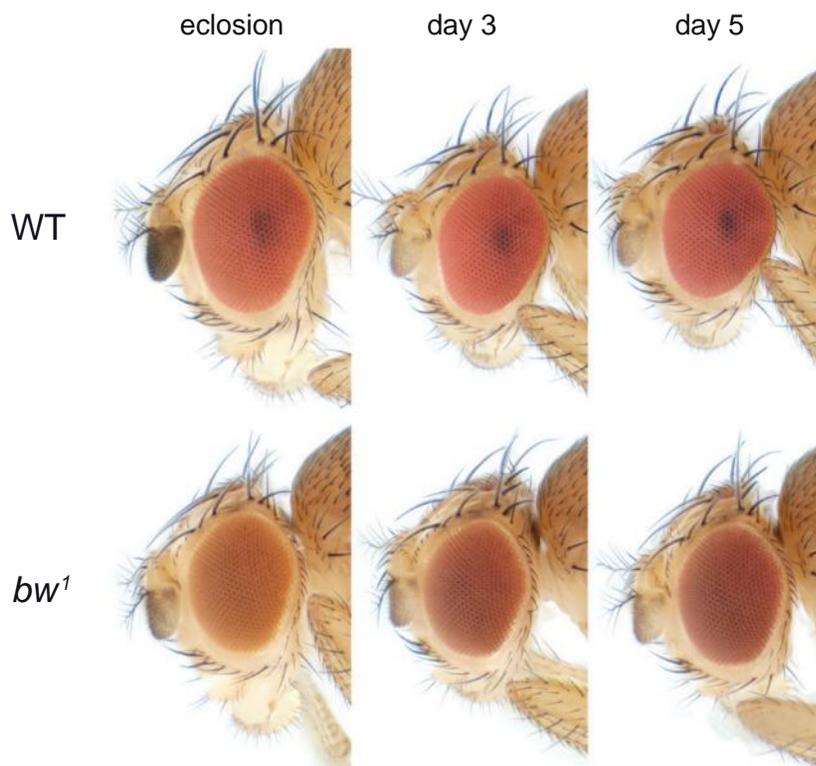
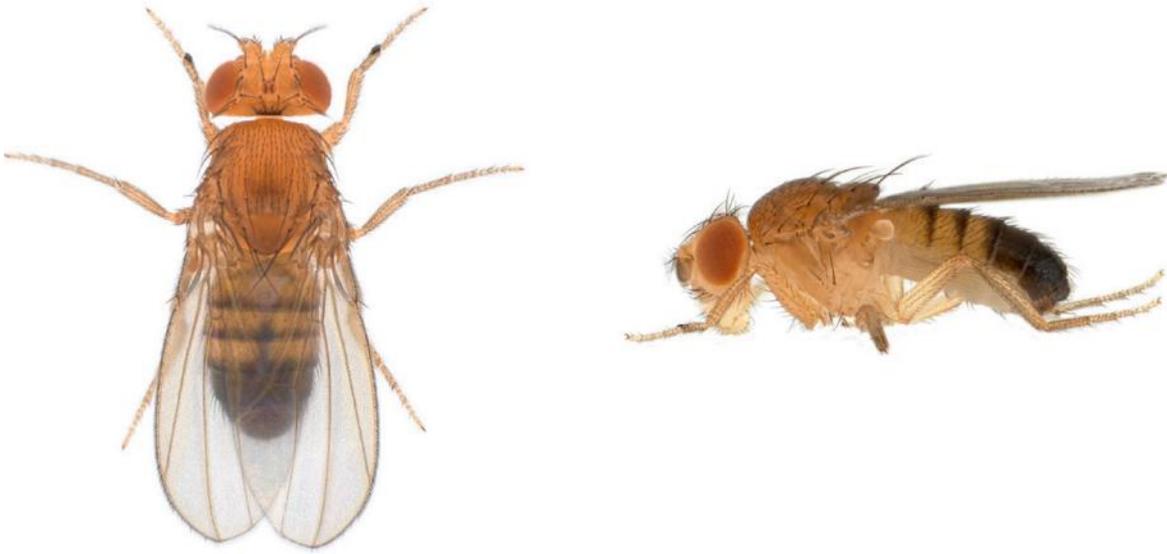
Expressivity variation



Similarity

Hue of compound eye not strikingly different from that of *claret*, *garnet*, *pink*, or *purple*

brown interacts with *cinnabar*, *scarlet*, and *vermillion*: combination with either results in white eyes



claret

ca



Flybase ID: FBgn0000247

Chromosome: 3R

Cytogenetic location: 99C2

Recombination map: 3-100.7

Sequence location: 3R:25,632,970...25,640,782 [+]

Description

Compound eyes dull red, lacking pseudopupil
Ocelli colorless

Allele information

*ca*¹ shown

Temperature dependence

None

Age dependence

Darkens with age

Penetrance

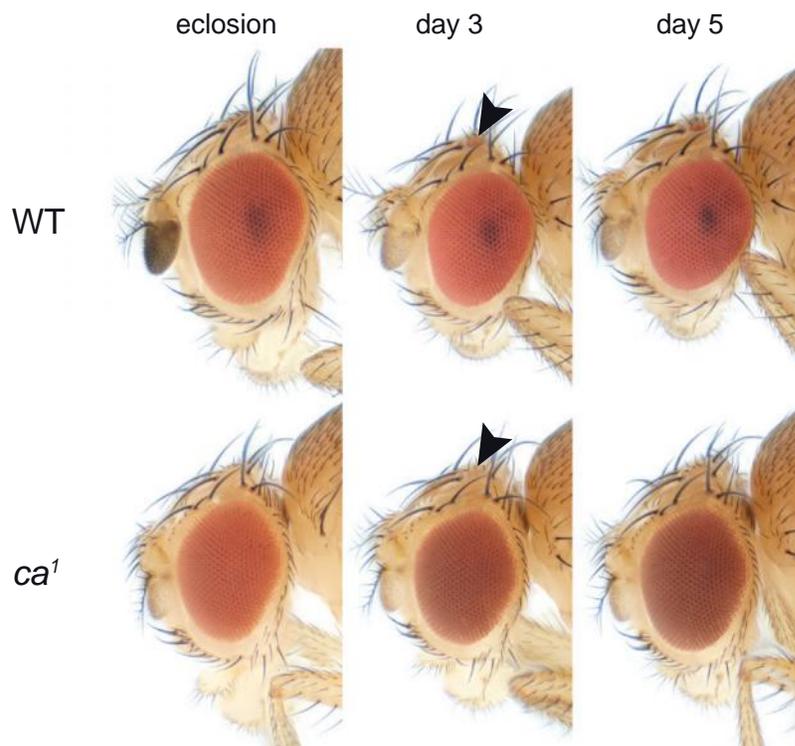
100%

Expressivity variation



Similarity

Hue of compound eye not strikingly different from that of *garnet*,
pink, *purple*, and *rosy*



cinnabar

cn



Flybase ID: FBgn0000337

Chromosome: 2R

Cytogenetic location: 43E16

Recombination map: 2-57.5

Sequence location: 2R:3,670,302..3,672,711 [-]

Description

Compound eyes bright red, pseudopupil invisible at eclosion

Ocelli colorless

Allele information

*cn*¹ shown

*cn*² very weak recessive marker on CyO

Temperature dependence

None

Age dependence

Darkens slightly with age

Pseudopupil absent at eclosion; present but very faint after a few days

Penetrance

100%

Expressivity variation

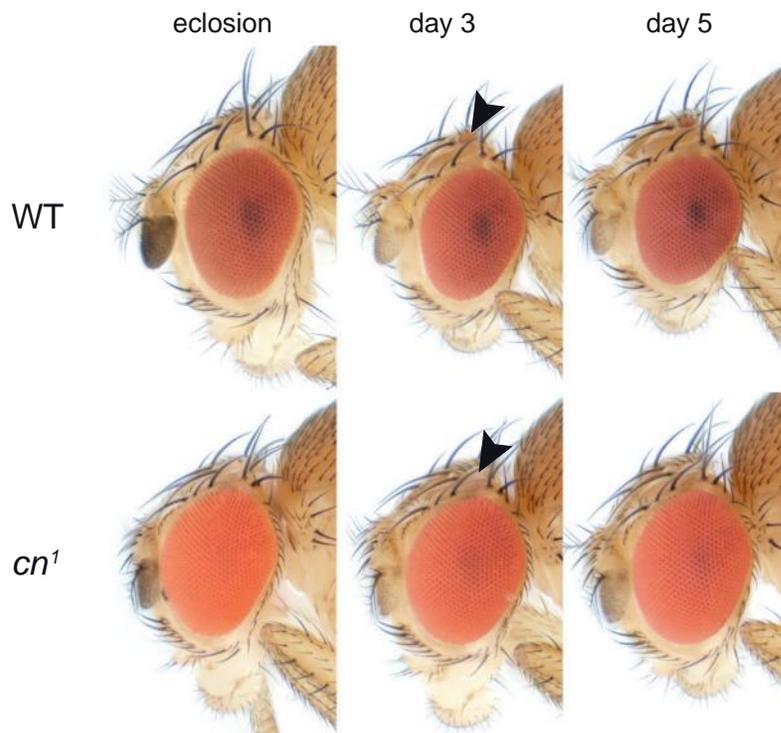
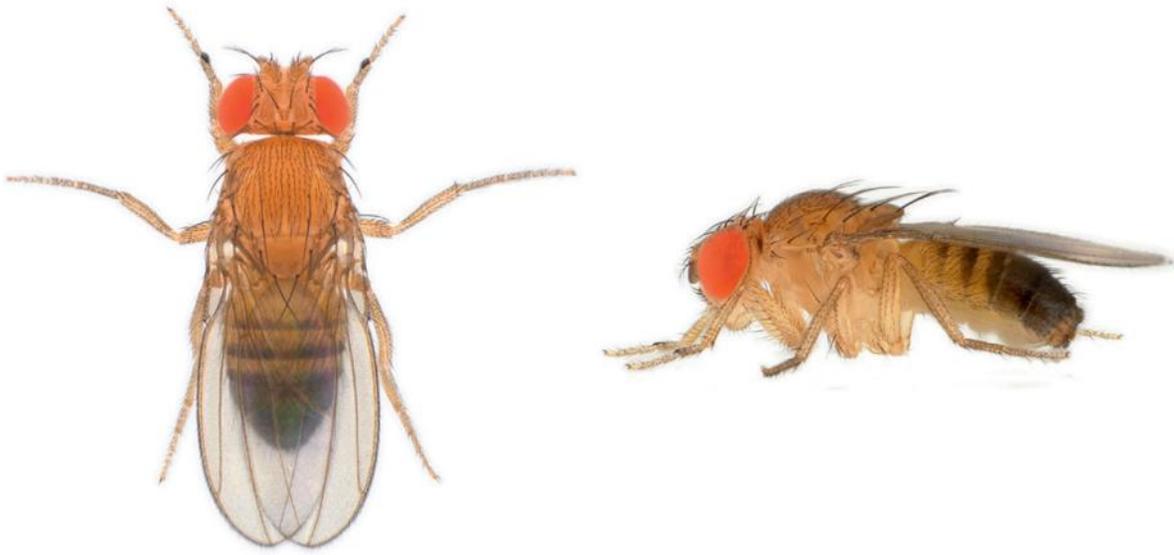


Similarity

Indistinguishable from *scarlet* and *vermillion*

karmoisin: pseudopupil faint but visible at eclosion

Results in white eyes when combined with *brown*



garnet

g



Flybase ID: FBgn0001087

Chromosome: X

Cytogenetic location: 12B4

Recombination map: 1-44.4

Sequence location: X:13,621,237..13,630,311 [-]

Description

Compound eyes dull red, lacking pseudopupil

Allele information

g^1 shown

g^4 recessive marker on FM7c

Temperature dependence

None

Age dependence

Darkens slightly with age

Penetrance

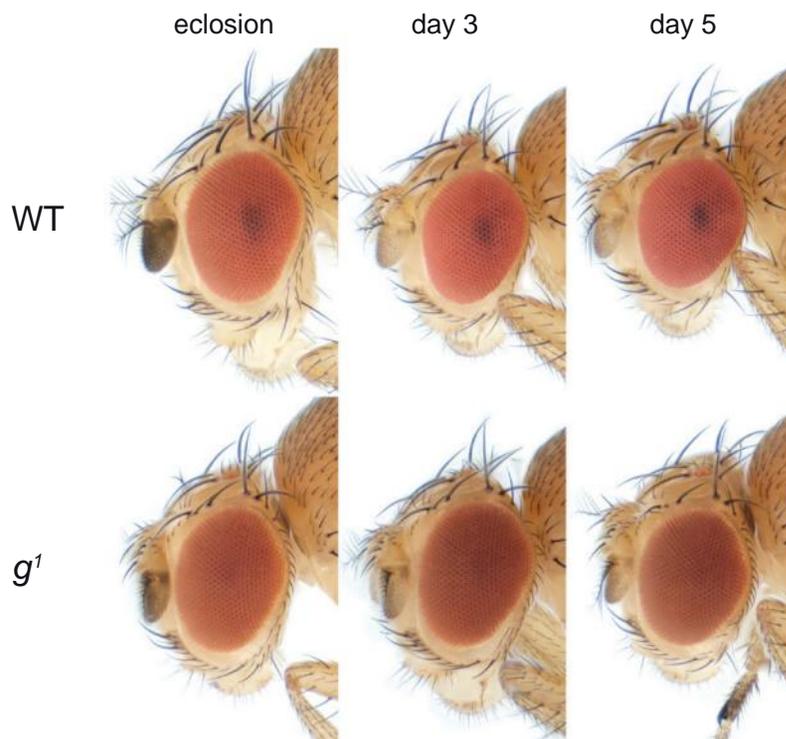
100%

Expressivity variation



Similarity

Hue of compound eye not strikingly different from that of *claret*, *pink*, *purple*, or *rosy*



Henna

Hn



Flybase ID: FBgn0001208

Chromosome: 3L

Cytogenetic location: 66A12

Recombination map: 3-23.0

Sequence location: 3L:7,753,577...7,756,268 [+]

Description

Compound eyes dark brown

Ventral male abdomen uniformly yellowish

Allele information

Hn^{rs} shown, recessive allele

Hn^P dominant marker on TM6

Temperature dependence

None

Age dependence

Darkens slightly with age

Penetrance

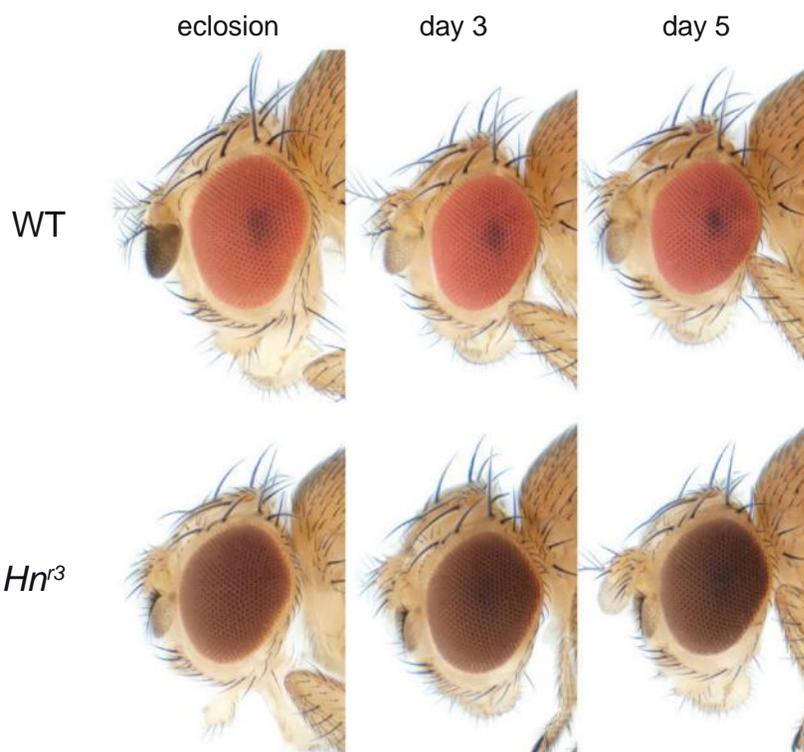
100%

Expressivity variation



Similarity

sepia: eyes dark at eclosion getting progressively darker to almost black



karmoisin

kar



Flybase ID: FBgn0001296

Chromosome: 3R

Cytogenetic location: 87C5

Recombination map: 3-51.7

Sequence location: 3R:8,507,908..8,515,089 [-]

Description

Compound eyes bright red, pseudopupil faint but visible
Ocelli colorless

Allele information

*kar*² shown

*kar*¹ recessive marker on MKRS

Temperature dependence

None

Age dependence

Darkens slightly with age

Penetrance

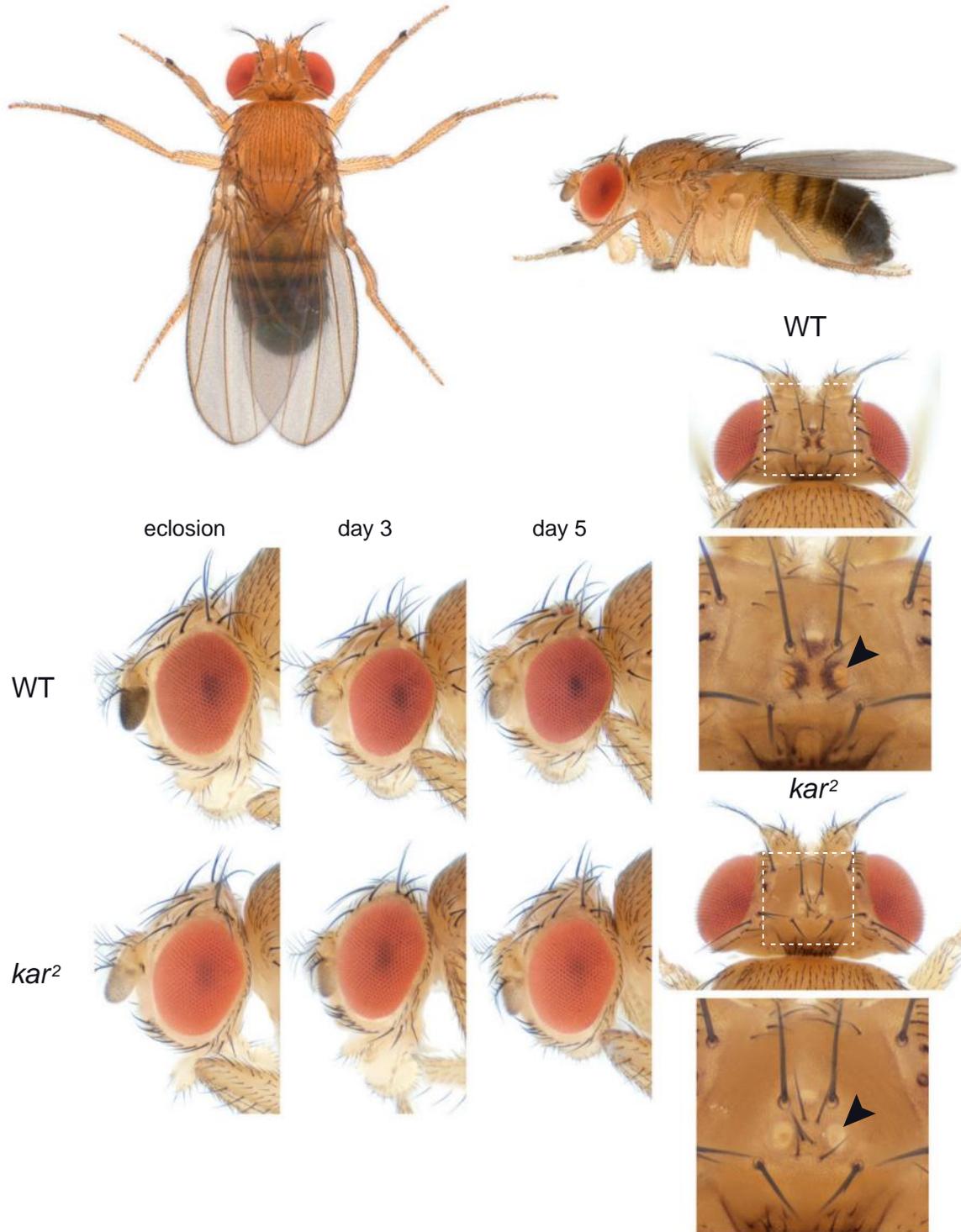
100%

Expressivity variation



Similarity

WT: has pigmented ocelli



light

lt



Flybase ID: FBgn0002566

Chromosome: 2L

Cytogenetic location: 40F

Recombination map: 2-55.0

Sequence location: 2L:22,811,944..22,834,955 [+]

Description

Compound eyes pale red with center of the eye appearing lighter

Allele information

lt¹ shown

lt^v recessive marker on SM5

Temperature dependence

None

Age dependence

Orange at eclosion, darkens with age

Penetrance

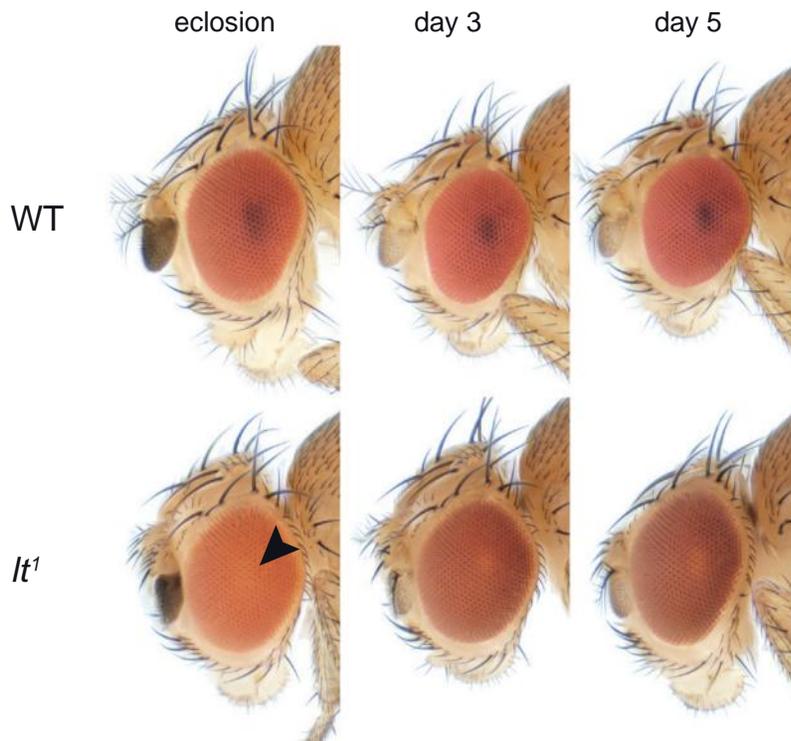
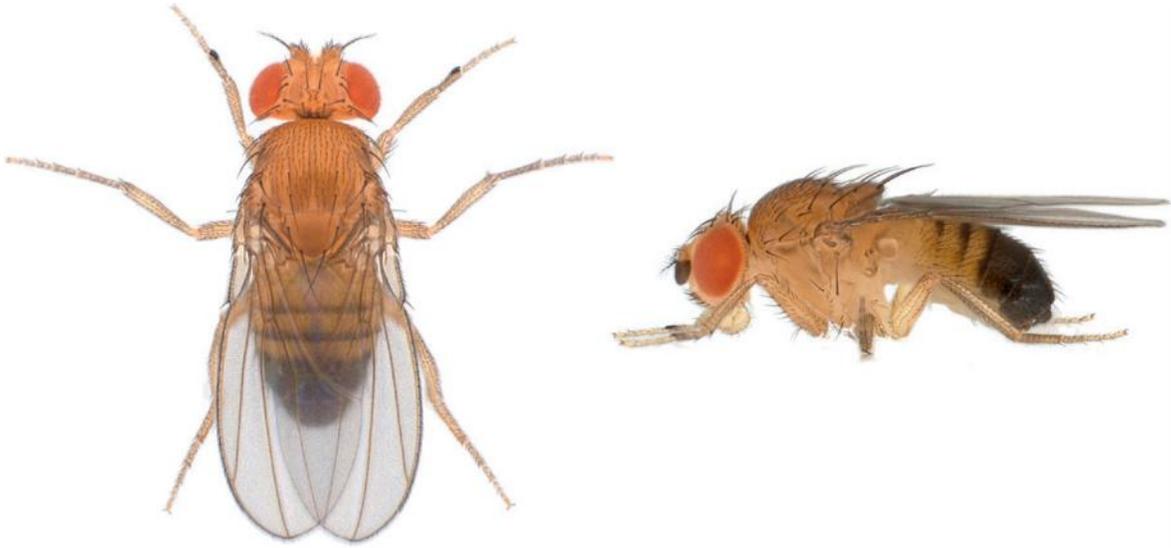
100%

Expressivity variation



Similarity

None



Moiré

Mé



Flybase ID: FBgn0002704

Chromosome: 3L

Cytogenetic location: 64C12-65E1

Recombination map: 3-19.2

Sequence location: N/A

Description

Compound eyes have a shimmering pigmentation pattern
Pseudopupil surrounded by six ill-defined dark markings changing position with the observation angle

Allele information

*Mé*¹ shown, dominant marker on TM1

Temperature dependence

None

Age dependence

Difficult to score at eclosion, becomes obvious after a day

Penetrance

100%

Expressivity variation

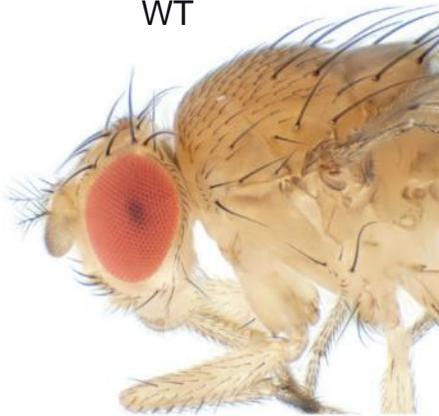


Similarity

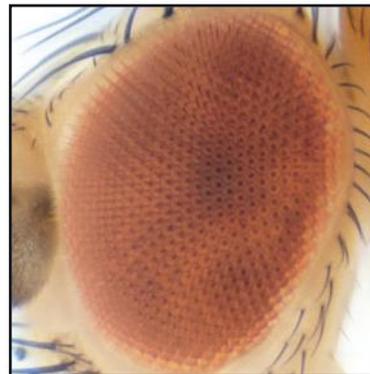
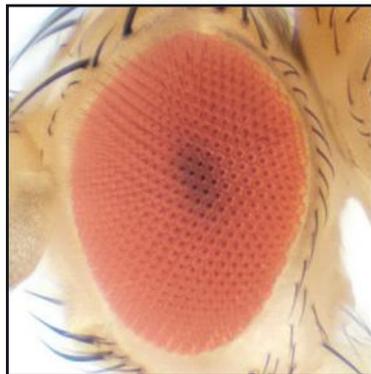
None



WT



M61+



pink

p



Flybase ID: FBgn0086679

Chromosome: 3R

Cytogenetic location: 85A6

Recombination map: 3-48.0

Sequence location: 3R:4,486,625..4,489,607 [-]

Description

Compound eyes dull red with faint pseudopupil

Allele information

*p*¹ shown

p^p recessive marker on TM3

Temperature dependence

None

Age dependence

Pink at eclosion turning to dull red within a few days

Pseudopupil absent at eclosion becoming faintly visible within few days

Penetrance

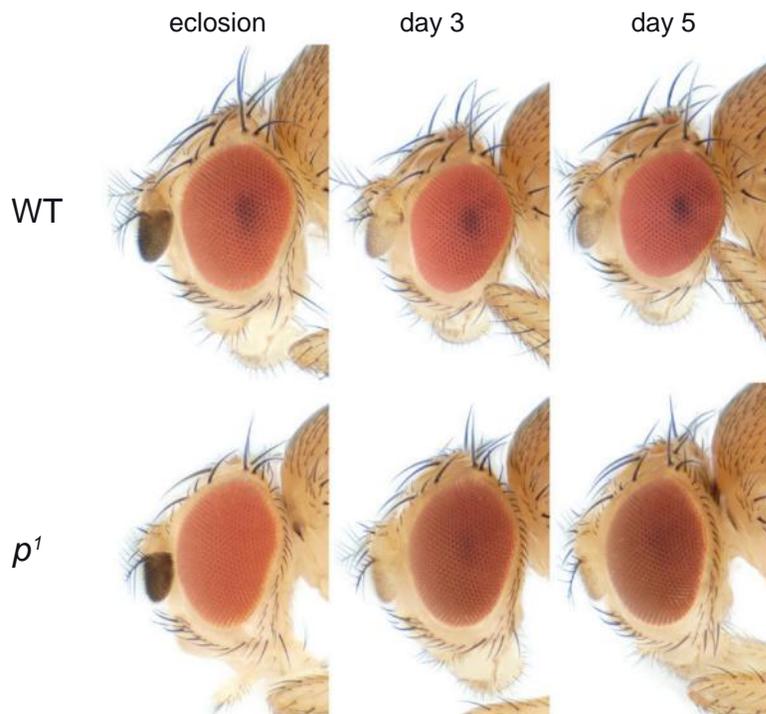
100%

Expressivity variation



Similarity

Hue of compound eye not strikingly different from that of *claret*, *garnet*, *purple*, or *rosy*



purple

pr



Flybase ID: FBgn0003141

Chromosome: 2L

Cytogenetic location: 38B3

Recombination map: 2-54.5

Sequence location: 2L:20,073,719..20,075,467 [-]

Description

Compound eyes reddish purple, lacking pseudopupil

Allele information

*pr*¹ shown

pr^P recessive marker on TM3

Temperature dependence

None

Age dependence

None

Penetrance

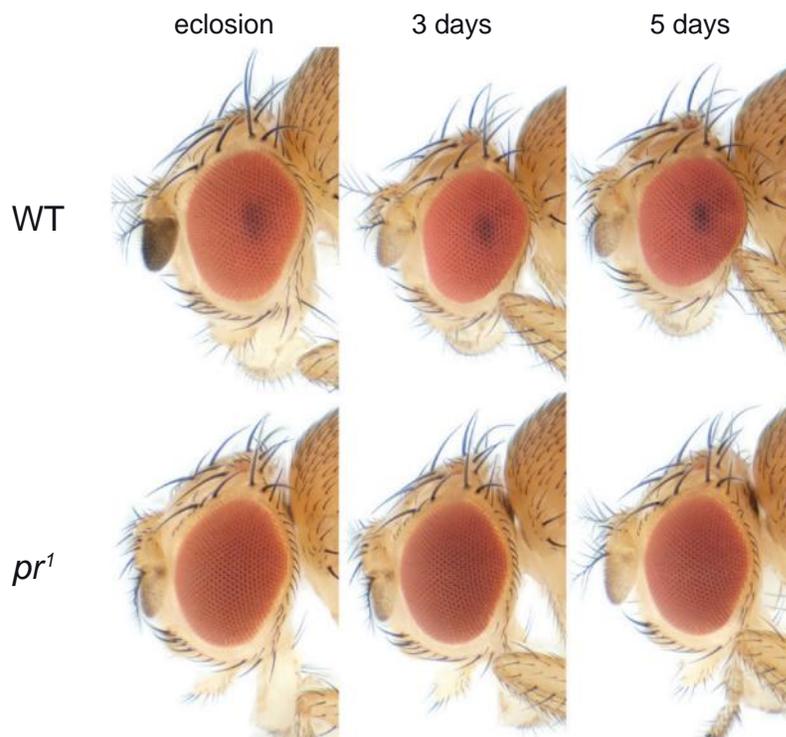
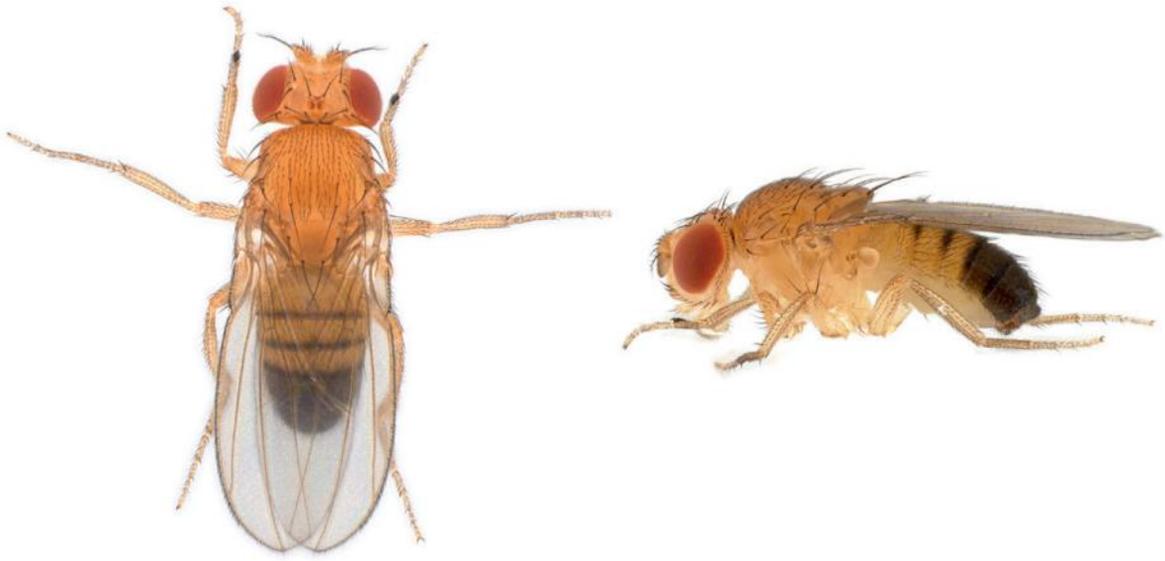
100%

Expressivity variation



Similarity

Hue of compound eye not strikingly different from that of *claret*, *garnet*, *pink*, or *rosy*



rosy

ry



Flybase ID: FBgn0003308

Chromosome: 3R

Cytogenetic location: 87D9

Recombination map: 3-52.0

Sequence location: 3R:8,858,259..8,863,748 [+]

Description

Compound eyes reddish brown

Allele information

*ry*¹ shown

*ry*² recessive marker on MRS and MKRS

Temperature dependence

None

Age dependence

Lighter than WT at eclosion, darkens significantly with age

Penetrance

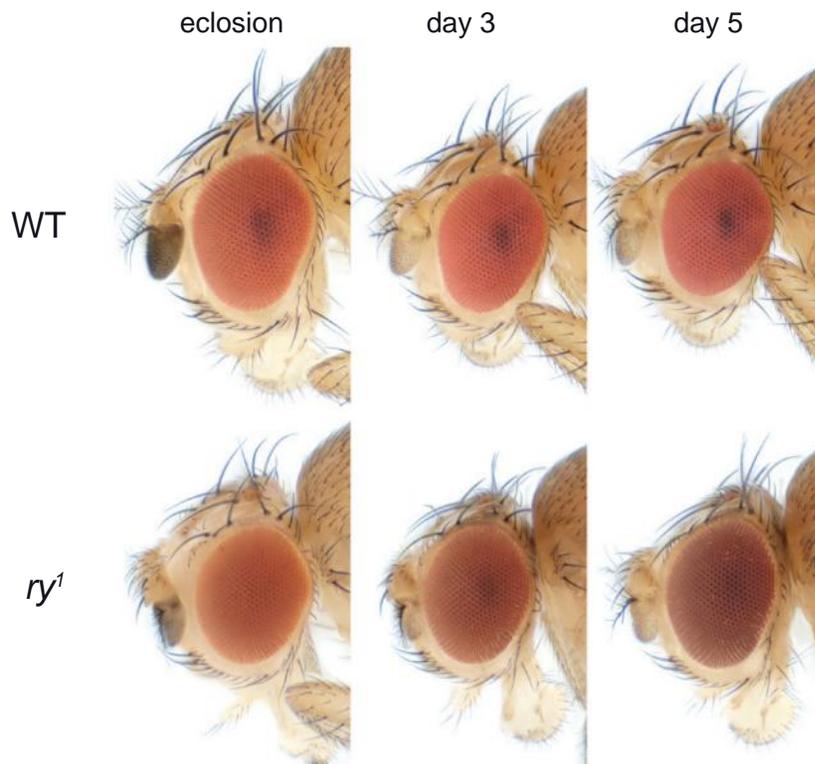
100%

Expressivity variation



Similarity

Hue of compound eye not strikingly different from that of *claret*, *garnet*, *pink*, or *purple*



sepia

se



Flybase ID: FBgn0086348

Chromosome: 3L

Cytogenetic location: 66D5

Recombination map: 3-26.0

Sequence location: 3L:8,513,652..8,514,589 [+]

Description

Compound eyes dark brown to almost black

Allele information

*se*¹ shown

Temperature dependence

None

Age dependence

Dark brown at eclosion to almost black within few days

Penetrance

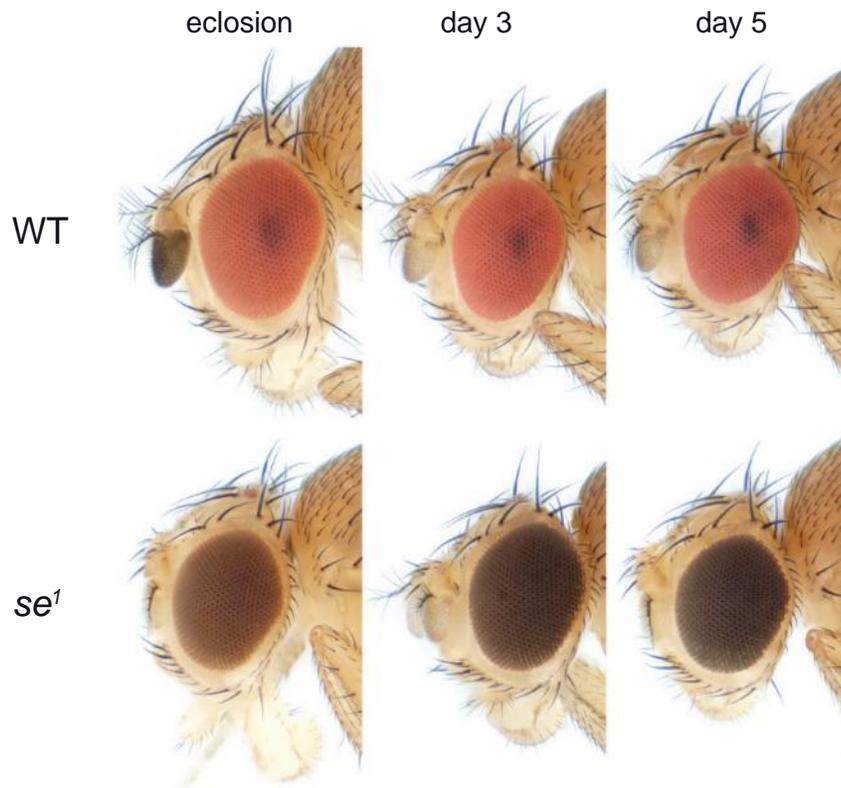
100%

Expressivity variation



Similarity

Henna: lighter brown, pseudopupil visible at eclosion



scarlet

st



Flybase ID: FBgn0003515

Chromosome: 3L

Cytogenetic location: 73A3

Recombination map: 3-44.0

Sequence location: 3L:16,490,751..16,493,563 [+]

Description

Compound eyes bright red, pseudopupil fainter than in WT
Ocelli colorless

Allele information

*st*¹ shown, recessive marker on TM8 and TM9

Temperature dependence

None

Age dependence

Darkens slightly with age, pseudopupil becomes more visible with age

Penetrance

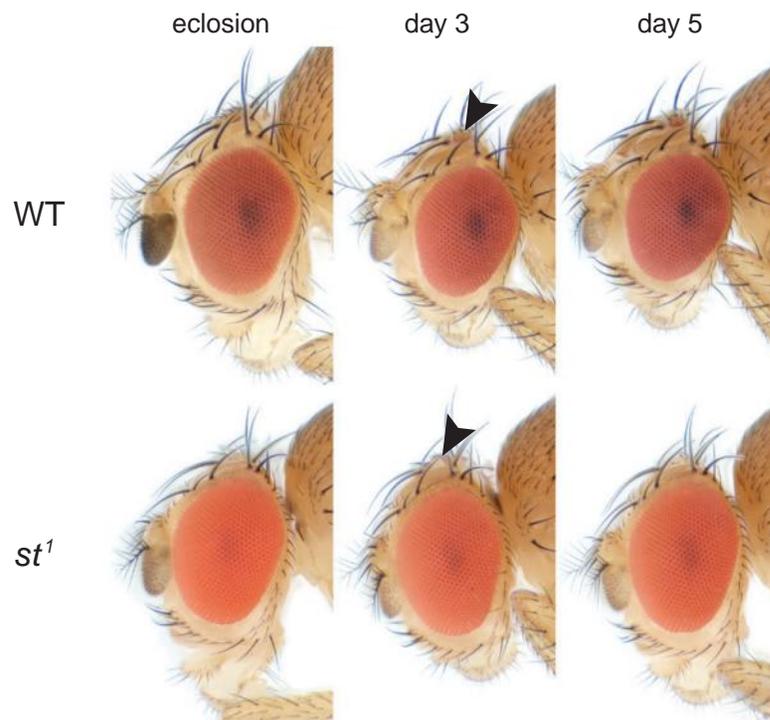
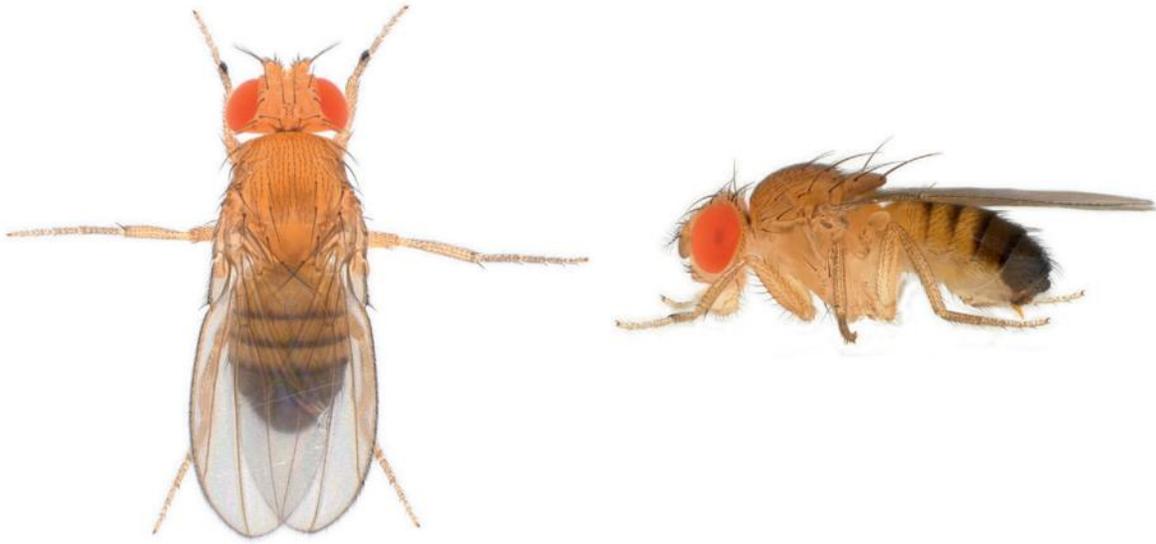
100%

Expressivity variation



Similarity

Indistinguishable from *cinnabar* and *vermillion*
Results in white eyes when combined with *brown*
Easy to score against WT



vermillion

v



Flybase ID: FBgn0003965

Chromosome: X

Cytogenetic location: 9F11

Recombination map: 1-33.0

Sequence location: X:10,818,005..10,819,664 [+]

Description

Compound eyes bright red, pseudopupil fainter than in WT
Ocelli colorless

Allele information

*v*¹ shown

v^{Of} recessive marker on FM7a and FM7c

Temperature dependence

None

Age dependence

Darkens slightly with age, pseudopupil becomes more visible with age

Penetrance

100%

Expressivity variation

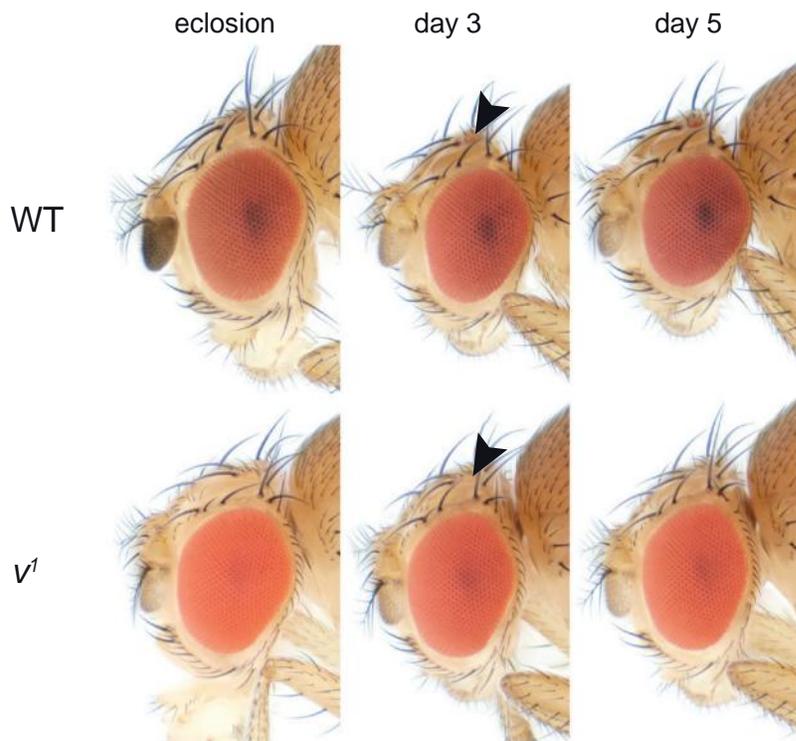
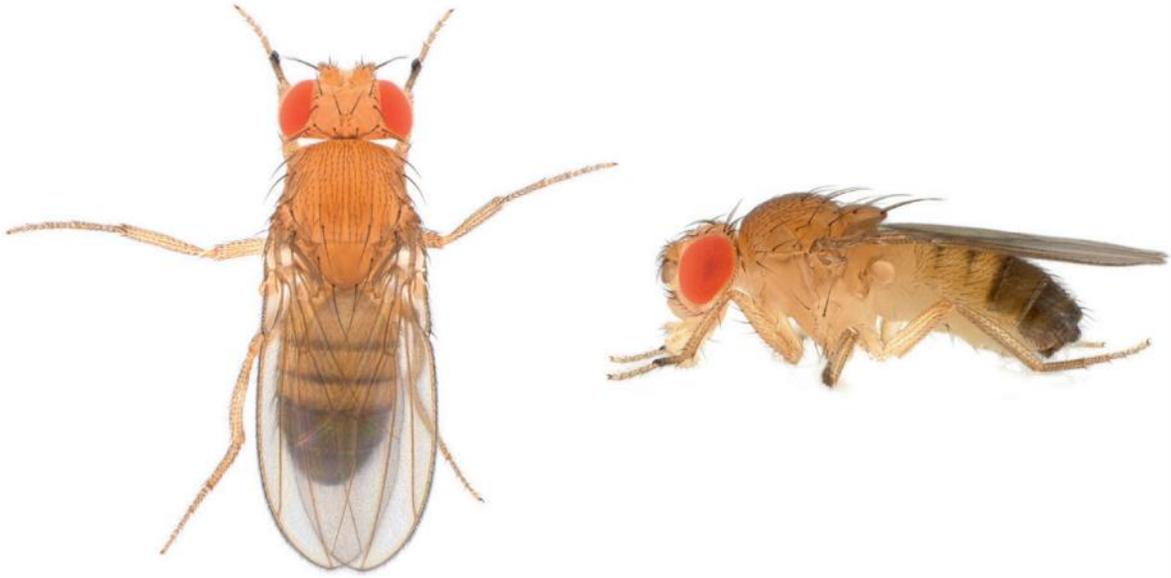


Similarity

Indistinguishable from *cinnabar* and *scarlet*

Results in white eyes when combined with *brown*

Easy to score against WT



white

w**Flybase ID:** FBgn0003996**Chromosome:** X**Cytogenetic location:** 3B6**Recombination map:** 1-1.5**Sequence location:** X:2,684,632..2,690,499 [-]

Description

Compound eyes and ocelli orange to entirely white

Allele information

*w*¹¹¹⁸ shown

w^a detail shown, recessive marker on FM7a and FM7c

*w*¹ recessive marker on FM7i

A modified version of the *white* locus, *mini-white*, is often used as a marker of transformation for transgenesis with mobile elements (e.g., P{w+}) in a *white* background. The extent of the red pigmentation rescue varies in a dose-dependent and position-dependent manner

Temperature dependence

None

Age dependence

None

Penetrance

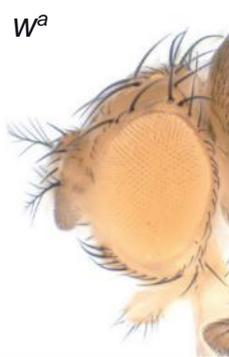
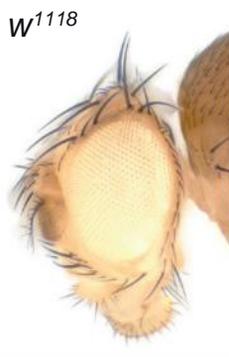
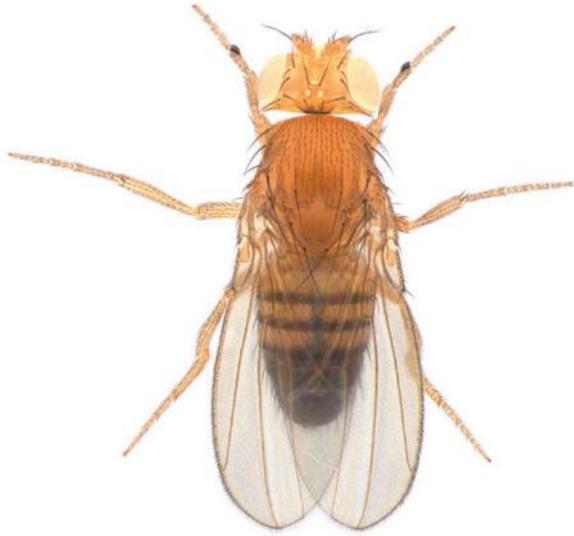
100%

Expressivity variation

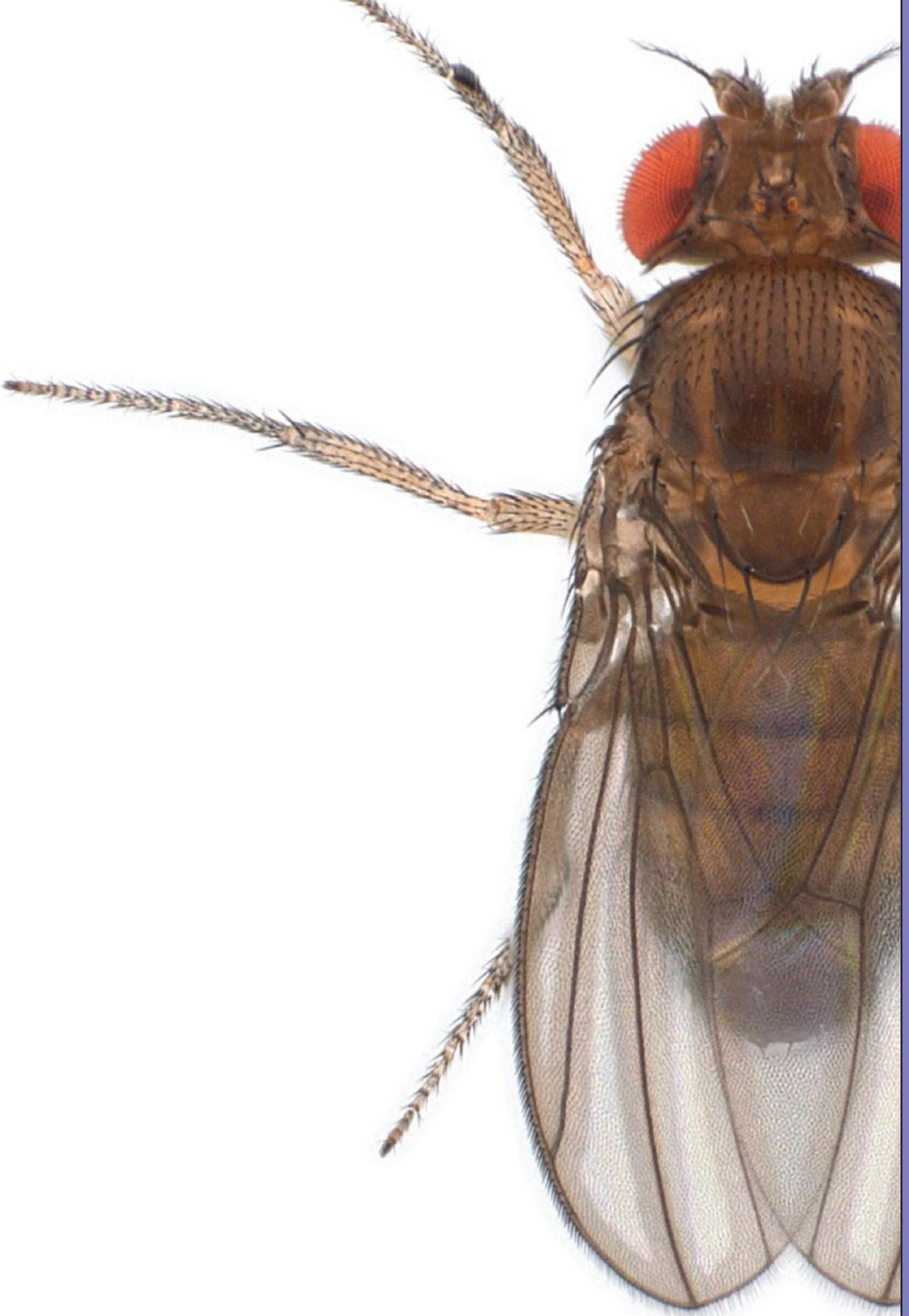


Similarity

White eye color can also result from *brown* interaction with *cinnabar*, *scarlet*, or *vermillion*



Body markers



Black cells

Bc



Flybase ID: FBgn0261382
Chromosome: 2R
Cytogenetic location: 54F6
Recombination map: 2-80.6
Sequence location: N/A

Description

Integument of larva, and to a lesser extent pupa and adult, displaying dark speckles (crystal cells)

Allele information

*Bc*¹ shown, unique allele

Temperature dependence

*Bc*¹/+ larvae have fewer speckles when raised at elevated temperatures

Age dependence

Speckles most numerous in the third instar larvae

Penetrance

100%

Expressivity variation

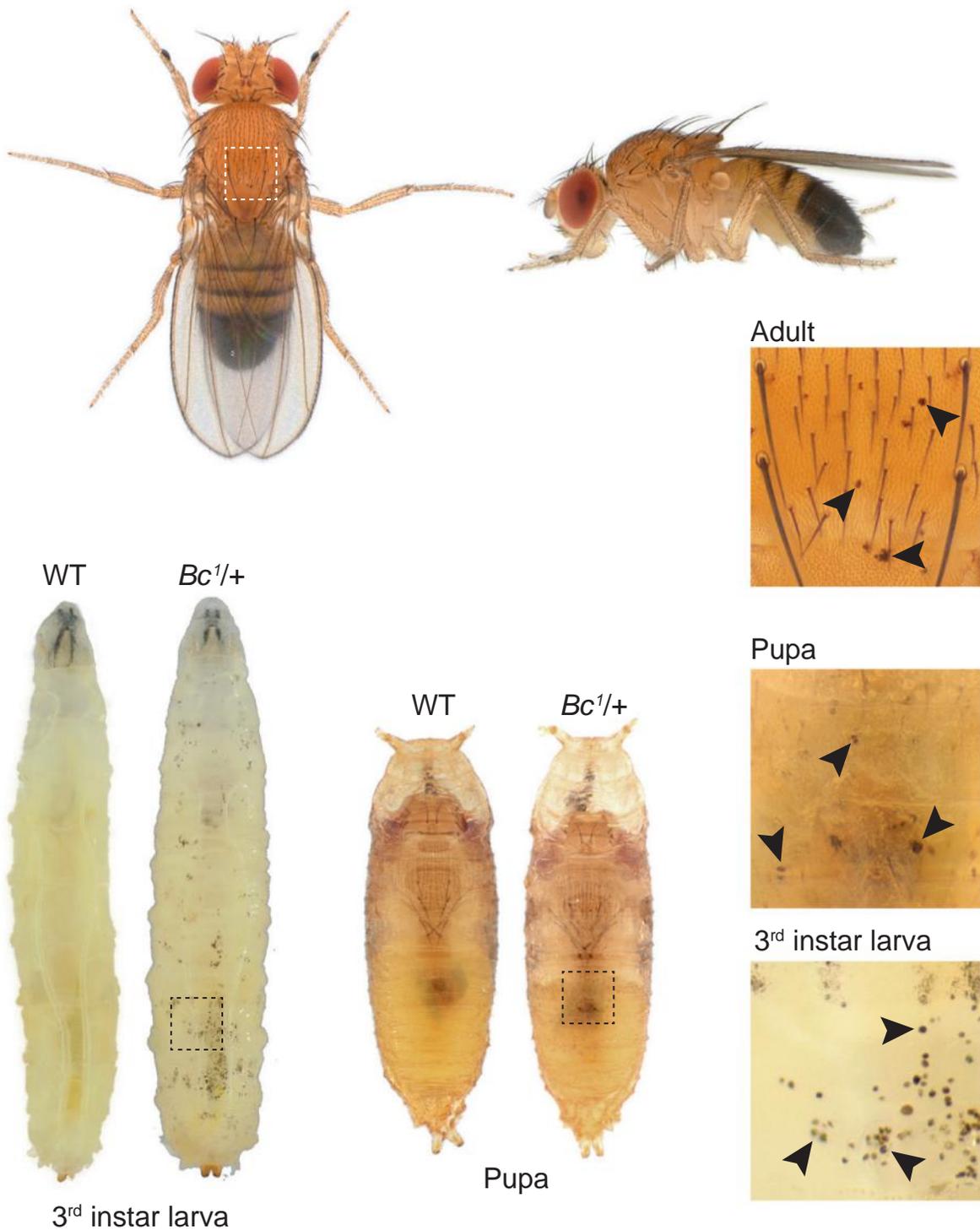


Similarity

None

Easy to score in larvae, pupae, and newly eclosed adults

Difficult to score in *ebony* background adults



ebony

e



Flybase ID: FBgn0000527

Chromosome: 3R

Cytogenetic location: 93C7-D1

Recombination map: 3-70.7

Sequence location: 3R:17,055,561..17,062,900 [-]

Description

Cuticle pigmentation much darker than WT

Darkening roughly homogeneous but reveals pigmentation patterns on thorax in some alleles (trident)

Wing pigmentation darker anterior to L5 vein

Allele information

e¹ shown, recessive marker on TM3, TM6, TM6B, TM6C, TM8, and TM9

e^S shown, recessive marker on TM2

Temperature dependence

None

Age dependence

Already obvious at emergence, darkening further with age

Dark pigmentation spreads around wing veins over the next 72 h following eclosion

Penetrance

100%

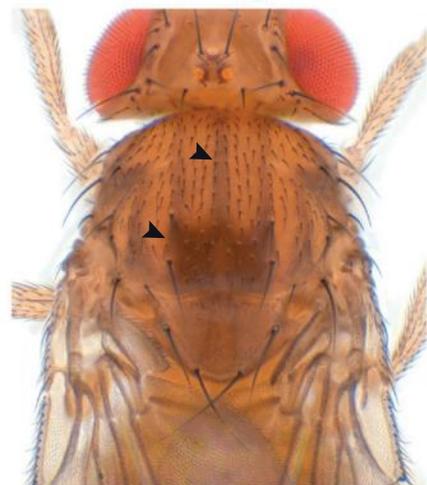
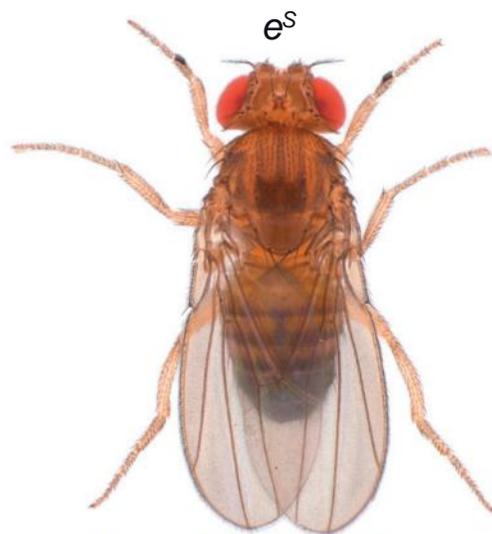
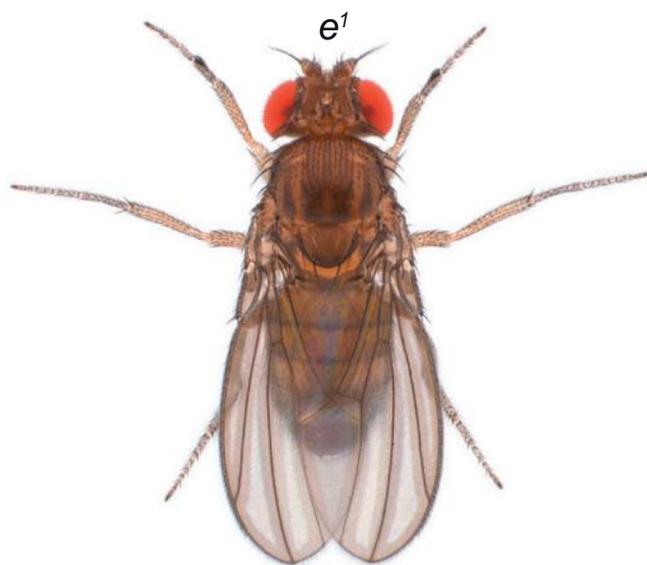
Expressivity variation



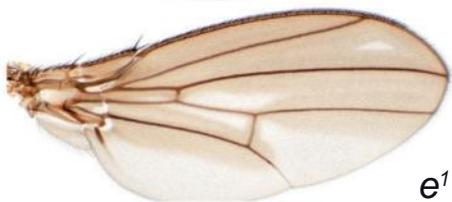
Similarity

Easy to score

Several other pigmentation mutants are also dark



day 3



day 2



day 1



pentagon

ptg



Flybase ID: FBgn0003158
Chromosome: X
Cytogenetic location: 8A1-5
Recombination map: 1-23.2
Sequence location: N/A

Description

Darker pigmentation pattern resembling a trident on scutum
Darkly pigmented scutellum

Allele information

*ptg*¹ shown, recessive marker on FM7i

Temperature dependence

Stronger at 19°C

Age dependence

Difficult to score in young flies, becomes more visible with age

Penetrance

100%

Expressivity variation



Similarity

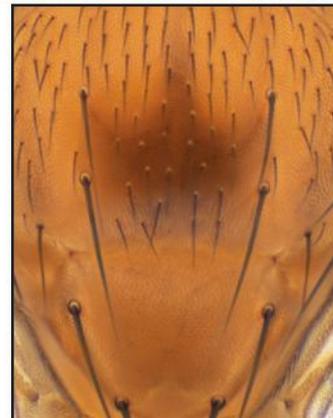
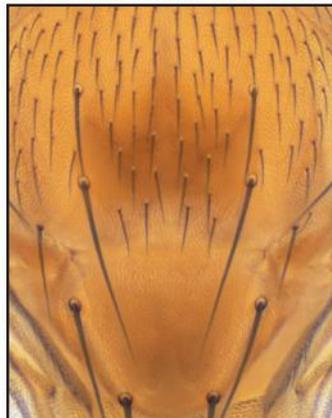
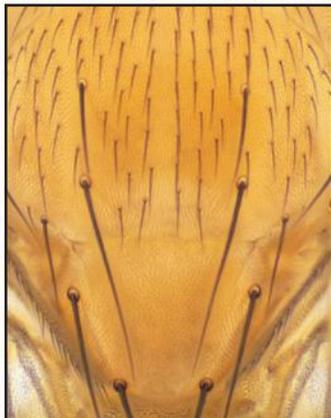
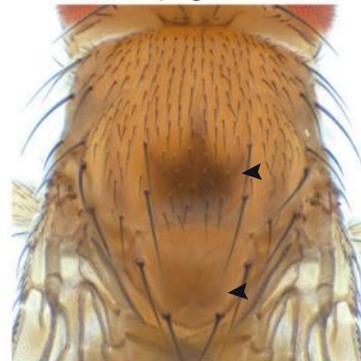
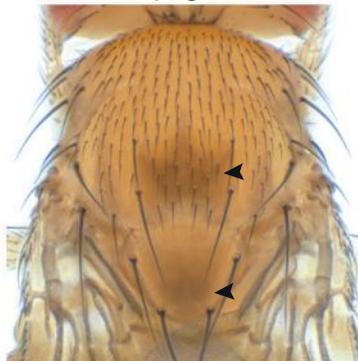
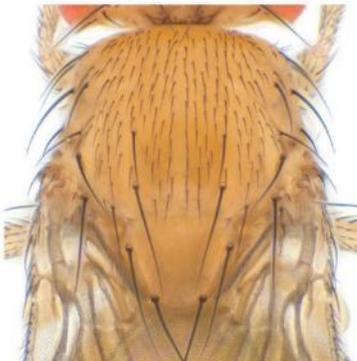
Trident pattern appears in some natural populations, in some *ebony* semidominant alleles and in some genetic backgrounds



WT

eclosion
ptg¹

day 3
ptg¹



speck

sp



Flybase ID: FBgn0003466

Chromosome: 2R

Cytogenetic location: 60C1-2

Recombination map: 2-107.0

Sequence location: N/A

Description

Body color darker than WT with dark specks on axils of wings

Pupae darker than WT (not shown)

Allele information

*sp*¹ shown

*sp*² darker than *sp*¹, recessive marker on SM1, SM5, SM6a, and SM6b balancers

Temperature dependence

None

Age dependence

None

Penetrance

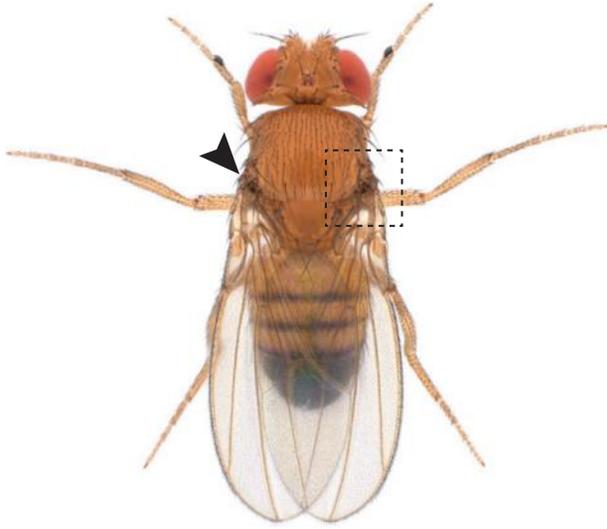
100%

Expressivity variation

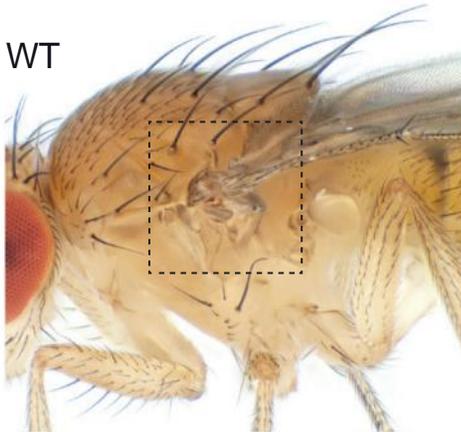


Similarity

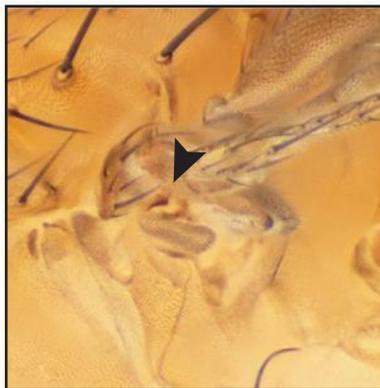
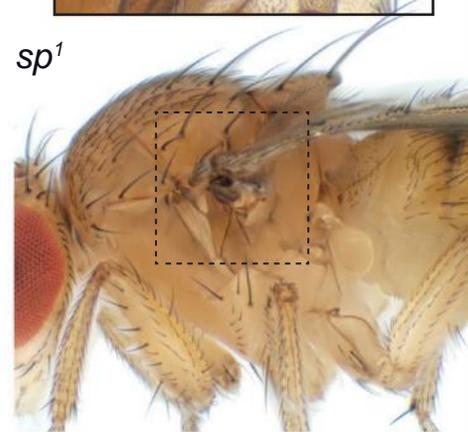
None



WT



*sp*¹



Tubby

Tb



Flybase ID: FBgn0243586

Chromosome: 3R

Cytogenetic location: 97C3

Recombination map: 3-90.6

Sequence location: 3R:22,482,168...22,483,253 [+]

Description

Larvae, pupae, and adults short and stout

Allele information

*Tb*¹ shown, dominant marker on several variants of TM balancers. Homozygous viable, phenotype same as *Tb*/+

Temperature dependence

None

Age dependence

None

Penetrance

100%

Expressivity variation



Similarity

Easy to score in larvae and pupae, much less obvious in adults

yellow

y



Flybase ID: FBgn0004034
Chromosome: X
Cytogenetic location: 1A5
Recombination map: 1-0.0
Sequence location: X:250,542..255,278 [+]

Description

Cuticle pigmentation much paler than WT, yellowish, either uniformly (type-1 alleles) or with hairs and bristles of WT color (type-2 alleles)

Allele information

y^1 shown, type-1 allele

y^2 details shown, type-2 allele

y^{31d} shown on balancer plate 4, type-2 allele, recessive marker on FM6, FM7a, FM7c, and FM7d

y^{93j} , type-2 allele, recessive marker on FM7i

Temperature dependence

None

Age dependence

None

Penetrance

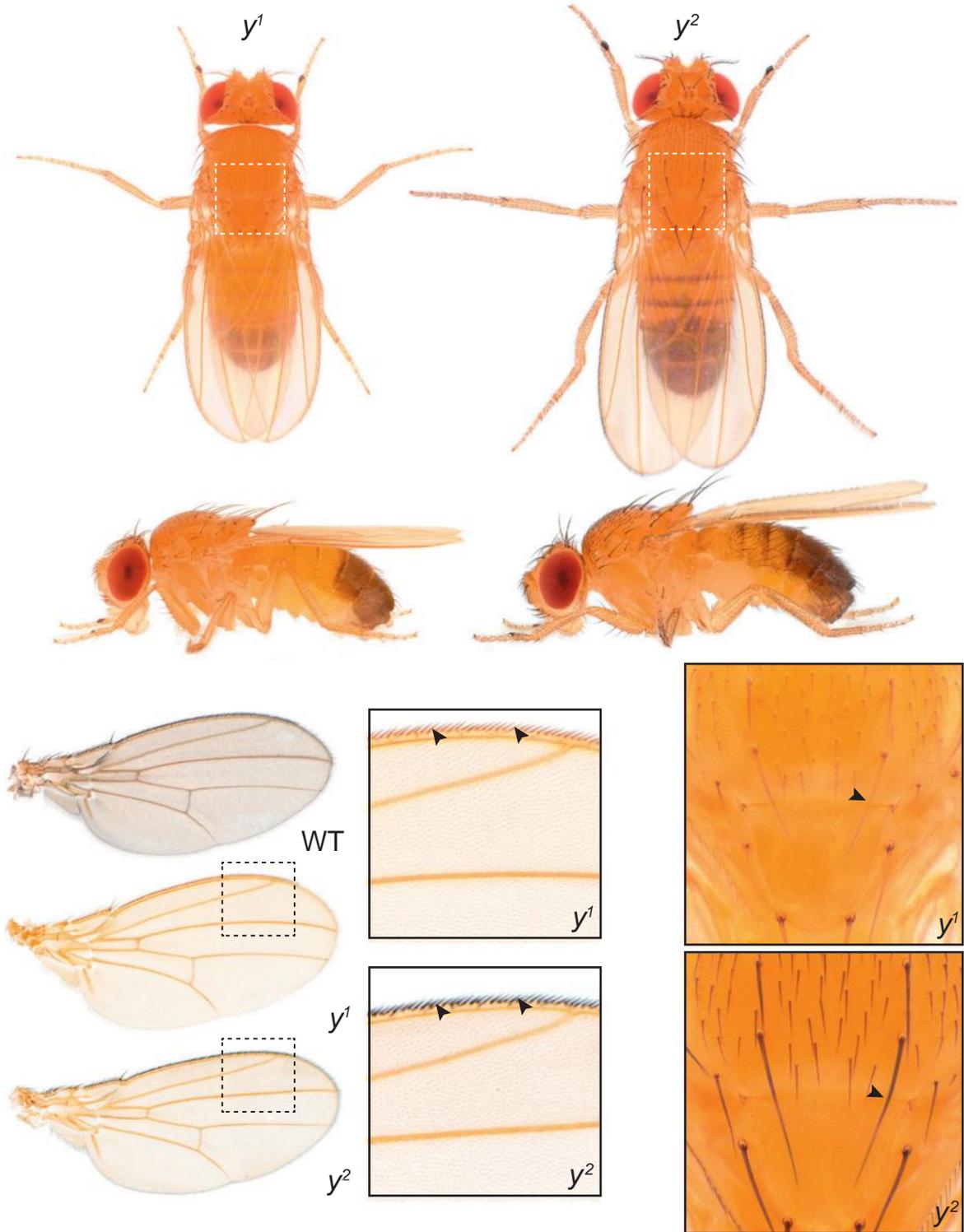
100%

Expressivity variation



Similarity

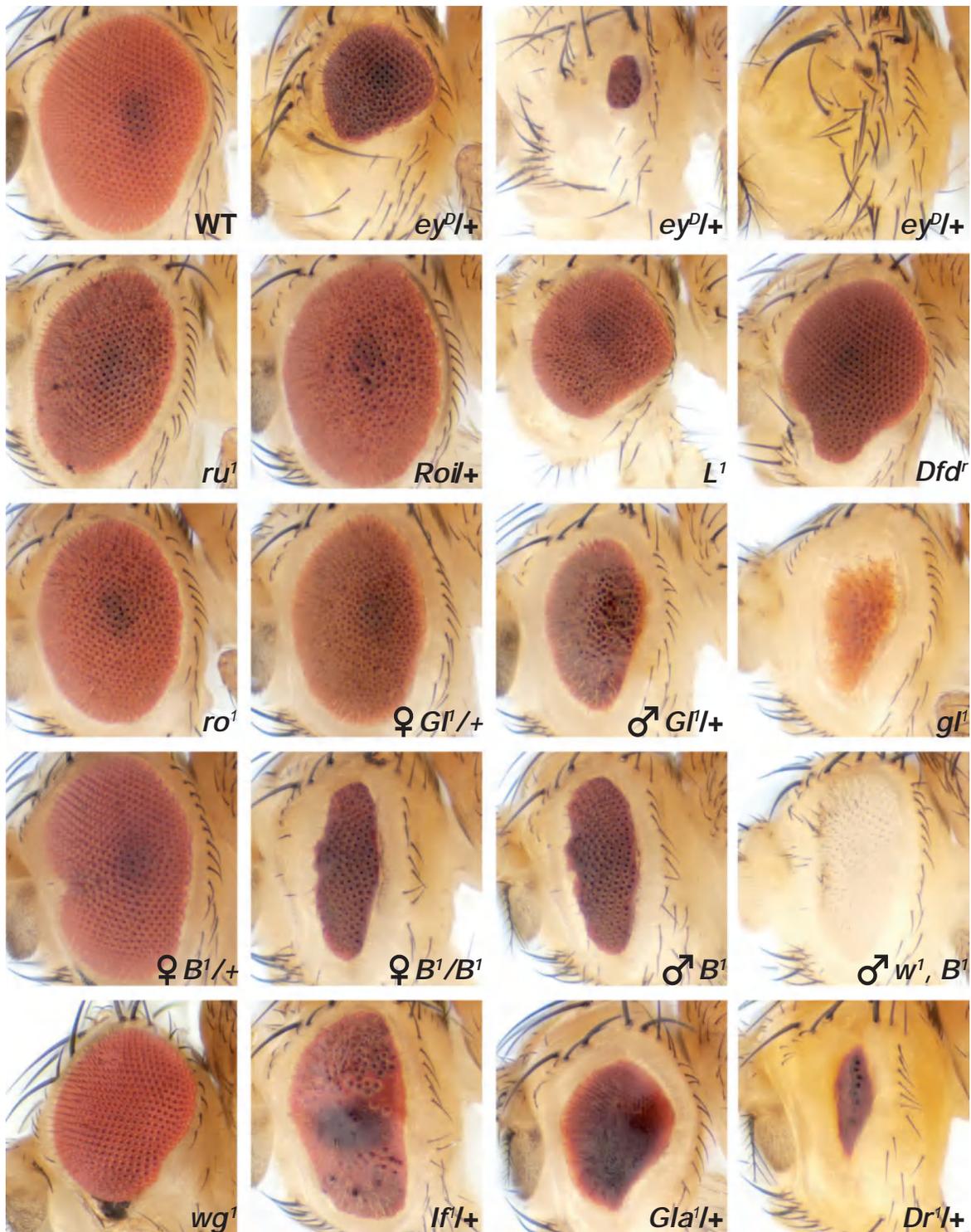
tan: (not covered in this book)



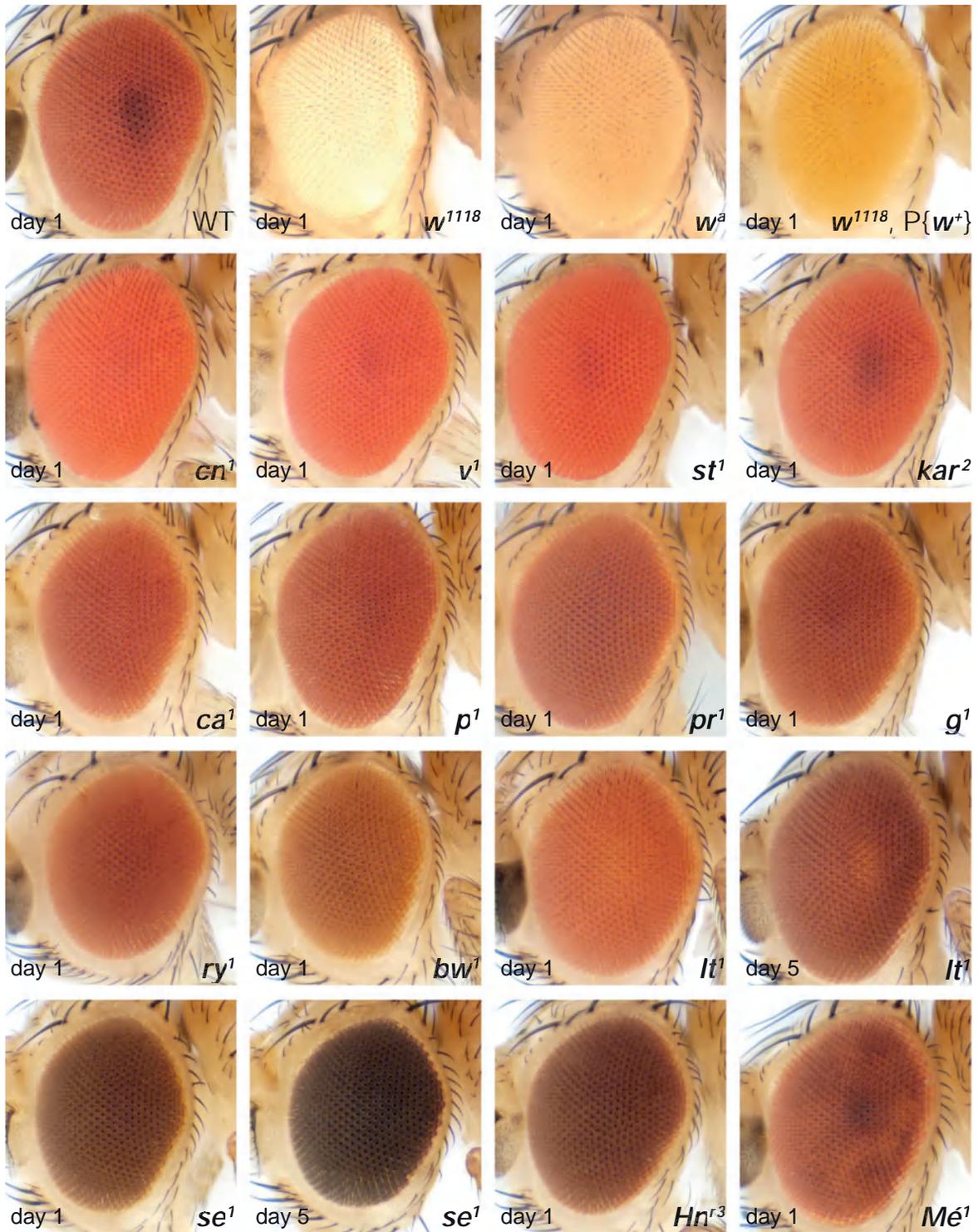
Thorax



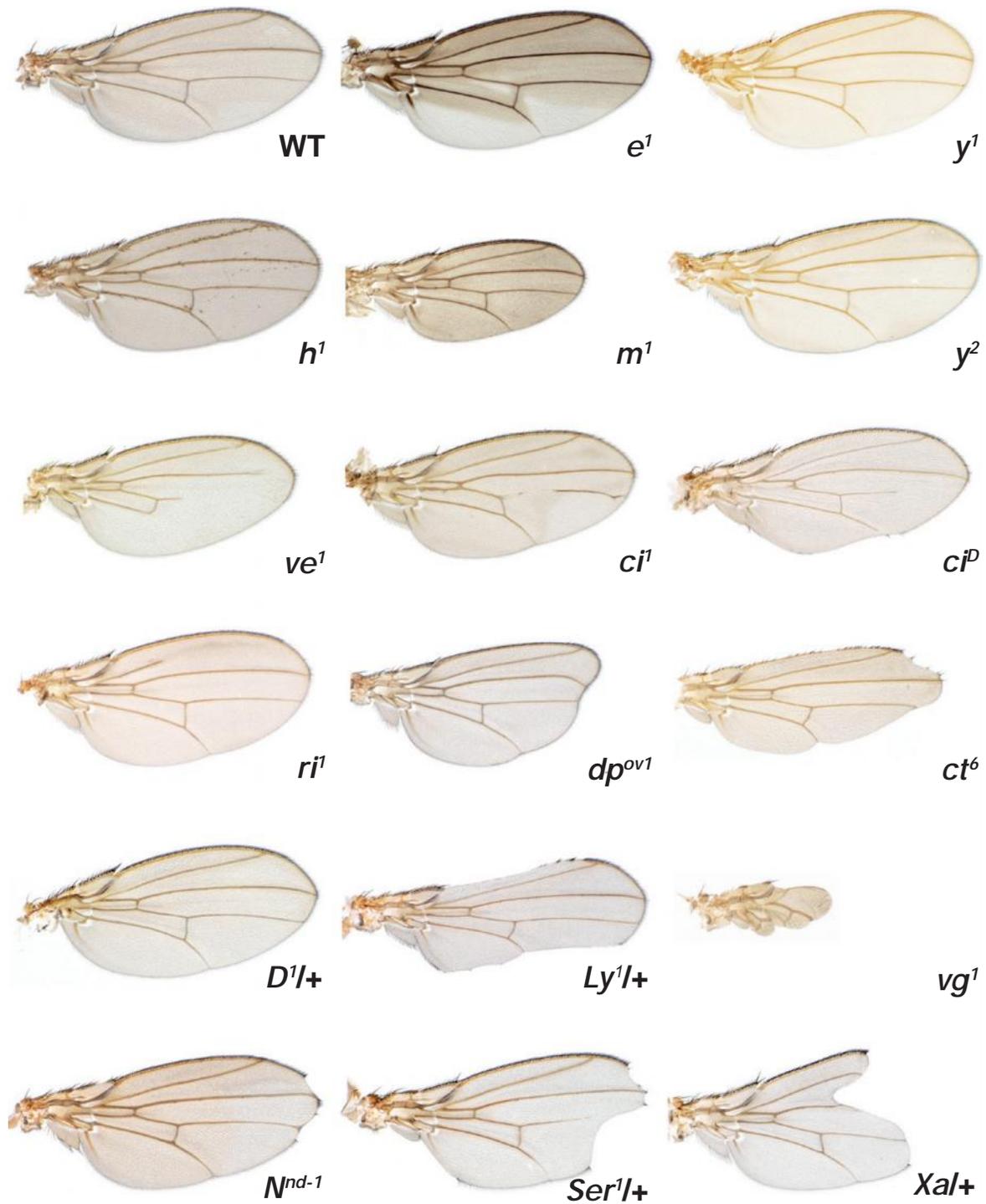
Eye shape



Eye color



Wings



Balancer chromosomes



First Multiple 6

FM6



Flybase ID: FBba0000003

Chromosome: X

Genotype

In(1)FM6 y^{31d} sc^8 dm^1 B^1

Dominant marker

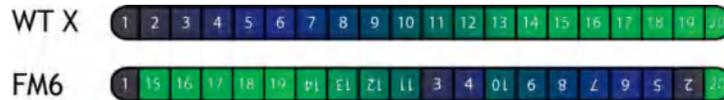
B^1

Recessive markers

y^{31d} , sc^8 , dm^1

Cytology

1Lt-1B2 | (20B-20B) | 15E-20A | 15D11F4 | (4E-4E) | 3C-4D7 |
11F2-4F | 3C-1B3 | 20D1-1Rt



First Multiple 7a

FM7a



Flybase ID: FBba0000007

Chromosome: X

Genotype

$\text{In}(1)\text{FM7 } y^{31d} \text{ } sc^8 \text{ } w^a \text{ } v^{Of} \text{ } B^1$

Dominant marker

B^1

Recessive markers

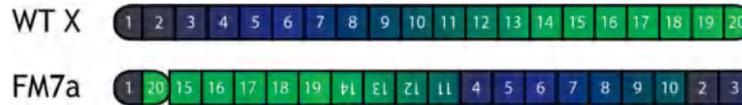
$y^{31d}, sc^8, w^a, v^{Of}$

Cytology

1Lt-1B2 | 20F-20A | 15D-20A | 15D-11F4 | 4E1-11F2 |
4D7-1B3 | 1Rt

Notes

Males viable and fertile





First Multiple 7c

FM7c

Flybase ID: FBba0000009

Chromosome: X

Genotype

In(1)FM7 *y^{31d} sc⁸ w^a sn^{X2} v^{Of} g⁴ B¹*

Dominant marker

B¹

Recessive markers

y^{31d}, sc⁸, w^a, sn^{X2}, v^{Of}, g⁴

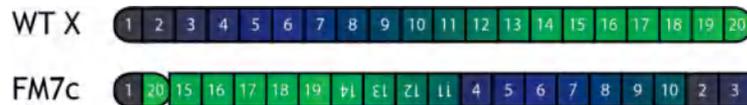
Cytology

1Lt-1B2 | 20F-20A | 15D-20A | 15D-11F4 | 4E1-11F2 |
4D7-1B3 | 1Rt

Notes

Males viable and fertile

Homozygous females viable but sterile (due to *sn^{X2}*)



First Multiple 7d

FM7d



Flybase ID: FBba0000216

Chromosome: X

Genotype

In(1)FM7 *y*^{31d} *sc*⁸ *B*¹

Dominant marker

*B*¹

Recessive markers

y^{31d}, *sc*⁸

Cytology

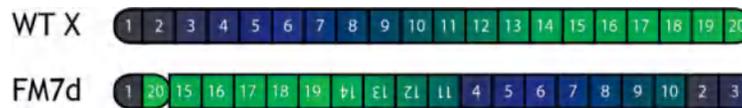
1Lt-1B2 | 20F-20A | 15D-20A | 15D-11F4 | 4E1-11F2 |
4D7-1B3 | 1Rt

Notes

Derived from FM7a

Males and heterozygous females viable and fertile

Most FM7d variants carry *oc*¹ which is female sterile



First Multiple 7i

FM7i



Flybase ID: FBba0000226

Chromosome: X

Genotype

In(1)FM7 *y^{93j} sc⁸ w¹ oc¹ ptg¹ B¹*

Dominant marker

B¹

Recessive markers

y^{93j}, sc⁸, w¹, oc¹, ptg¹

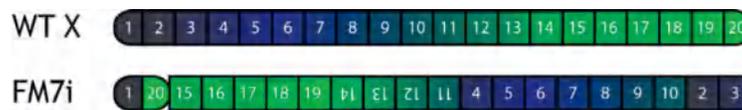
Cytology

1Lt-1B2 | 20F-20A | 15D-20A | 15D-11F4 | 4E1-11F2 |
4D7-1B3 | 1Rt

Notes

Derived from FM7a

Males viable and fertile

Most FM7i variants carry *oc¹* which is female sterile

Curly of Oster

CyO



Flybase ID: FBba0000025

Chromosome: 2

Genotype

 $\text{In}(2\text{LR})\text{O } \text{Cy}^1 \text{ dp}^M \text{ pr}^1 \text{ cn}^2$

Dominant marker

 Cy^1

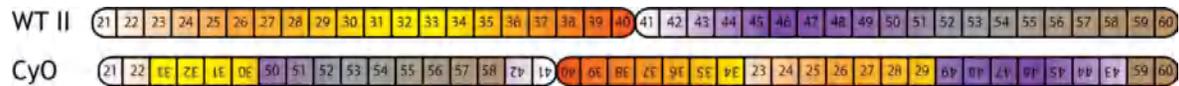
Recessive markers

 $\text{dp}^M, \text{pr}^1, \text{cn}^2$

Cytology

2Lt-22D1 | 33F5-30F | 50D1-58A4 | 42A2-34A1 | 22D2-30E |
50C10-42A3 | 58B1-2Rt

Notes

 cn^2 is a weak allele of *cinnabar*, cn^1/cn^2 is distinguishable from wild-type in young flies



Second Multiple 1

SM1

Flybase ID: FBba0000037

Chromosome: 2

Genotype

In(2LR)SM1 *al*¹ *Cy*¹ *cn*² *sp*²

Dominant marker

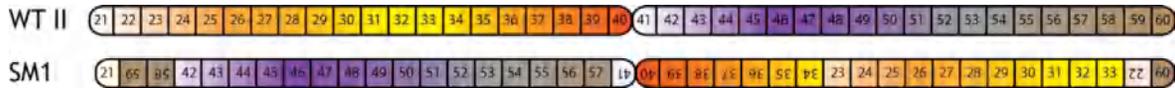
*Cy*¹

Recessive markers

*al*¹, *cn*², *sp*²

Cytology

2Lt-22A3 | 60B-58B1 | 42A3-58A4 | 42A2-34A1 | 22D2-33F5 |
22D1-22B1 | 60C-2Rt



Second Multiple 5

SM5



Flybase ID: FBba0000038

Chromosome: 2

Genotype

In(2LR)SM5 *al*² *ds*⁵⁵ *Cy*¹ *It*^v *cn*² *sp*²

Dominant marker

*Cy*¹

Recessive markers

*al*², *ds*⁵⁵, *It*^v (temperature sensitive), *cn*², *sp*²

Cytology

2Lt-21D2 | 36C-40F | 29C-22D2 | 34A1-36C | 21D3-22A3 |
 60B-58B1 | 42A3-42D | 42D-42A3 | 58B1-58F | 53C-42D |
 53C-58A4 | 42A2-40F | 29E-33F5 | 22D1-22B1 | 60C-2Rt

Notes

Heterozygotes less viable and less fertile than SM1





Second Multiple 6a

SM6a

Flybase ID: FBba0000039

Chromosome: 2

Genotype

In(2LR)SM6 *al*² *Cy*¹ *dp*^{lvi} *cn*^{2P} *sp*²

Dominant marker

*Cy*¹

Recessive markers

*al*², *dp*^{lvi}, *cn*^{2P} (amorphic derivative of *cn*²), *sp*²

Cytology

2Lt-22A3 | 60B-58B1 | 42A3-50C10 | 30E-22D | 34A1-42A2 |
58A4-50D1 | 30F-33F5 | 22D1-22B1 | 60C-2Rt



Second Multiple 6b

SM6b

**Flybase ID:** FBba0000040**Chromosome:** 2

Genotype

 $\text{In}(2\text{LR})\text{SM6 } a^2 \text{ Cy}^1 \text{ dp}^{M1} \text{ Roi}^1 \text{ cn}^{2P} \text{ sp}^2$

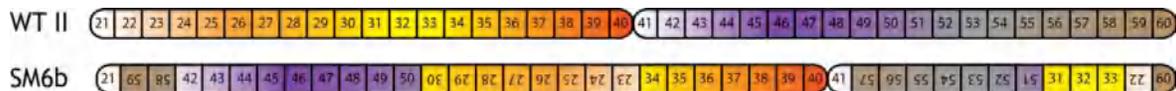
Dominant marker

 $\text{Cy}^1 \text{ Roi}^1$

Recessive markers

 $a^2, \text{ dp}^{M1}, \text{ cn}^{2P}$ (amorphic derivative of cn^2), sp^2

Cytology

2Lt-22A3 | 60B-58B1 | 42A3-50C10 | 30E-22D | 34A1-42A2 |
58A4-50D1 | 30F-33F5 | 22D1-22B1 | 60C-2Rt

Translocation

CyO-TM9

T(2;3)CyO-TM9



Flybase ID: FBab0023073
Chromosome: 2, 3

Genotype

T(2;3)CyO-TM9, CyO:TM9, *cn² dp^M e¹ l(3)DTS4¹ pr¹ st¹ th¹*

Dominant marker

Cy¹, Sb¹, l(3)DTS4¹ (dominant temperature sensitive allele: lethal at 29°C during larval development)

Recessive markers

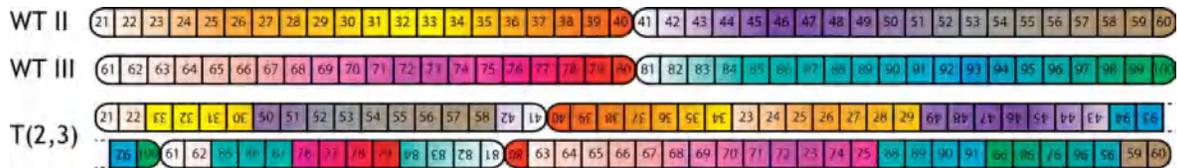
cn², dp^M, e¹, pr¹, st¹, th¹

Cytology

2Lt-22D1 | 33F5-30F | 50D1-58A4 | 42A2-34A1 | 22D2-30E
 | 50C10-42A3 | 58B1-59F|94A-92E1|100F3-3Rt; 3Lt-62D2 |
 85A-87A | 76F-80C | 85A-80C | 62D7-76F | 87A-92D1 | 100F2-
 94A|59F - 2Rt

Notes

Multichromosome balancer
 Suppresses crossing over in chromosomes 2 and 3



Minute-Rosy-Stubble

MRS



Flybase ID: FBba0000068

Chromosome: 3

Genotype

$Tp(3;3)MRS M(3)76A^1 ry^2 Sb^1$

Dominant marker

Sb^1

$M(3)76A^1$

Recessive markers

ry^2

Cytology

3Lt-71B2 | 92E-93C | 87F1-92E | 71C2-87E8 | 93C-3Rt

Notes

Minute phenotype nearly undetectable

Effective balancer only for proximal 3L and 3R



Minute-Karmoisin- Rosy-Stubble

MKRS



Flybase ID: FBba0000066
Chromosome: 3

Genotype

Tp(3;3)MRS *M(3)76A¹ kar¹ ry² Sb¹*

Dominant marker

Sb¹
M(3)76A¹

Recessive markers

kar¹, ry²

Cytology

3Lt-71B2 | 92E-93C | 87F1-92E | 71C2-87E8 | 93C-3Rt

Notes

Minute phenotype nearly undetectable
Effective balancer only for proximal 3L and 3R



Third Multiple 1

TM1

**Flybase ID:** FBba0000042**Chromosome:** 3

Genotype

 $\text{In}(3\text{LR})\text{TM1 } \text{M}\acute{\text{e}}^1 \text{ } r\text{i}^1 \text{ } \text{Sb}^{\text{sb}d-1}$

Dominant marker

 $\text{M}\acute{\text{e}}^1$

Recessive markers

 $r\text{i}^1, \text{Sb}^{\text{sb}d-1}$

Cytology

3Lt-63C | 72E1-69E | 91C-97D | 89B-72E2 | 63C-69E | 91C-89B |
97D-3Rt



Third Multiple 2

TM2

Flybase ID: FBba0000062

Chromosome: 3

Genotype

In(3LR) Ubx¹³⁰ emc² Ubx¹³⁰ e^S

Dominant marker

Ubx¹³⁰

Recessive markers

emc², e^S

Cytology

3Lt-61A | 96B-93B | 89D-74 | 61C-74 | 89E-93B | 96A-3Rt



Third Multiple 3

TM3

**Flybase ID:** FBba0000047**Chromosome:** 3

Genotype

 $\text{In}(3\text{LR})\text{TM3 } ri^1 \text{ } vl^{sep} \text{ } p^D \text{ } I(3)89Aa^1 \text{ } Ubx^{bx-34e} \text{ } e^1$

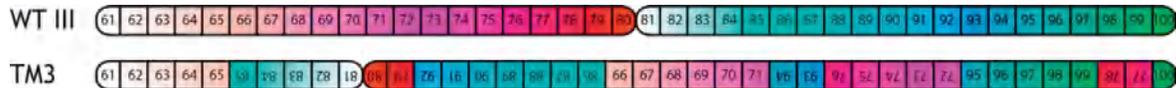
Dominant marker

 Ser^1 , most often with Sb^1

Recessive markers

 ri^1 , vl^{sep} , p^D , Ubx^{bx-34e} , e^1

Cytology

3Lt-65E | 85E-79E | 100C-100F2 | 92D1-85E | 65E-71C | 94D-93A
| 76C-71C | 94F-100C | 79E-76C | 93A-92E1 | 100F3-3Rt



Third Multiple 6

TM6

Flybase ID: FBba0000056

Chromosome: 3

Genotype

In(3LR)TM6 Hn^P ss^{aP88} Ubx^{P15} Ubx^{bx-34e} e¹

Dominant marker

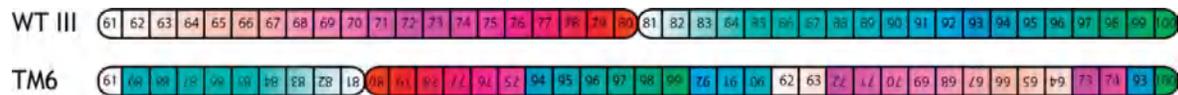
Hn^P, Ubx^{P15}

Recessive markers

ss^{aP88}, Ubx^{bx-34e}, e¹

Cytology

3Lt-61A | 89C2-75C | 94A-100F2 | 92D1-89C4 | 61A2-63B8 |
72E1-63B11 | 72E2-75C | 94A-92E1 | 100F3-3Rt



Third Multiple 6B

TM6B



Flybase ID: FBba0000057

Chromosome: 3

Genotype

In(3LR)TM6B *Hu e*¹

Dominant marker

Hu, most often with *Tb*¹, less often with *D*³

Recessive markers

*e*¹

Cytology

3Lt-61A1 | 87B2-86C8 | 84F2-86C7 | 84B2-84F2 | 84B2-75C |
94A-100F2 | 92D1-87B4 | 61A2-63B8 | 72E1-63B11 | 72E2-75C |
94A-92E1 | 100F3-3Rt





Third Multiple 6C

TM6C

Flybase ID: FBba0000071

Chromosome: 3

Genotype

In(3LR)TM6C *e*¹

Dominant marker

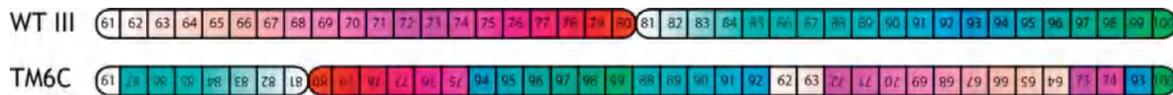
Usually carries *Sb*¹, sometimes carries *Tb*¹

Recessive markers

*e*¹, sometimes also carries *ca*¹

Cytology

3Lt-61A1 | 87B2-75C | 94A-100F2 | 92D1-87B4 | 61A2-63B8 |
72E1-63B9 | 72E2-75C | 94A-92D9 | 100F3-3Rt



Third Multiple 8

TM8



Flybase ID: FBba0000060

Chromosome: 3

Genotype

In(3LR)TM8 *l(3)DTS4¹ th¹ st¹ Sb¹ e¹*

Dominant marker

Sb¹, l(3)DTS4¹ (dominant temperature sensitive allele: lethal at 29°C during larval development)

Recessive markers

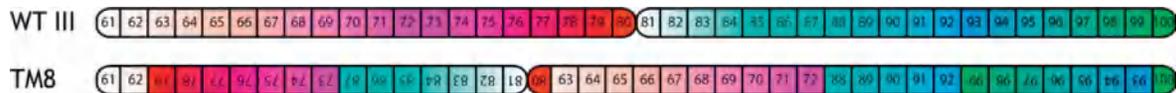
th¹, st¹, e¹

Cytology

3Lt-62D2 | 80C-73F | 87D2-80C | 62D7-73F | 87D3-92D1 | 100F2-92E1 | 100F3-3Rt

Notes

Same markers as TM9 but different breakpoints





Third Multiple 9

TM9

Flybase ID: FBba0000061

Chromosome: 3

Genotype

In(3LR)TM8 I(3)DTS4¹ th¹ st¹ Sb¹ e¹

Dominant marker

Sb¹, I(3)DTS4¹ (dominant temperature sensitive allele: lethal at 29°C during larval development)

Recessive markers

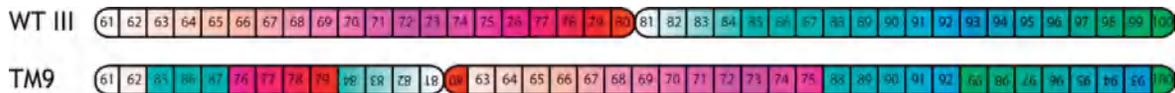
th¹, st¹, e¹

Cytology

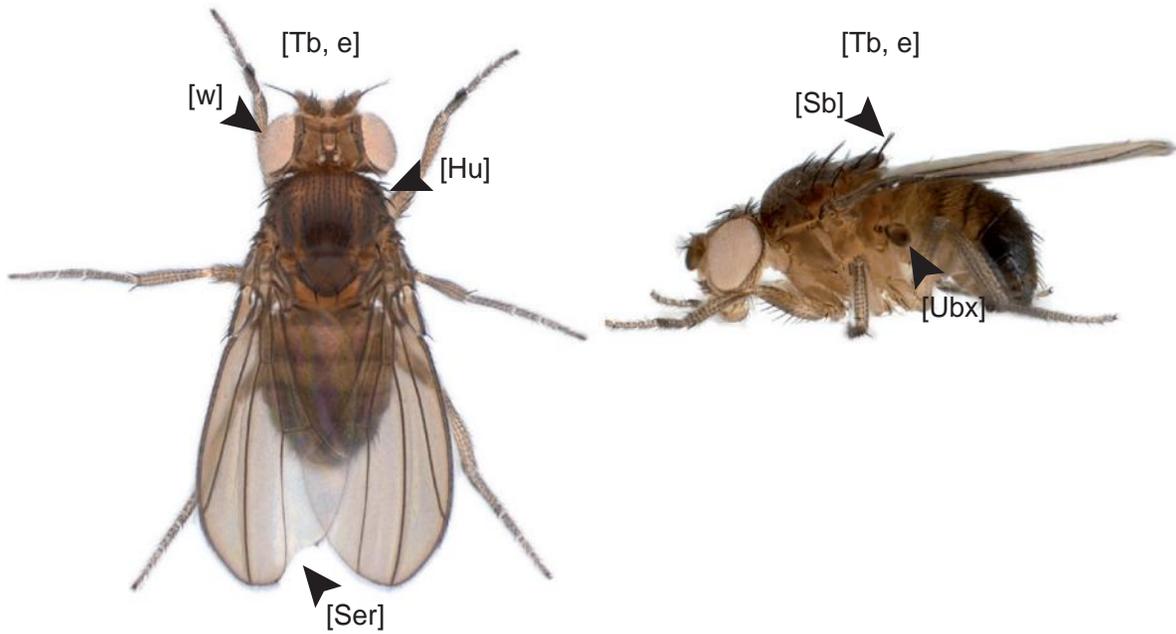
3Lt-62D2 | 85A-87A | 76F-80C | 85A-80C | 62D7-76F | 87A-92D1 | 100F2-92E1 | 100F3-3Rt

Notes

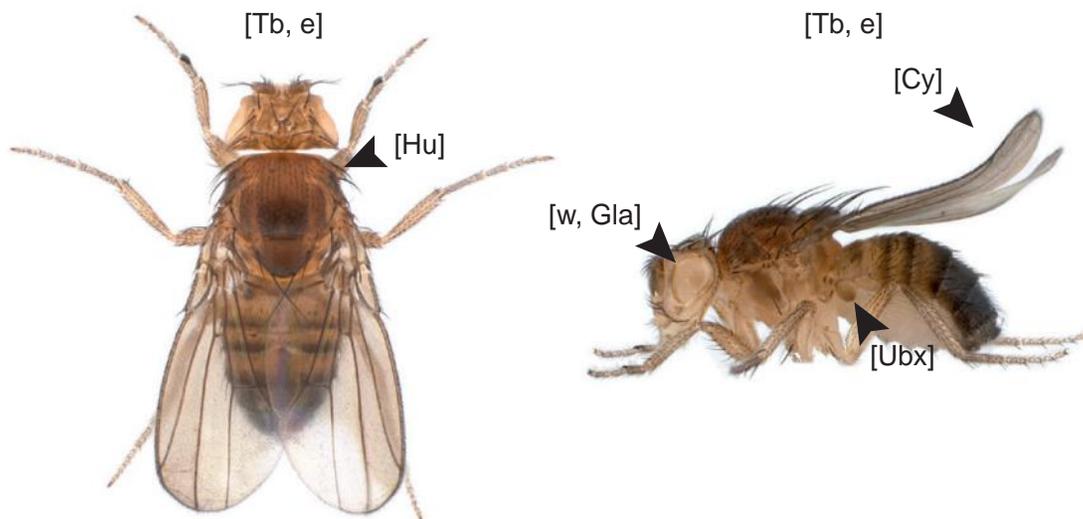
Same markers as TM8 but different breakpoints



w^{}; TM3, Sb¹ Ser¹/TM6B, Tb¹*



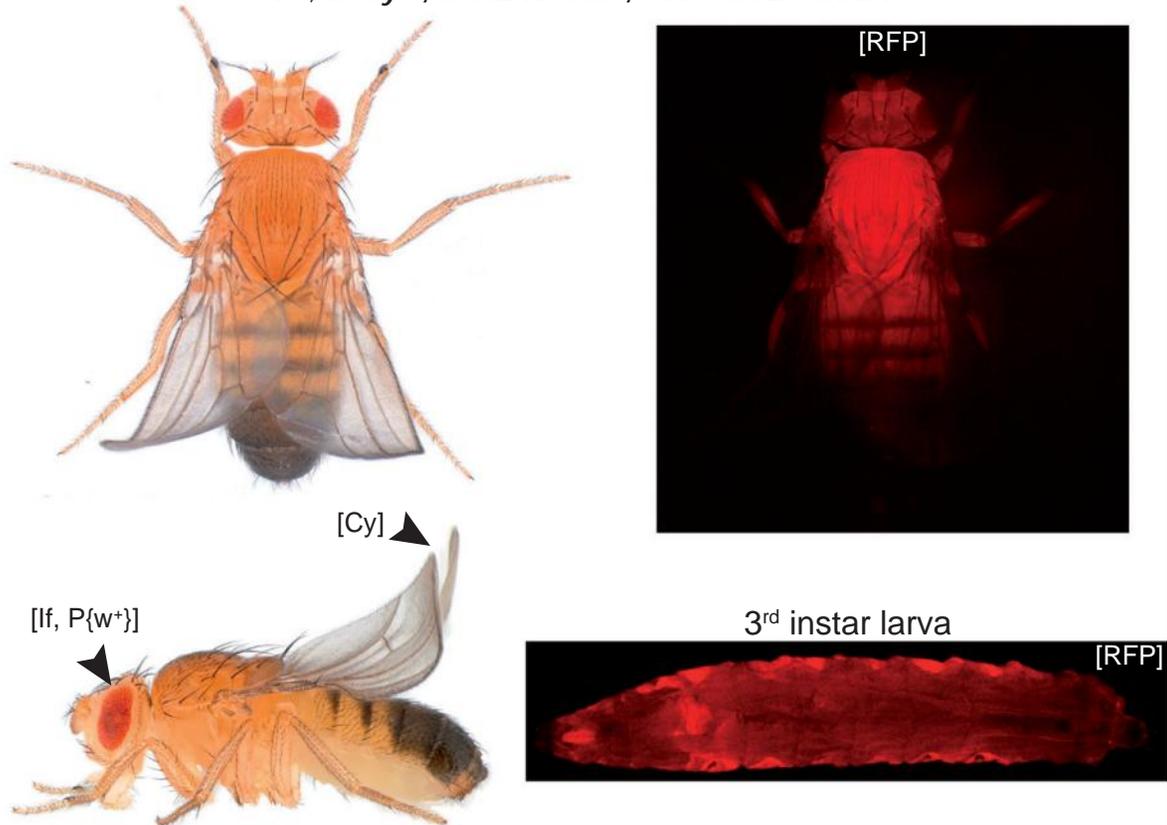
w^{}; Gla Bc/CyO; TM2, Ubx¹³⁰/TM6B, Tb¹*



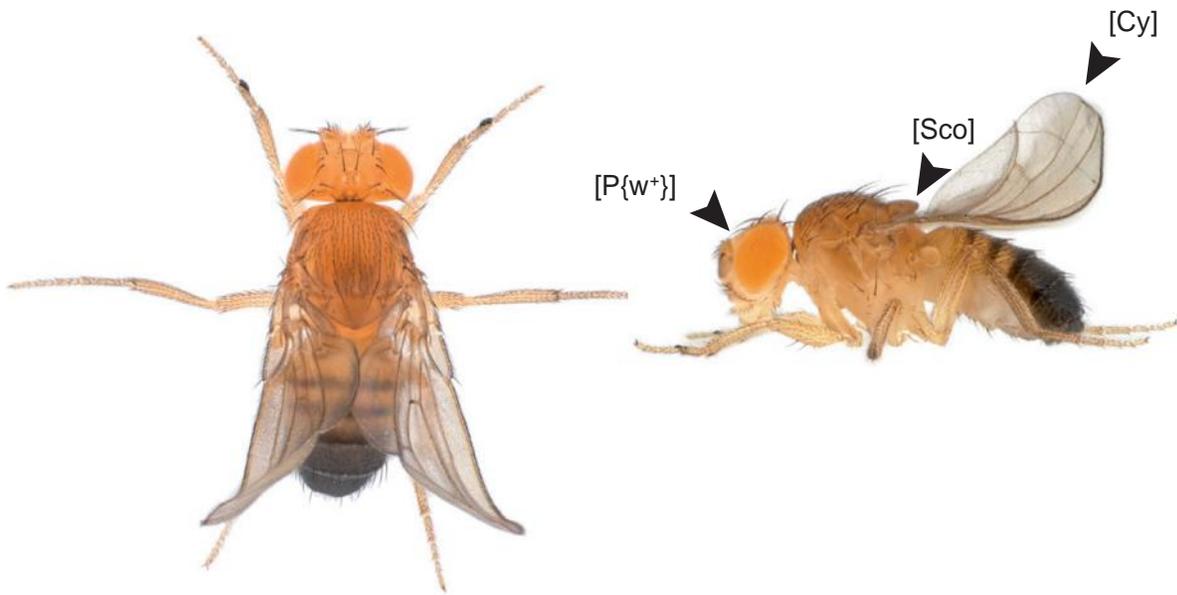
FM6, B⁺/?; SM5, Cy/Dp(?;2) bw^D Sp¹; TM3, y⁺ Ser¹/Sb¹



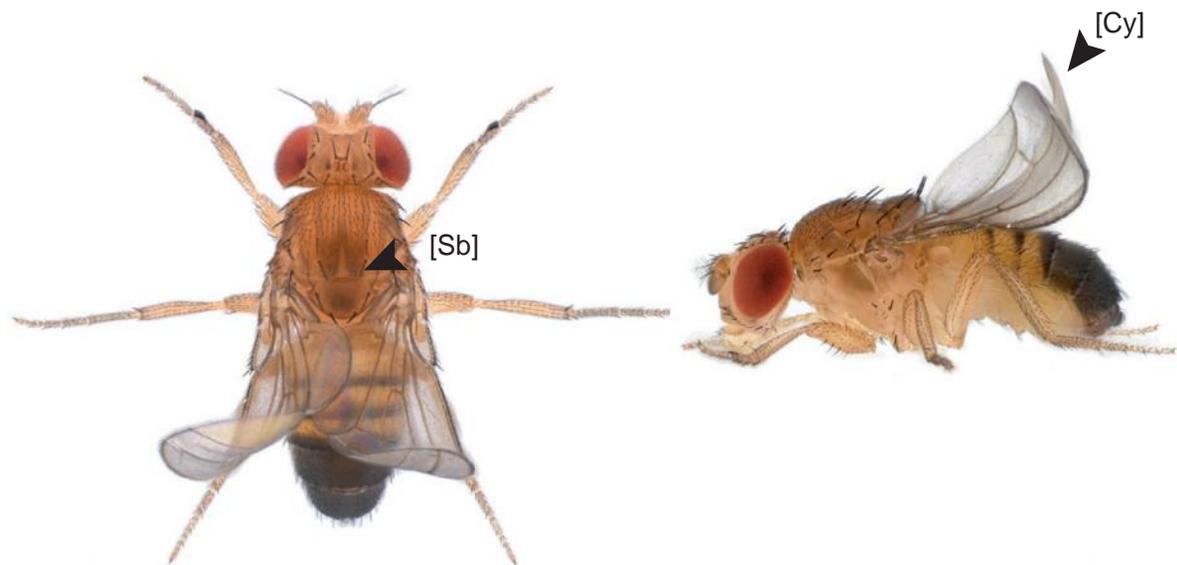
w^{}; If/CyO, Mef2.R-Gal4, UAS-mCD8.mRFP*



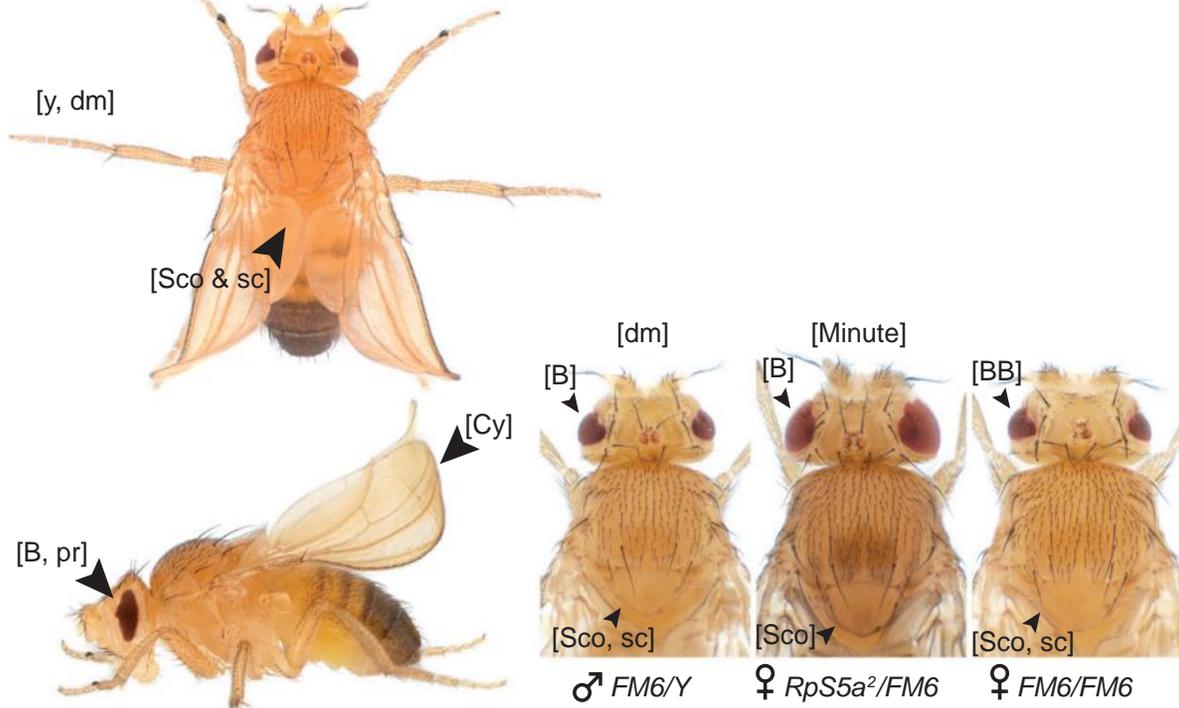
w¹¹¹⁸; Sco/SM6a, Cy¹ hsILMiT



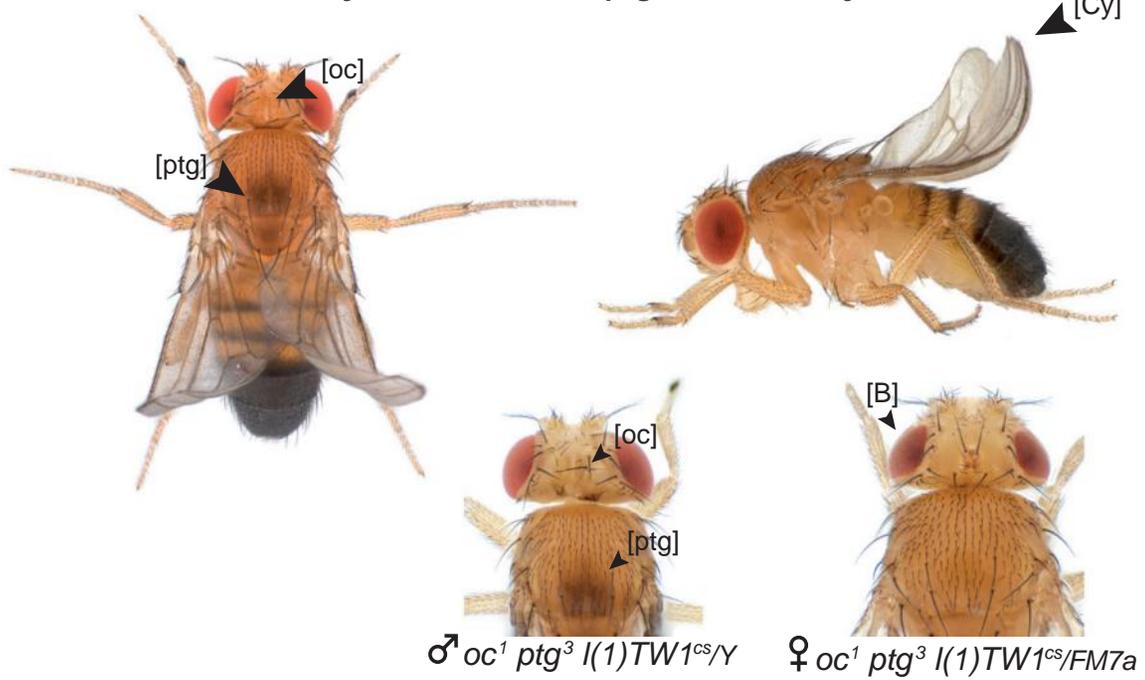
T(2;3)CyO-TM9, CyO: TM9, I(3)DTS4[1]/Tp(3;3)h[M3], h[49]

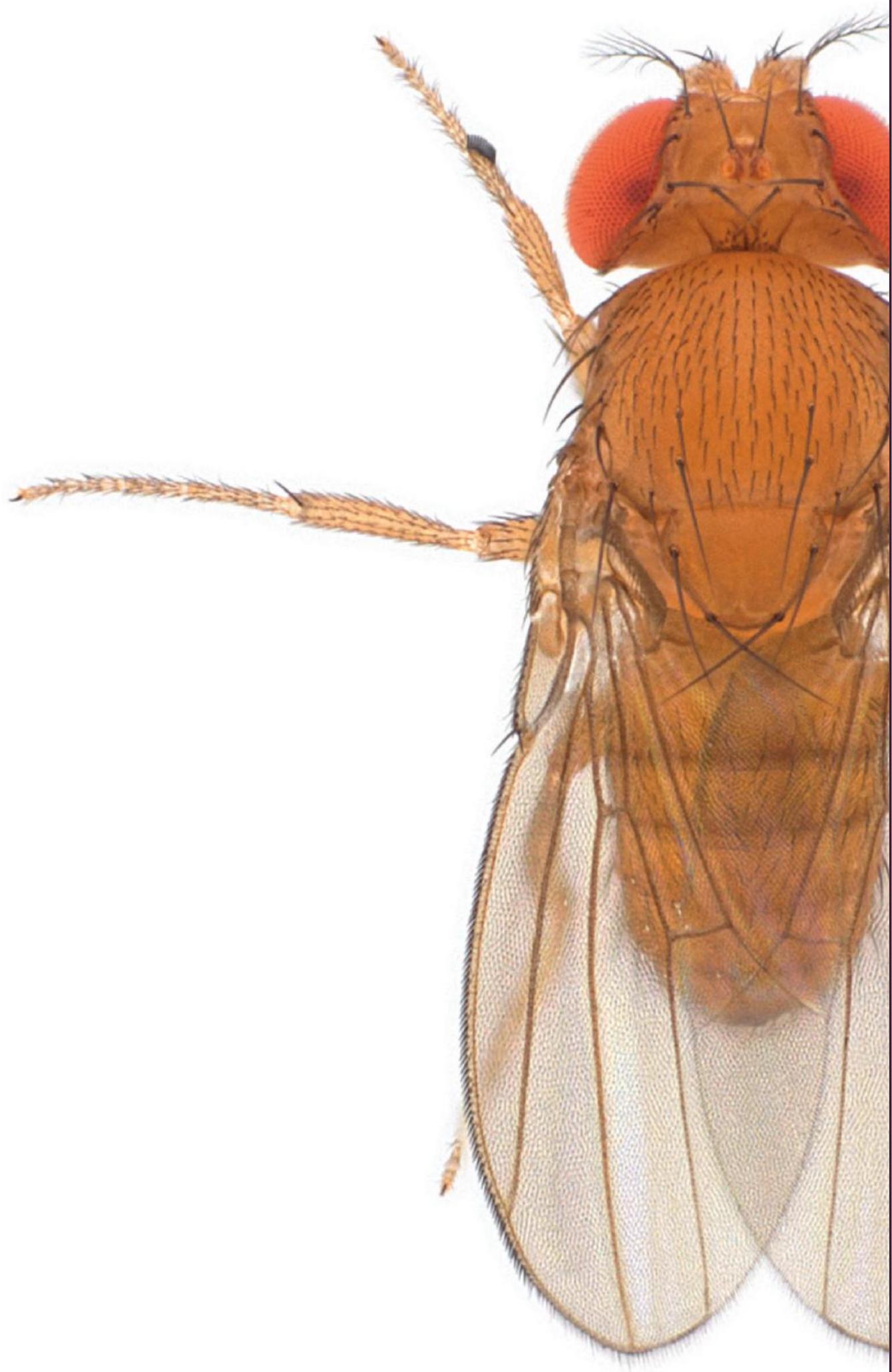


RpS5a²/FM6, B¹ dm¹ sc⁸ y^{31d}; Sco Aats-asn⁴ pr¹/CyO



FM7a, B¹ sc⁸ v^{Of} w^a y^{31d} I(1)TW24¹/oc¹ ptg³ I(1)TW1^{cs}; CyO/I(2)DTS91¹





D. melanogaster subgroup species

Taxonomy and distribution

Drosophila melanogaster Meigen, 1830
Cosmopolitan

Drosophila simulans Sturtevant, 1919
Cosmopolitan

Drosophila sechellia Tsacas & Bächli, 1981
Africa: Seychelles

Drosophila mauritiana Tsacas & David, 1974
Africa: Mauritius

Drosophila teissieri Tsacas, 1971
West Central Africa

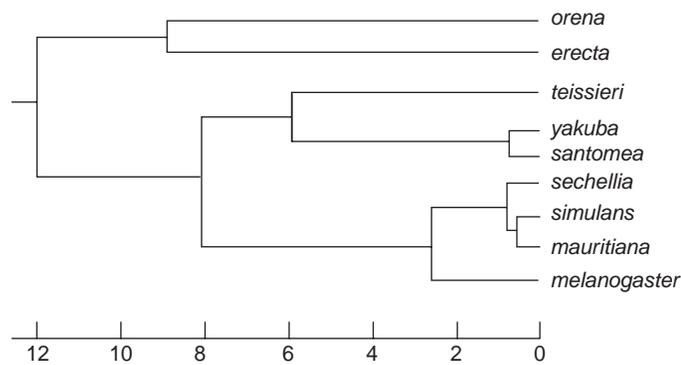
Drosophila erecta Tsacas & Lachaise, 1974
Africa: Ivory Coast, Congo

Drosophila orena Tsacas & David, 1978
Africa: Cameroon mountains

Drosophila yakuba Burla, 1954
Subsaharan tropical Africa

Drosophila santomea Lachaise & Harry, 2000
Africa: São Tomé island

Phylogeny



Subgroup phylogeny redrawn from Obbard et al. (2012) *Estimating divergence dates and substitution rates in the Drosophila phylogeny*. Mol Biol Evol. doi:10.1093/molbev/mss150

Male epandria (external genitalia) (p 220)

Note the variation in shape of clasper, a reliable morphological criterion to identify species.

D. melanogaster



♂

♀

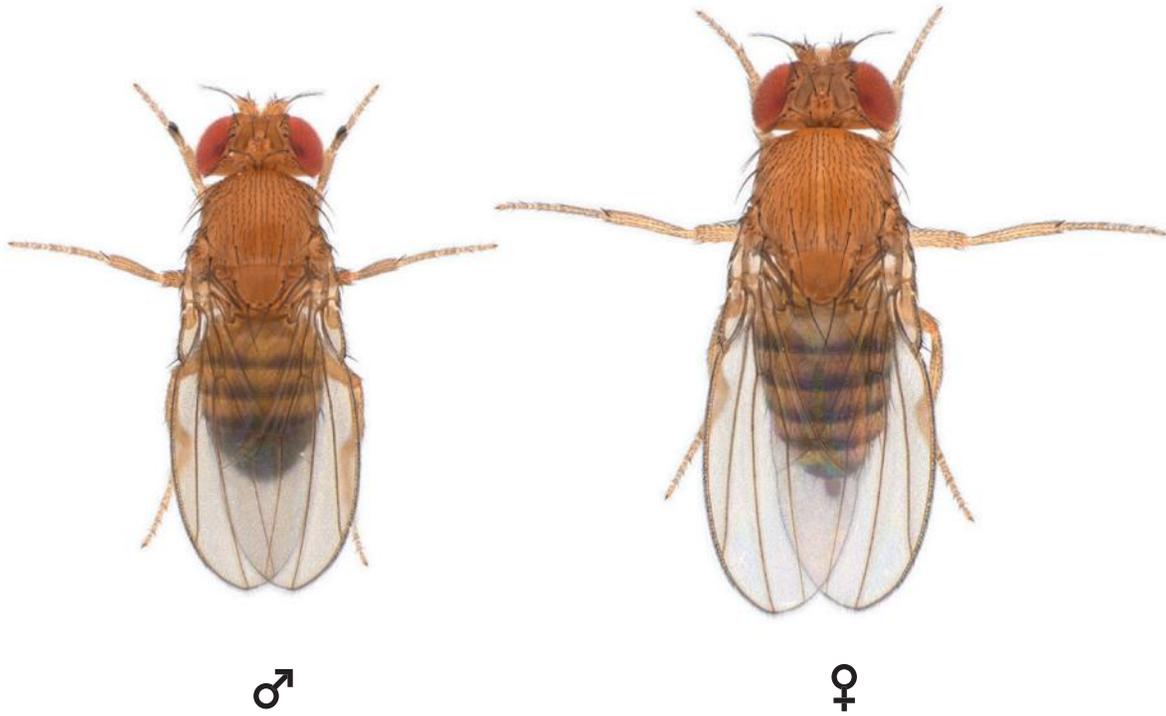


♂



♀

D. simulans



D. sechellia



♂

♀

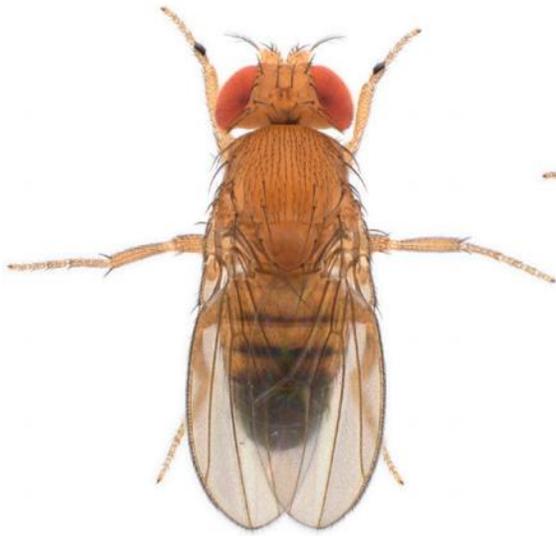


♂



♀

D. mauritania



♂



♀

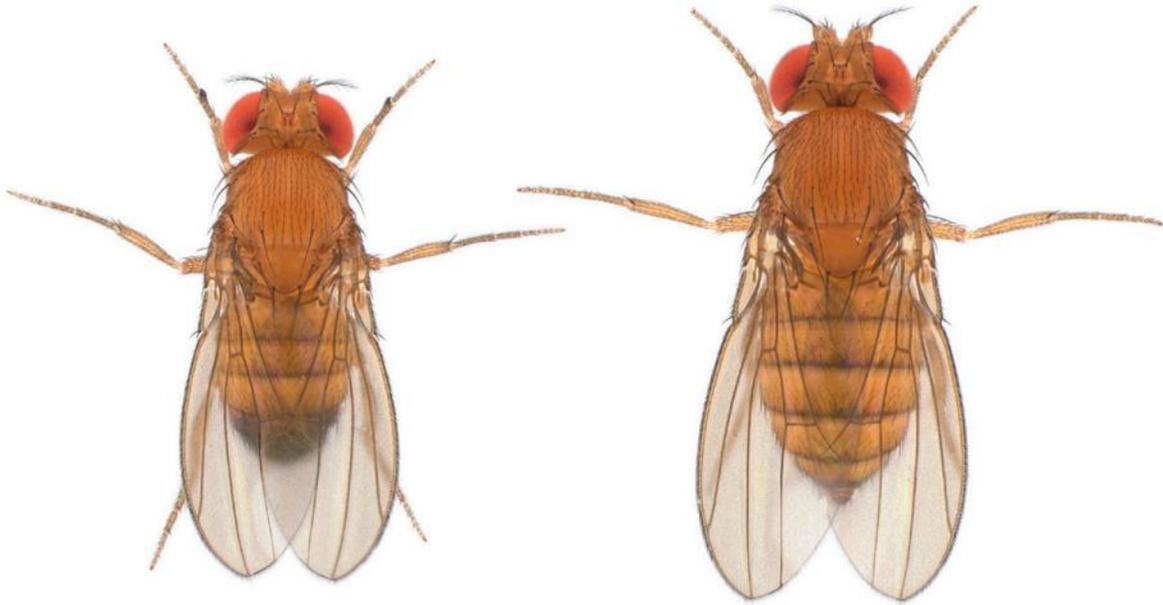


♂



♀

D. teissieri



♂

♀

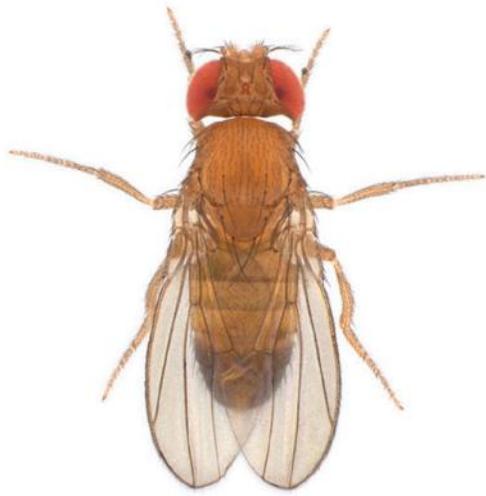


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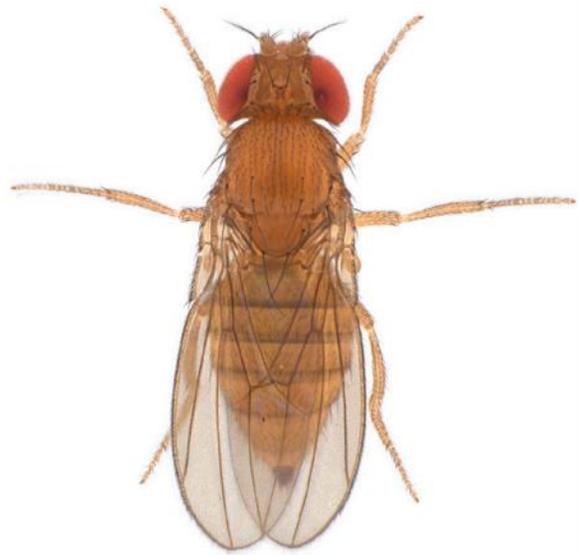


♀

D. erecta



♂



♀

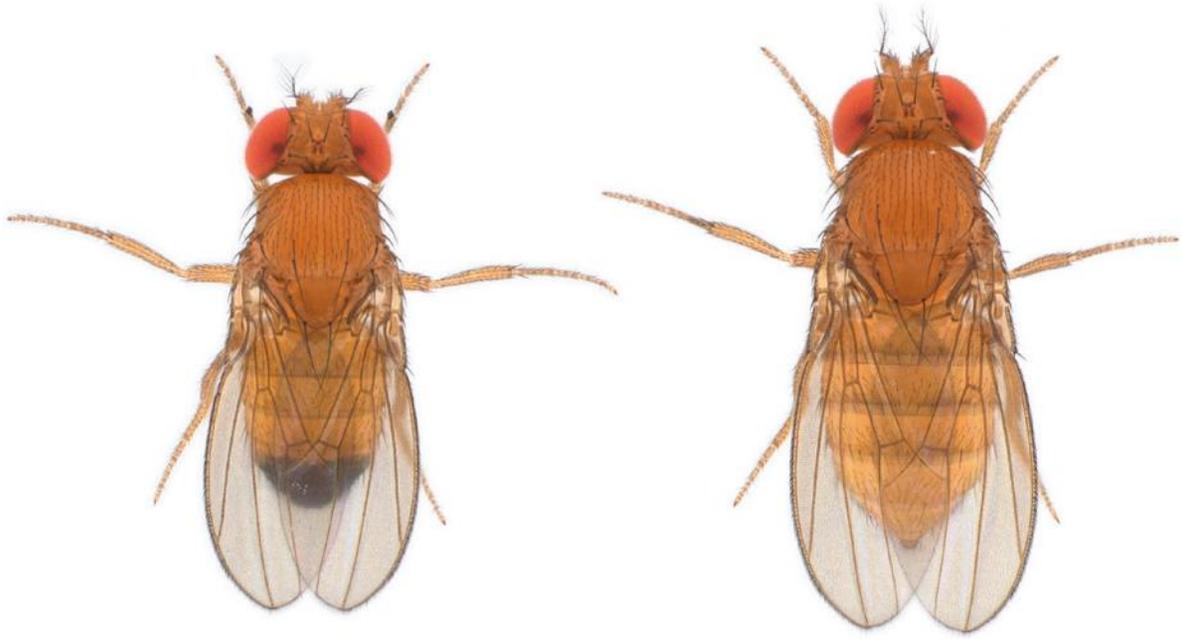


♂



♀

D. orena



♂

♀

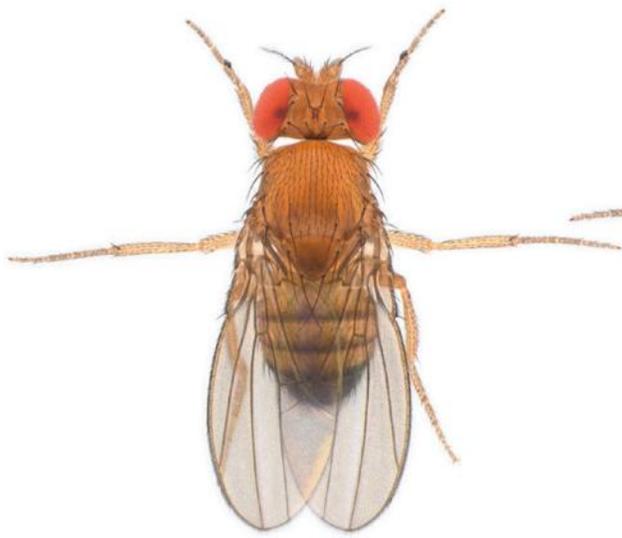


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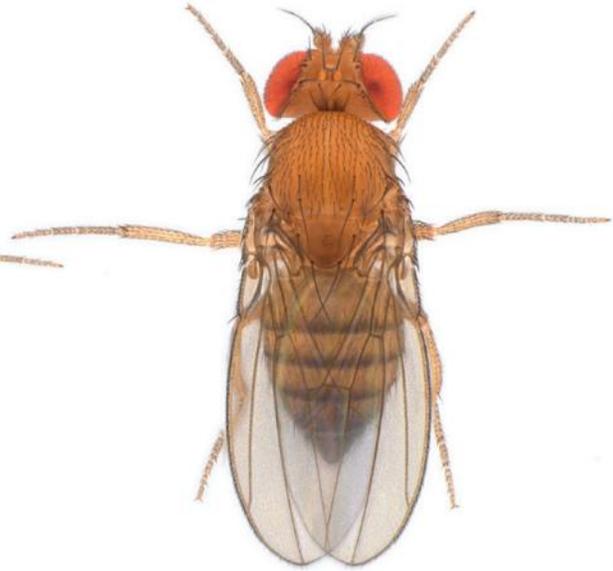


♀

D. yakuba



♂



♀

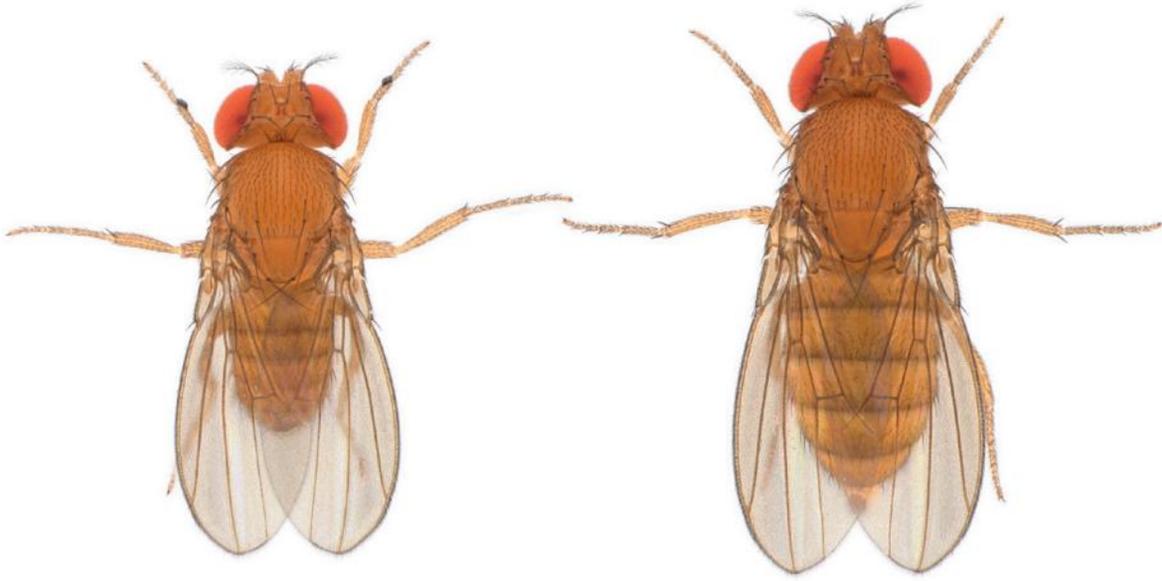


♂



♀

D. santomea



♂

♀

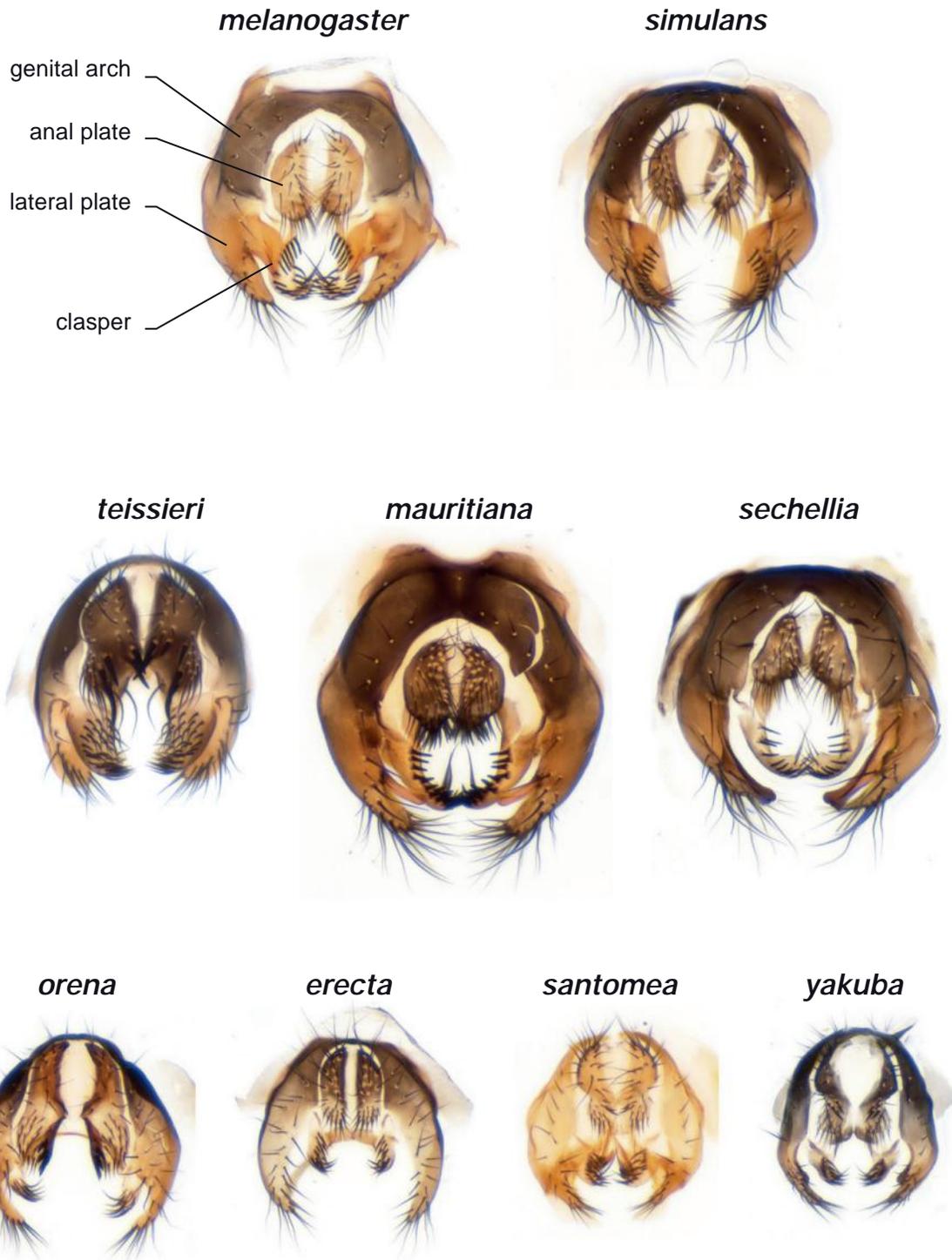


♂



♀

Male epandria summary plates



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