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Comparisons of pupae oil fatty acids composition and development parameters in a mulberry- and artificial diet- fed insect pest, *Spodoptera litura*

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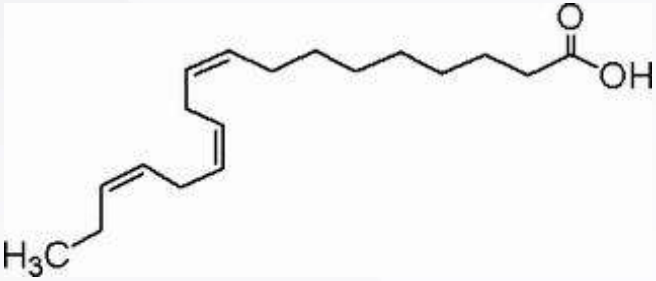
1. Background

Silkworm pupae

Bo

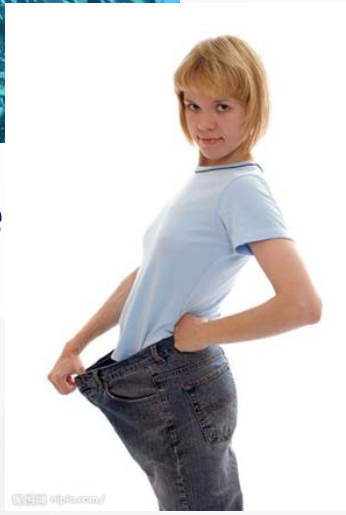


Linseed

α-linolenic acid (ALA)

C18:3

Deep-se



Perilla frutescens

common cutworm

Spodoptera litura (Lepidoptera, noctuidae)

Major destructive insect pest in China and Asian countries

eggs

Newly hatched larvae

Earlier stage larvae

Later stage larvae

pupa

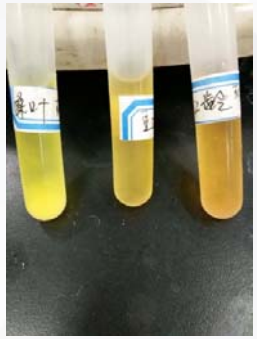
Adult moth

Lepidoptera Insects
Similar Feeding habit

?

Fatty acid composition

Metabolic pathways



2. Experimental design

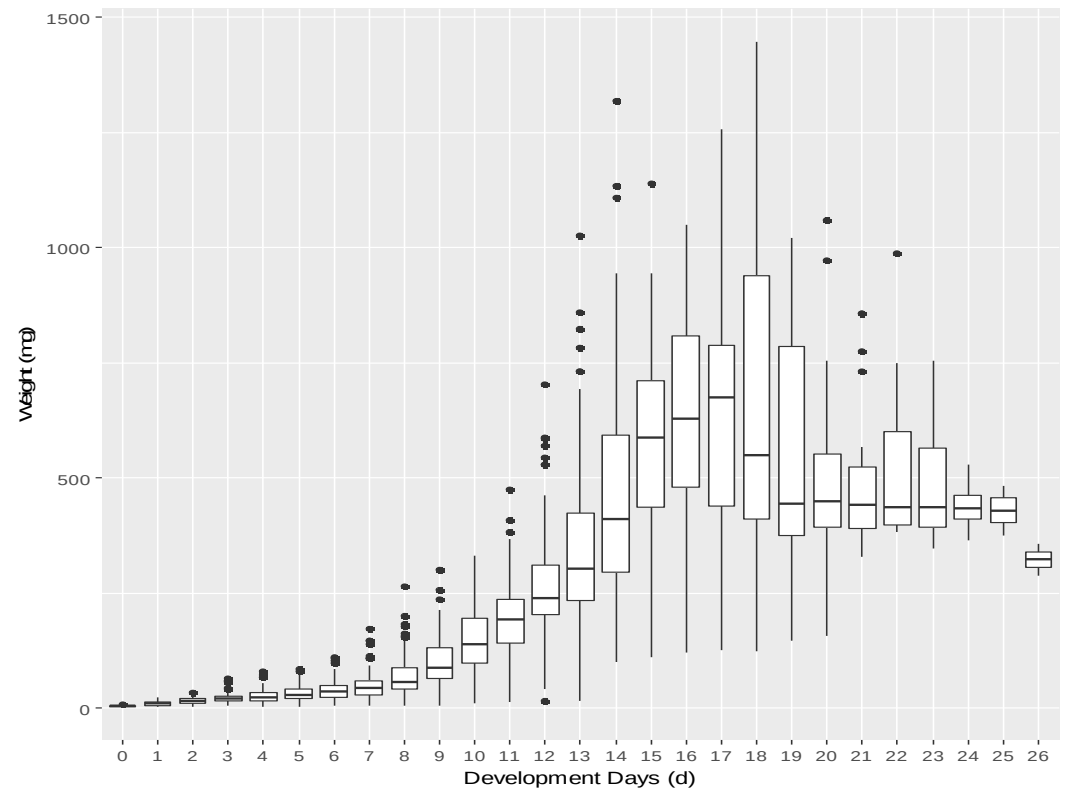
- ***Developmental parameters of S. Litura When feeding different foods***

- ***Measurements of fatty acids composition and contents in S. Litura pupae oil***

- ***Identifications of different expressed genes related to development and fatty acid biosynthesis in S. Litura pupae***

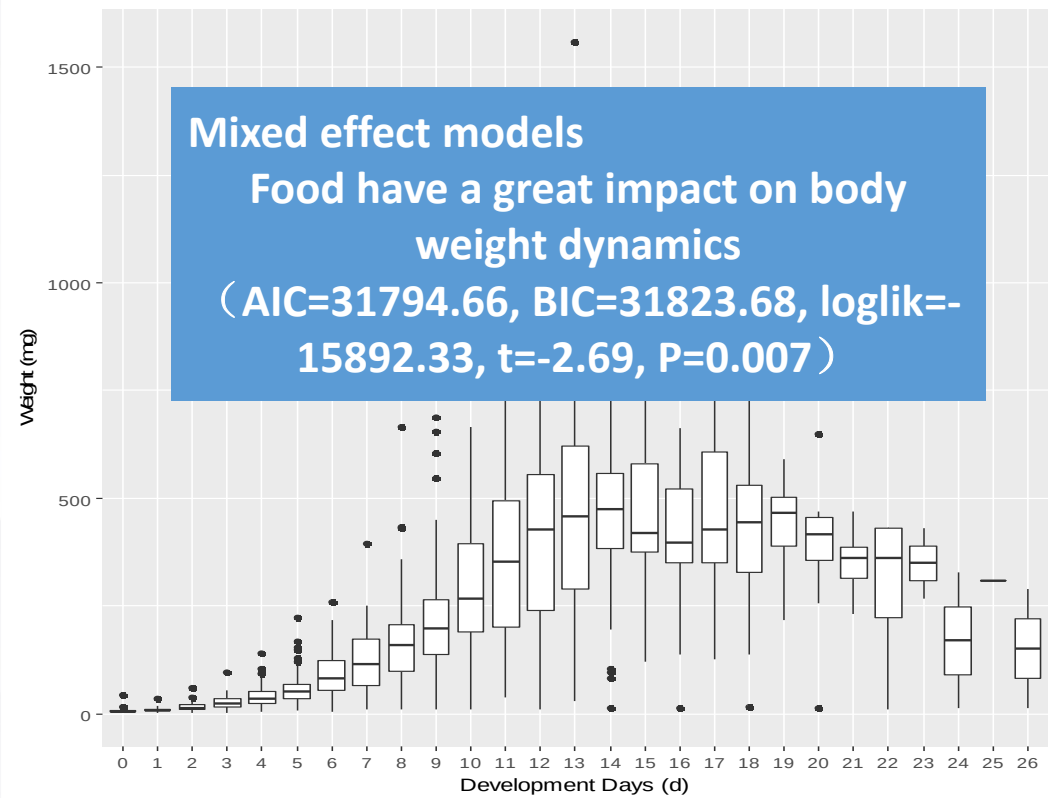
3. Results

3.1 Bodyweight dynamics



L1 L2 L3 L4 L5 Pre pupae

Feeding on mulberry foliage



Mixed effect models

Food have a great impact on body weight dynamics

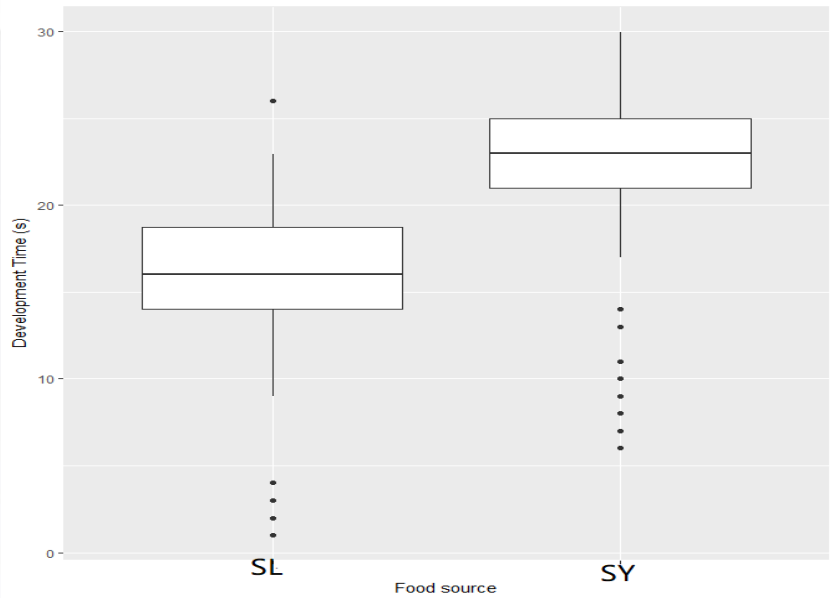
（AIC=31794.66, BIC=31823.68, loglik=-15892.33, t=-2.69, P=0.007）

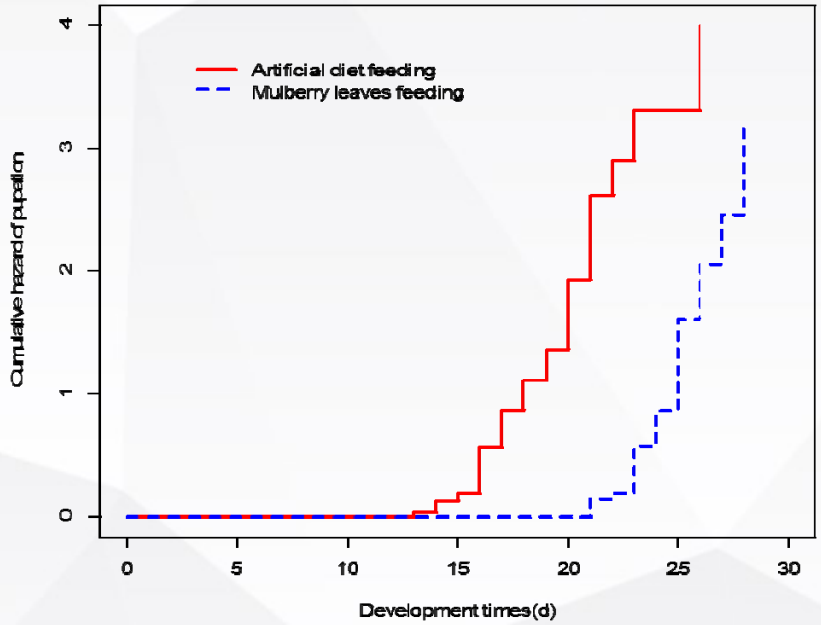
L1 L2 L3 L4 L5 Pre pupae

Feeding on artificial diet

3.2 Development time

$$h(t) = h_0(t)\exp\left\{\sum_{i=1}^{n} \beta_i z_i\right\}$$



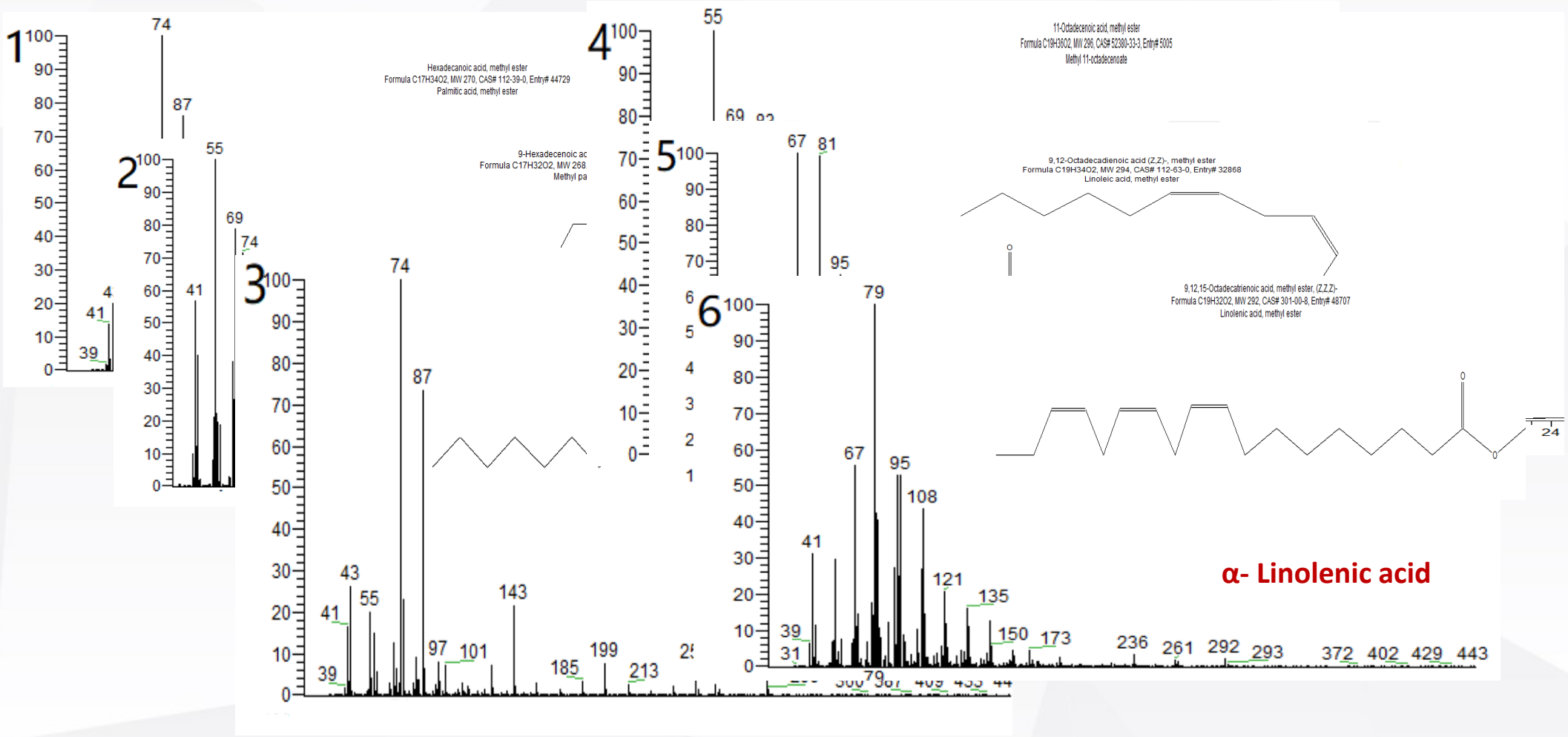


Mulberry-fed larvae: 21.70±0.68d

Artificial diets-fed larvae:15.53±0.62d

Longer developmental time in MF larvae

3.3 Compositions of pupae oil fatty acid

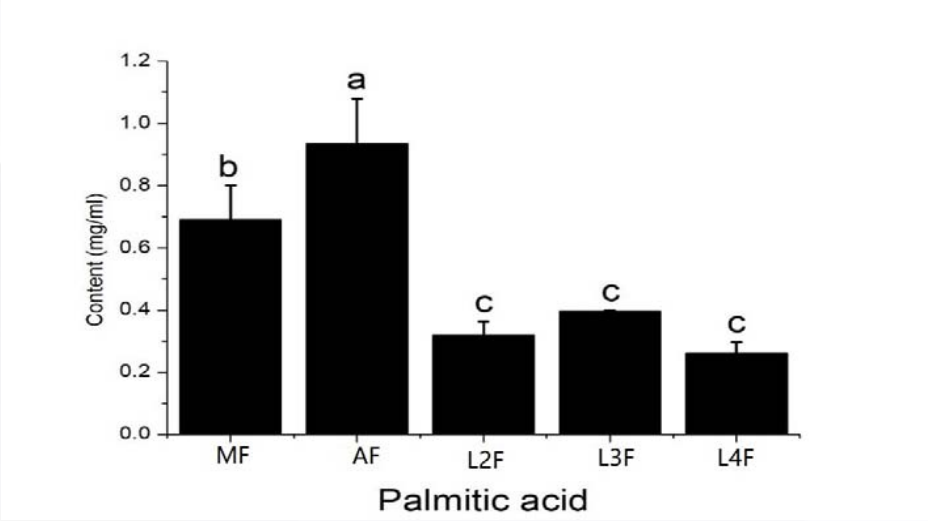


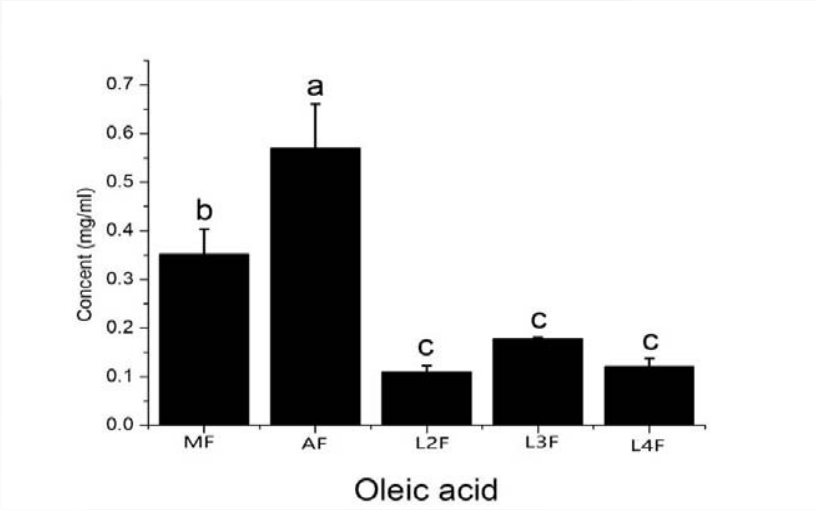
3.4 Relative contents of pupae oil fatty acid

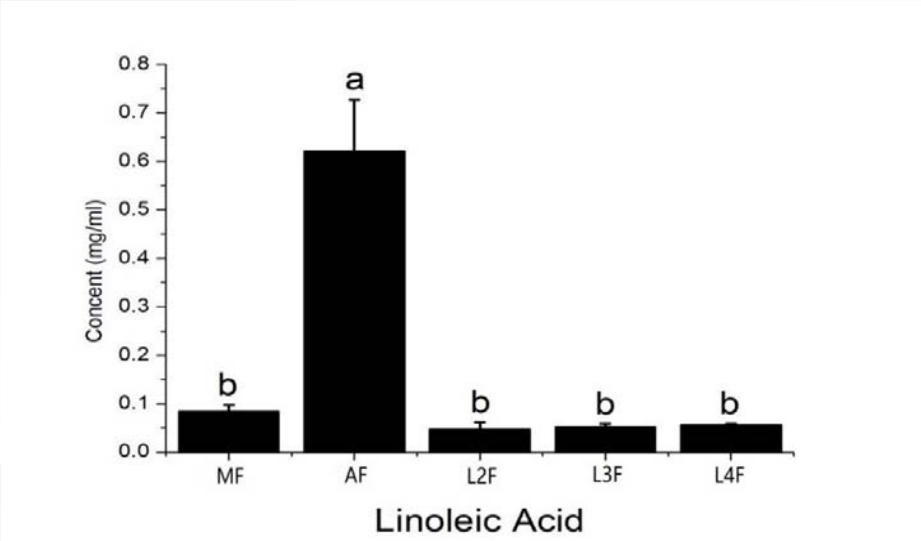
Treatment	Palmitic acid (%)	Palmitoleic acid (%)	Stearic acid (%)	Oleic acid (%)	Linoleic acid (%)	α- Linolenic acid (%)
MF	44.13±0.0057[a]	2.28±0.0004[a]	5.60±0.0026[a]	26.33±0.0025[ab]	4.21±0.0006[c]	17.45±0.0050[b]
AF	35.53±0.0072[a]	1.77±0.0003[a]	1.73±0.0002[d]	24.40±0.0002[ab]	32.61±0.0042[a]	3.92±0.0007[d]
L2F	42.76±0.0067[a]	2.21±0.0007[a]	5.22±0.0043[a]	25.72±0.0025[ab]	4.86±0.0006[c]	19.24±0.0051[a]
L3F	41.26±0.0116[a]	2.00±0.0054[a]	4.28±0.0017[b]	27.52±0.0070[a]	5.45±0.0010[c]	19.48±0.0031[a]
L4F	48.23±0.0614[a]	2.14±0.059[a]	2.34±0.0046[c]	23.39±0.0307[b]	22.18±0.0226[b]	11.72±0.0136[c]

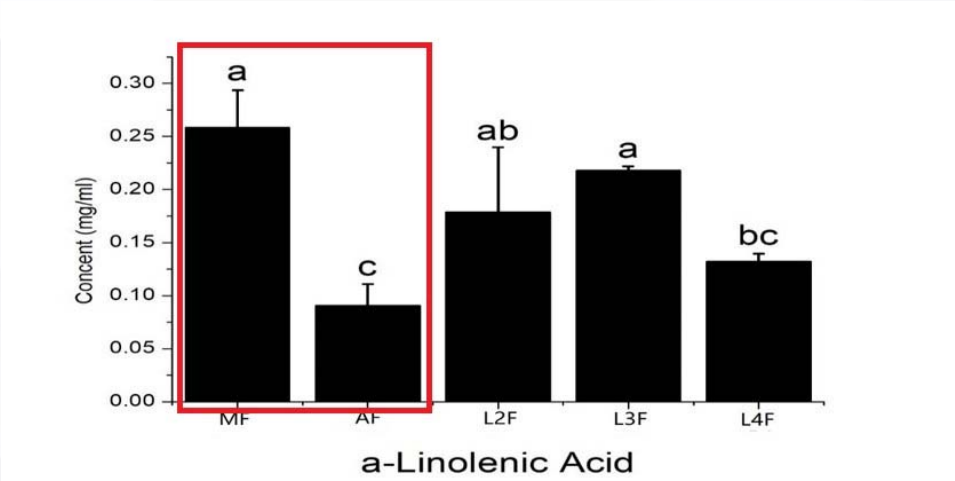
MF: Mulberry-fed, AF: Artificial diets-fed; L2F: 2nd instar changing food; L3F: 3rd instar changing food; L4F: 4th instar changing food

3.5 Absolute contents of pupae oil fatty acid





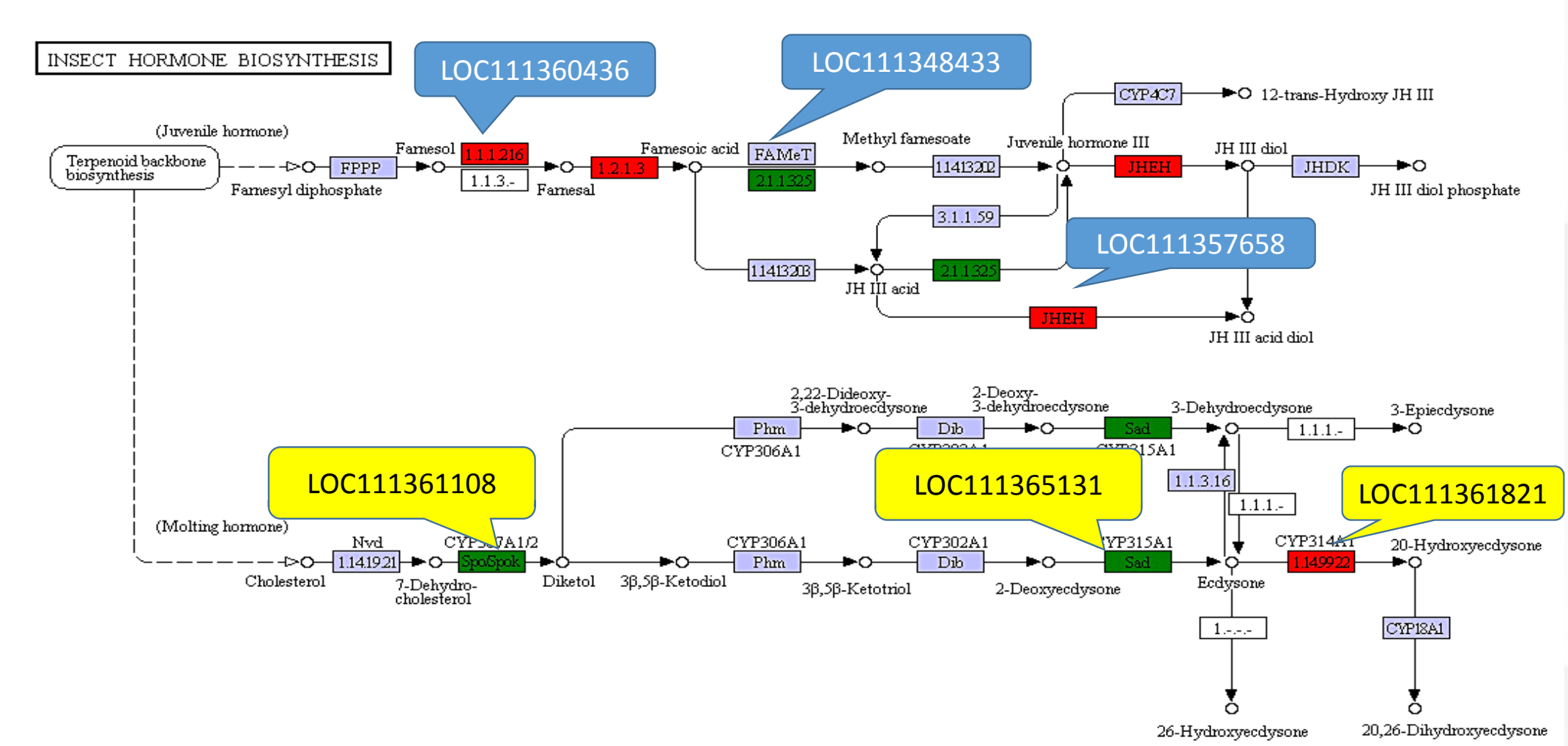




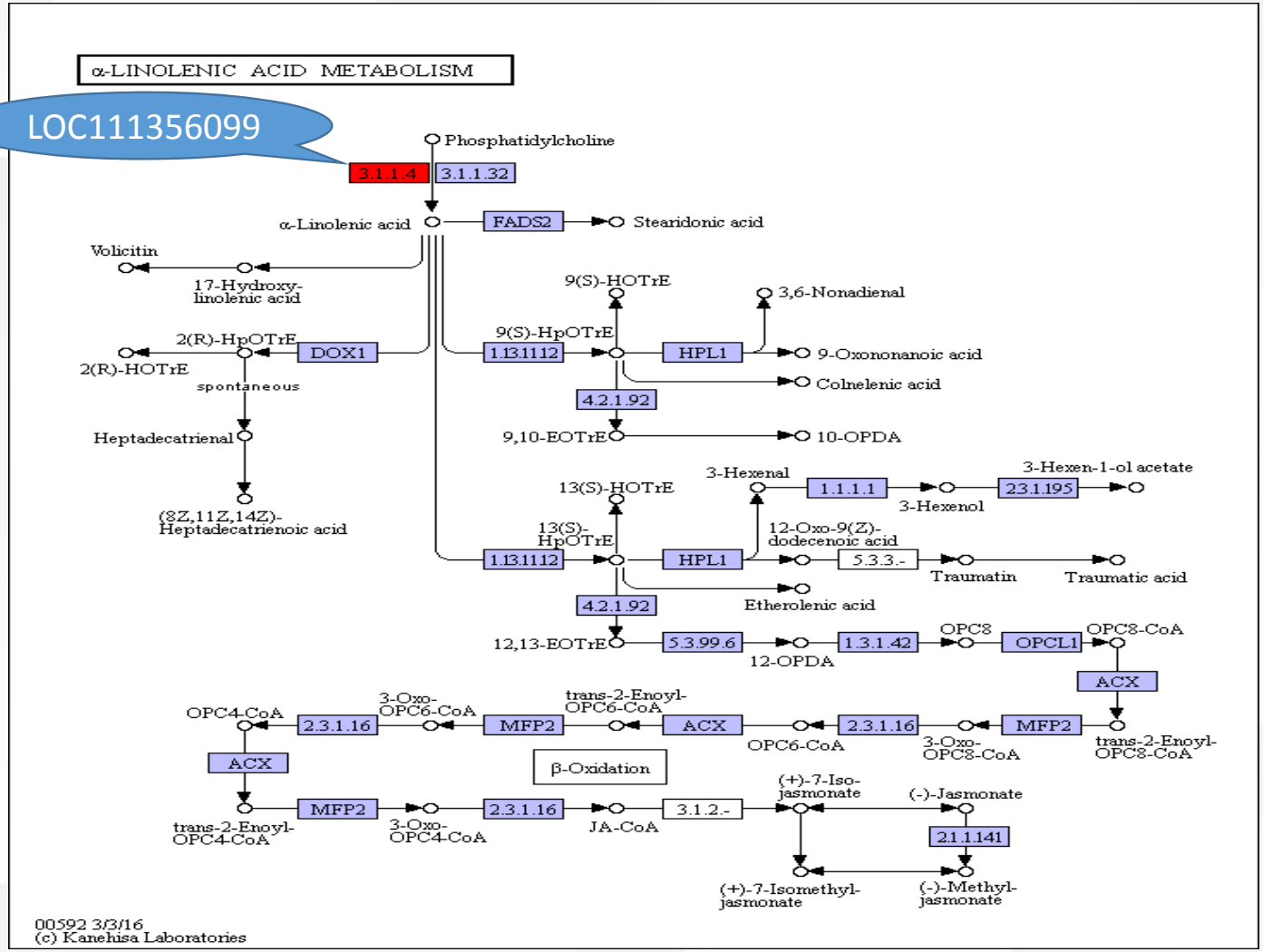
3.6 Differentially expressed genes identified from pupae transcriptome

Gene ID	Log_2FoldChange	Padj Value	Up_Down	Gene description	KEGG/GO term
Ecdysone					
LOC111364978	1.63	0.013	Up	Broad-complex core protein isoforms 1	response to ecdysone/regulation of development
LOC111365131	-1.97	0.024	Down	Cytochrome P450 315a1, mitochondrial	ecdysone biosynthetic process
LOC111361108	-2.85	0.0090	Down	Cytochrome P450 307a1	ecdysone biosynthetic process
LOC111361821	1.72	0.020	Up	Ecdysone 20-monooxygenase	ecdysone 20-monooxygenase activity
juvenile hormone					
LOC111348433	-3.84	0.00031	Down	Juvenile hormone acid Omethyltransferase	juvenile hormone biosynthetic process
LOC111351898	-1.39	0.045	Down	Juvenile hormone esterase	juvenile-hormone esterase activity
LOC111357658	2.15	0.020	Up	Juvenile hormone epoxide hydrolase	Insect hormone biosynthesis
LOC111358473	3.04	0.0029	Up	Juvenile hormone esterase	juvenile-hormone esterase activity
LOC111360436	2.47	0.00024	Up	Farnesol dehydrogenase	juvenile hormone biosynthetic process
ALA					
LOC111356099	4.93	0.0024	Up	Phospholipase A2	alpha-Linolenic acid metabolism
LOC111361908	2.15	0.0023	Up	Acyl-CoA desaturase	Biosynthesis of unsaturated fatty acids
LOC111347913	6.31	0.0010	Up	Acyl-CoA desaturase	Biosynthesis of unsaturated fatty acids
LOC111355209	4.69	0.0049	Up	Acyl-CoA desaturase	Biosynthesis of unsaturated fatty acids

3.7 KEGG Pathway enrichment of insect hormone biosynthesis



3.8 KEGG Pathway enrichment of ALA



Conclusion

1 Body weight dynamics were different when fed on artificial diet and mulberry, while pupae weight were not different significantly.

2 The content of α-linolenic acid was dramatically different between mulberry-fed pupae and artificial diets-fed ones, and the scenario of linoleic acid was opposite.

3 Four candidate genes which up-regulated in mulberry-fed pupae were identified by transcriptome deep sequencing.

THANKS for your attention!