__The genes A and B, which control the number of wings (gene A) and the color of wings (gene B) of Odonata, are independently transmitted on autosomal chromosome(s).__

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1. Introduction

In the initial cage, small numbers of six different phenotypes of Odonata (at least one male and one female of each phenotype) had been collected from the wild:

Number of wings	Wing color	Male Organisms	Female Organisms	Total
1	Black	1	2	3
1	Blue	3	2	5
1	Yellow	3	4	7
6	Black	3	2	5
6	Blue	4	1	5
6	Yellow	2	3	5

Table 1: Initial cage

These organisms differ in two traits – the number of wings and the wing color. Two different phenotypes regarding the number of wings and three different phenotypes regarding the wing color were to be found, which I define as follows:

- Number of wings: 1 → phenotype [1]
  6 → phenotype [6]
- Wing color: Black → phenotype [B]
  Blue → phenotype [R]
  Yellow → phenotype [Y]

In order to identify the correct genetic model of this initial cage, I pose several questions. How many genes are implicated in these two traits that I am looking at? Are any of these genes on sexual chromosomes? Are these genes linked or independently transmitted? Are the alleles dominant, recessive or co-dominant?

2. Results

On the basis of the initial cage, it could already be stated that there must exist at least two genes for these traits because of the variety of phenotype combinations and the different number of phenotypes of each trait.

P1 [1B]♀ X [6R]♂ **P2**

↓

F1 [6Y] X [6Y] **F1**

16♂ 9♀

↓ (Supercross 500)

F2 [1B] [1R] [1Y] [6B] [6R] [6Y]

20♂ 17♀ 18♂ 24♀ 25♂ 35♀ 47♂ 44♀ 40♂ 43♀ 99♂ 88♀

Figure 1: Crossings **P1**x**P2** and **F1**x**F1**

For the first crossing (Figure 1) I chose **P1** and **P2** from the initial cage, because each of these two parental organisms has a different phenotype from the other in both traits. The generation of **F1** turned out to be phenotypically homogeneous, so it can be concluded that the parents in this crossing are homozygous concerning at least all the genes that are implicated in the examined traits. The **F1**-phenotype shows us that the phenotype [6] is dominant over [1] and that the phenotype [Y] is an intermediate phenotype of [B] and [R]. It is obvious that there have to be at least two different genes responsible for the two traits, since the organisms of **F1** have a mixture of the dominant and an intermediate phenotype of the parental generation.

My first hypothesis is now that it is a monogenic determinism (MD) for each trait, meaning there are two genes in total. In order to confirm or reject the hypothesis, I continued with self-fertilization of **F1** (Figure 1) and will now look at it trait by trait.

a) <u>Number of wings (Figure 2)</u>

Anticipating a MD I expect ¼ of the descendants of the 2nd generation to have one wing [1] and ¾ of the organisms in **F2** to have six wings [6].

P1 [1] $(\frac{a}{a})$ X [6] $(\frac{A}{A})$ **P2**

↓

F1 [6] $(\frac{a}{A})$ X [6] $(\frac{a}{A})$ **F1**

↓ (Supercross 500)

F2 [1] [6]

139 361

γ F1 \ γ F1	**a** $\frac{1}{2}$	**A** $\frac{1}{2}$
$\frac{1}{2}$ **a**	[1]	[6]
$\frac{1}{2}$ **A**	[6]	[6]

expected: [1]:[6] ≅ 1:3

	O	**E**
[1]	139	125
[6]	361	375
Σ	500	500
	χ^2=	2,09
	dl=	1
	P_{Value}>	10%

Figure 2: Trait 1 with proposed genotypes // gamete table // observed and expected values for MD

The χ^2-test confirms my hypothesis showing a probability over 10% for a MD in this trait.

b) <u>Wing color (Figure 3)</u>

Since there is an intermediate phenotype [Y] regarding the wing color, the expected distribution of the phenotypes for an MD in **F2** are ¼ for each [B] and [R] and ½ for [Y].

P1 [B] $(\frac{B'}{B'})$ X [R] $(\frac{B*}{B*})$ **P2**

↓

F1 [Y] $(\frac{B'}{B*})$ X [Y] $(\frac{B'}{B*})$ **F1**

↓ (Supercross 500)

F2 [B] [R] [Y]

128 125 247

γ F1 \ γ F1	**B'** $\frac{1}{2}$	**B*** $\frac{1}{2}$
$\frac{1}{2}$ **B'**	[B]	[Y]
$\frac{1}{2}$ **B***	[Y]	[R]

expected: [B]:[R]:[Y] ≅1:1:2

	O	**E**
[B]	128	125
[R]	125	125
[Y]	247	250
Σ	500	500
	χ^2=	0,11
	dl=	2
	P_{Value}>	90%

Figure 3: Trait 2 with proposed genotypes // gamete table // observed and expected values for MD

Clearly the results of the χ^2-test state, with a probability of more than 90%, that it is a MD as well.

c) Test cross

To verify these results, I also did a test cross (Figure 4) checking the descendants (**F2***) of **F1** by **P3**.

F1 [6Y]♀ X [1Y]♂ **P3**

↓(Supercross 500)

F2*	[1B]	[1R]	[1Y]	[6B]	[6R]	[6Y]
	33♂ 30♀	26♂ 30♀	82♂ 64♀	22♂ 30♀	30♂ 28♀	70♂ 55♀

Figure 4: Test Cross **F1**x**P3**

The test cross also supports the first hypothesis of MD in the trait of the number of wings (Figure 5) and the MD in the trait of wing color (Figure 6) as the P_{Value} is in both cases higher than 10% using the χ^2-test.

F1 [6] $(\frac{a}{A})$ X [1] $(\frac{a}{a})$ **P3**

↓(Supercross 500)

F2* [1] [6]

265 235

γ P3 \ γ F1	a $\frac{1}{2}$	A $\frac{1}{2}$
1 a	[1]	[6]

expected: [1]:[6] ≅ 1:1

	O	E
[1]	265	250
[6]	235	250
Σ	500	500
χ^2=	1,8	
dl=	1	
P_{Value}>	10%	

Figure 5: Trait 1 with proposed genotypes // gamete table // observed and expected values for MD

F1 [Y] $(\frac{B'}{B*})$ X [Y] $(\frac{B'}{B*})$ **P3**

↓ (Supercross 500)

F2* [B] [R] [Y]

115 114 271

γ P3 \ γ F1	B' $\frac{1}{2}$	B* $\frac{1}{2}$
$\frac{1}{2}$ **B'**	[B]	[Y]
$\frac{1}{2}$ **B***	[Y]	[R]

expected: [B]:[R]:[Y] ≅1:1:2

	O	E
[B]	115	125
[R]	114	125
[Y]	271	250
Σ	500	500
χ^2=	3,53	
dl=	2	
P_{Value}>	10%	

Figure 6: Trait 2 with proposed genotypes // gamete table // observed and expected values for MD

d) Independence (Figure 7 & 8)

My second hypothesis is now that the two verified genes are independently transmitted.

P1 [1B] $(\frac{a}{a}\frac{B'}{B'})$ X [6R] $(\frac{A}{A}\frac{B*}{B*})$ **P2**

↓

F1 [6Y] $(\frac{a}{A}\frac{B'}{B*})$ X [6Y] $(\frac{a}{A}\frac{B'}{B*})$ **F1**

↓(Supercross 500)

F2	[1B]	[1R]	[1Y]	[6B]	[6R]	[6Y]
	37	42	60	91	83	187

γ F1 \ γ F1	a B' $\frac{1}{4}$	A B* $\frac{1}{4}$	a B* $\frac{1}{4}$	A B' $\frac{1}{4}$
$\frac{1}{4}$ **a B'**	[1B]	[6Y]	[1Y]	[6B]
$\frac{1}{4}$ **A B***	[6Y]	[6R]	[6R]	[6Y]
$\frac{1}{4}$ **a B***	[1Y]	[6R]	[1R]	[6Y]
$\frac{1}{4}$ **A B'**	[6B]	[6Y]	[6Y]	[6B]

Figure 7: Crossing **P1** x **P2** with proposed genotypes // gamete table with independent transmission

	[1B]	[1R]	[1Y]	[6B]	[6R]	[6Y]	Σ
	$\frac{1}{16}$	$\frac{1}{16}$	$\frac{2}{16}=\frac{1}{8}$	$\frac{3}{16}$	$\frac{3}{16}$	$\frac{6}{16}=\frac{1}{4}$	1
O	31,25	31,25	62,5	93,75	93,75	187,5	500
E	37	42	60	91	83	187	500
	χ^2=6,17	dl=5	P_{Value}>20%				

Figure 8: observed and expected values for independent transmission

With a probability over 20% (based on the χ^2-test) the two genes A and B are independently transmitted.

The second hypothesis can also be verified by the test cross (Figure 9) with a probability value over 20% after the χ^2-test (Figure 10).

F1 [6Y] ($\frac{a}{A}\frac{B'}{B*}$) X [1Y] ($\frac{a}{a}\frac{B'}{B*}$) **P3**

↓(Supercross 500)

F2 [1B] [1R] [1Y] [6B] [6R] [6Y]

63 56 146 52 58 125

γ F1 / γ P3	a B' $\frac{1}{4}$	A B* $\frac{1}{4}$	a B* $\frac{1}{4}$	A B' $\frac{1}{4}$
$\frac{1}{2}$ **a B'**	[1B]	[6Y]	[1Y]	[6B]
$\frac{1}{2}$ **a B***	[1Y]	[6R]	[1R]	[6Y]

Figure 9: Crossing **F1** x **P3** with proposed genotypes // gamete table with independent transmission

	[1B]	[1R]	[1Y]	[6B]	[6R]	[6Y]	Σ
	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{2}{8}=\frac{1}{4}$	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{2}{8}=\frac{1}{4}$	1
O	62,5	62,5	125	62,5	62,5	125	500
E	63	56	146	52	58	125	500
	χ^2=6,30	dl=5	P_{Value}>20%				

Figure 10: observed and expected values for independent transmission in test cross

Since every time the crossings resulted in the approximately same numbers of male and female descendants of each phenotype (Figure 1 & 4), it can be concluded, that none of the genes that are implicated in the traits I am looking at, are located on a sexual chromosome.

3. Conclusion

The traits "number of wings" and "wing color" of Odonata are controlled by two different, independently transmitted genes (in this report gene A and B). These genes are therefore on either two different chromosomes or on the same chromosome but far enough from each other in order to be transmitted independently. The two genes must be located on autosomal chromosomes, since no location on sexual chromosomes could be noticed. The final genotypes I am proposing after this analysis are:

- **P1** ($\frac{a}{a}\frac{B'}{B'}$)
- **P2** ($\frac{A}{A}\frac{B*}{B*}$)
- **F1** ($\frac{a}{A}\frac{B'}{B*}$)

The allele *A* is dominant over *a,* with phenotype [6] being dominant over [1] and the alleles *B'* and *B** are co-dominant, with [Y] being an intermediate phenotype of [B] and [R].