

Multimodal dynamic response of the *Buchnera aphidicola* pLeu plasmid to variations in leucine demand of its host, the pea aphid *Acyrtosiphon pisum*

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Supporting Information

Figure S1. Pathways for the biosynthesis of isoleucine, leucine and valine.

The pathways were modified from <http://acycliccyc.cycadsys.org/> and completed with data from Wilson and colleagues (Wilson *et al.*, 2010). The enzymes encoded by *B. aphidicola* but absent in the pea aphid, and *vice versa*, are specified in blue and in green, respectively.

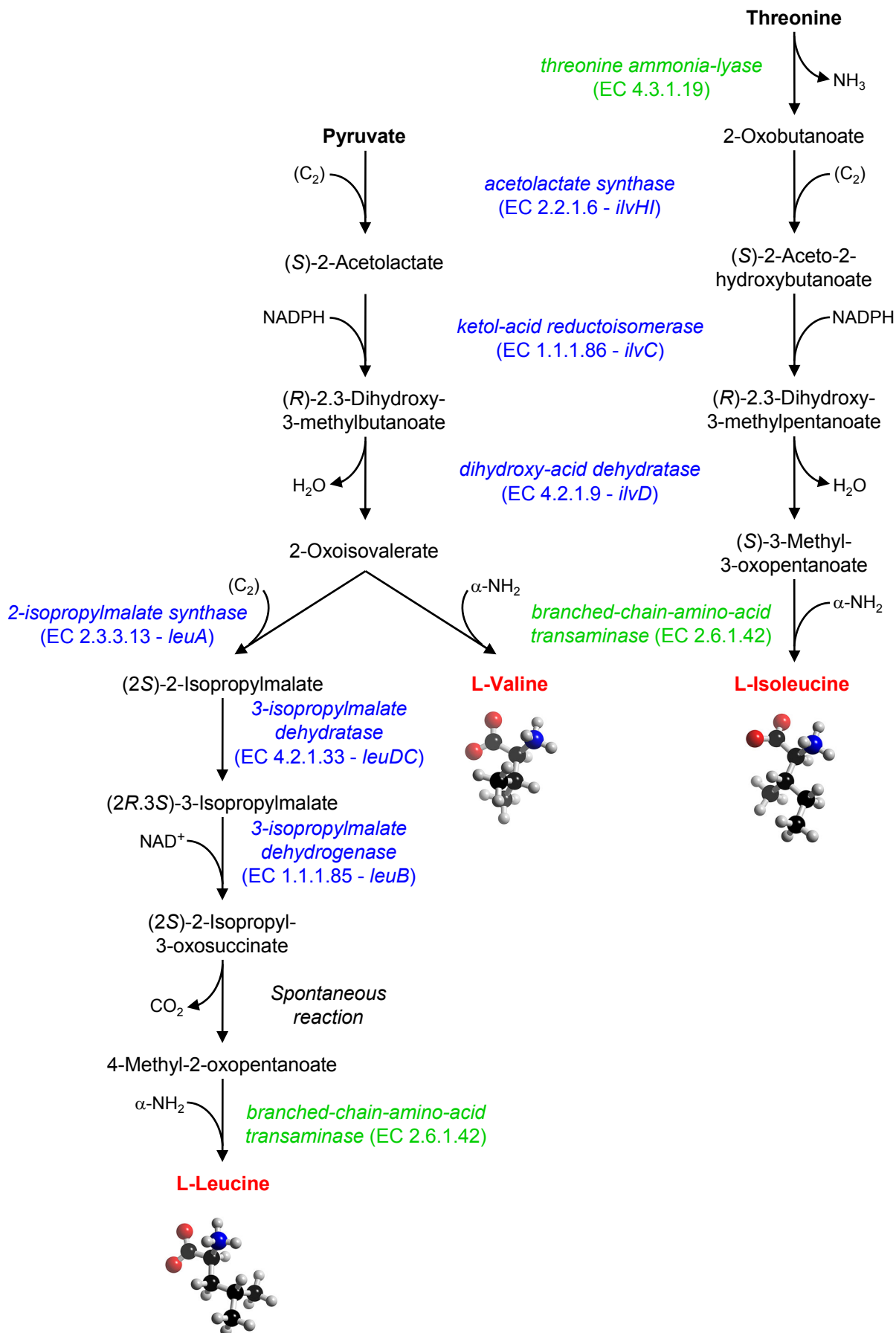
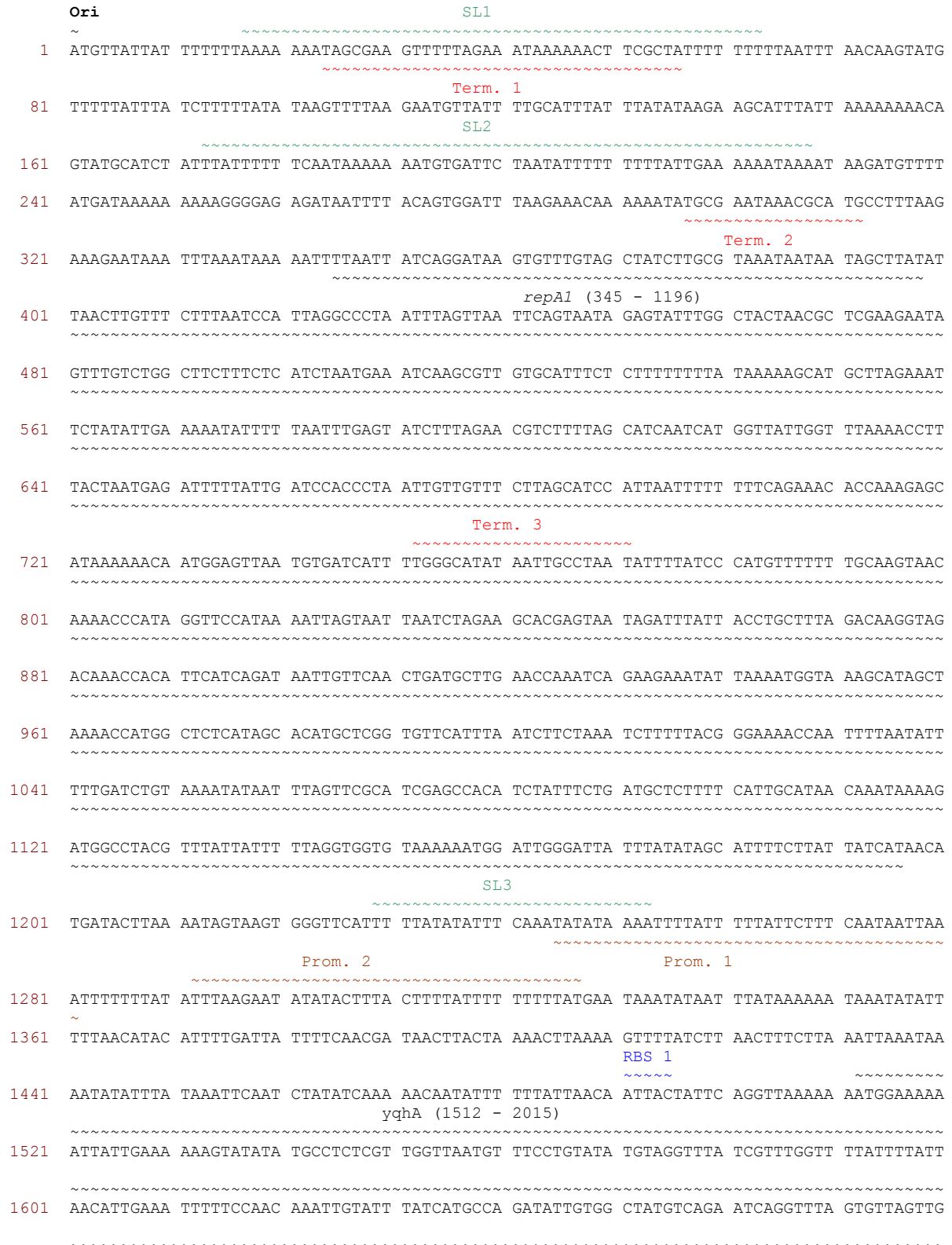


Figure S2. Features map of the reannotated pLeu plasmid in *B. aphidicola* from *A. pisum*.

Stem-loop structures are shown in green (SL), promoter sequences in brown (Prom.), rho-independent terminators in red (Term.) and ribosomal binding sites in blue (RBS).



1681 TTTTGTCAATT AATTGATATT GCATTAGTAG GTGGTCTATT AGTTATGGTT ATGTTTTCTG GATATGAAAA TTTTATTTCT
~
1761 AAAATGGATA TACAAGATAA TCAGAAAAGA TTAGGGTGGG TGGGAACCAT GGATGTTAAT TCAATAAAAA ACAAAGTAGC
~
1841 ATCTTCAATA GTTGCCATAT CTTCTGTTCA TCTTTTACGT CTTTTTATGG AAGCAGAAAA AATATTAGAT GATAAAATTA
~
1921 TGTATGTGT TATTATTCAT TTAACTTTTG TATTATCGGC TTTTGGAAATG GCATATATTTG ATAAAAATGAG CAAAAAATAA
~
~ Prom. 3 ~
2001 CATATCCTTC ATTAGTTTTT GTTTAAAAAA AATTTATTTT TTTTATTAA TTTTTTATAT TTTTTTAAAA AAACATAAT
~
~ RBS 2 ~
2081 AAAAGTATAT TGTTC AATAT ATGATTTATC AAAA ACTCTT CTTTTAAAAA AATATTTTAC TTTTAATTAA GTGTATTTAG
~ repA2 (2160 - 2912) ~
2161 TGCCTAGAAA AAATTATATA TATAATCTAA AACCATTTTT TAATCCATCT AAAAATGAAA GAAAAAATC TACATTTATT
~
2241 TGTATGCAA TGAAAAAGT ATCAGAAATA GACGTGCTA GAAGTCATTT AAATCGTGCA TTATTACCA TAGATCCTAA
~
2321 AACTGGTAAT GTTCTGCCTC GATTCAGACG ATTAATAATA CATCGAGCAT GTGCTATGAG AGCTATAGTA CCTGCTATGT
~
2401 TGTATTATTT TAATATTGAC TCTAAATTAG TCGAAGCTTC TATTGAAAAA TTAGCAGATG AATGTGGATT ATCTACTTTA
~ Term. 4 ~
2481 TCAGATTCTG GTAATAAATC CATCACTCGC GCTTCTCGTT TAATAAGTGA GTTTTTGGAA CCAATGGGTT TTGTTAAATG
~
2561 TAAAAAATA AATAGTAAAT CAATGAGTAA TTATATACCT AAAAAAATTT TTTTAACTCC CATGTTTTTT ATGTTATGTG
~
2641 GTATTCACC ATCAGAAATA AATCATTTTT TATCAAAAAA AATAAAACCA TTAAAAAAT TAAAAAACA AGAAAAAGT
~
2721 GCATTTATTT CTTTTACAGA TATGAAGATT ATATCGCAAT TAGATGAAAG ATCAGCTAGA ACAAATTTT TAAATGCTTT
~
2801 AATTAATTAT TACACAGCTA GTGAATTAAC AAAAATAGGT CCGAAGGGTT TAAAAAATAA GATAGATATT GAATATAGTA
~ SL4 ~
~ Prom. 4 ~
2881 ATTTATGTAA TTTATATAAA AAAAAATCAT AAAATAAATT TATACAATAA AAATTTTCATG AGACATCATA TACAAAATTA
~ RBS 3 ~
2961 TTTTGTATAT GATGTCTTAT GAAATTTTTA TTGTATAAAT TTATTTTTAT CCAATAAAAC ATTCATTAC CTTAATTTGG
~ leuA (3051- 4610) ~
3041 AAAAAATTTT GTGAAATCTA AAGTTGTTAT TTTTGATACC ACGCTACGCG ATGGAGAACA AGCATTACAA GCAAGTCTTA
~
3121 GTGTTAAAGA AAAATTACAA ATTGCACTAT CTTTAGAAAA ATGTGGGATA GACATTTTAG AAATAGGATT TCCTGTTTCA
~
3201 TCACCCGGAG ATTTTAAATC AGTTCAAAC ATATCTAAAA ATATTAATAA TAGTCGAATA TGTAGTTAG CTCGTTGTAT
~
3281 AGAAAAAGAC ATCGATGCAG CCGGAGAAGC TATGTCTTCA TCTGATTCTT TTCGAATTCA TATTTTTTTA GCTACTTCAA
~
3361 CACTTCATAT GGAATCTAAA TTAAGAAAA ATTTTAACGA AATAATAGAT ATGGCTGTTT TTTCAGTAAA AAAAGCCTTA
~
3441 CGTTATACTG ATGATATTGA ATTTTCTTGT GAAGATGCTA CTAGAACTAC AATGGATAAT TTATGTCGTA TTGTAGAAAC
~
3521 ATTAATTAATA TCAGGTGTGA AAACAATTAA TATCCCCGAT ACAGTAGGAT ATACTGTACC CAACGAATTA TCTTGTATAA
~

3601 TAAAAAATTT GCTTGAAAGA GTACCTAACA TTCATAAATC TATAATTTCA GTTCATTGTC ATGACGATTT AGGCATGGCT
~~~~~  
3681 GTGGGAAATT CAATATCAGC TATACAGGCA GGTGCTAGAC AAATAGAAGG GACTATAAAC GGAATTGGCG AAAGAGCTGG  
~~~~~  
3761 TAATACAGCA TTAGAAGAAA TAATTATGGC TATAAAAGTA AGAGAAGATA TCTTAAGTGT TTCCACTAAT ATTAATTATA
~~~~~  
3841 AAGAAATTTA TCGAACTAGT AAAATTGTTA GTCAGATTTG TAATATGCCA ATCCCATCTA ATAAAGCTAT AGTAGGTAGT  
~~~~~  
3921 AATGCGTTTG CACATTCCTC AGGTATCCAC CAAGATGGTG TATTAATAAAA TAGAAAAAAT TATGAAATTA TGGAAACCAAG
~~~~~  
4001 TAGTATTGGT TTAAAAGAAG TAAACTTAA CTTAACCTCT CGTTCTGGAA GAGCAGCAGT AAAACATTAT ATGGATGAAA  
~~~~~  
4081 TGGGTTATAA TAATAGTGAT TATAATATAG ATGAACTTTA TATTGCTTTT TTAAAGTTAG CAGATAAAAA AGGTCAGGTT
~~~~~  
4161 TTTGACTATG ATTTAGAAGC ATTAGCTTTT ATTAATAAAC AACAAGATGA ATGGGAATAC TTTTCTTTAA AATTTTTTAG  
~~~~~  
4241 TGTGCAGTCT ATTTCTAATA GTTTATCTAC TGCATCAGTA AAATATTAT GTGGCAAAAA AACATACACA GAATCTTCTA
~~~~~  
Prom. 5  
~~~~~  
4321 CTACAAGCAA TGGACCAGTT GATGCTATTT ACCAAGCATT AAATAGAATT GCATGTTTTC CTATTATATT AAAAAAATTT
~~~~~  
4401 CAACTTGTAG CTAAGGGGAA GGGTAAAGAT GCGTTAGGTC AAGTAGATAT CTGCGTTGAA CATAAAAAA GGAAGTTTCA  
~~~~~  
4481 TGGAGTGGGT TTGGCTACTG ATATTATTGA AGCATCAGCT CAAGCAATGA TCAATGTACT AAATAACATA TGGAAAGCAA
~~~~~  
RBS 4  
~~~~~  
4561 AACAGTTAA CAAAAATTA AAAATTTTAA AAGATTTTAA AAAAAATAA TACATCTAGA TATAGAAATA TAATATTTTT
~~~~~  
leuB (4671- 5762)  
~  
4641 TGTGATTTT TATTAAGAG AAAAATTTTT ATGAAAAAA ATTATCGTAT CGCTGTATTA TCTGGTGATG GAATAGGTCC  
~~~~~  
SL5
~~~~~  
Term. 5  
~~~~~  
4721 TGAAGTCATG CAAGAAGCAT GTAAAATTTT AAATGTTTTA AAAAAATAT TTTTCTATC TTAGAAATA CAAAAATTTA
~~~~~  
4801 ATATTGGTGG TATAGCTATT GAACGTGAAG GTGTTGCTTT GCCAAAACT ACATTGCTAG GATGTGAAAA TTCTGATTCA  
~~~~~  
4881 ATTTTATTAG GTTCTGTAGG TGGTAAGAAG TGGGATAACC TTCCAGTAGA ACAACGTCTT GAAAGAGCAG CTTTATTGCC
~~~~~  
4961 TTAAAGAAAA TACTTTAATC TTTTTTCTAA TTAAAGACCA GCAAAATAT ATCCAGAACT AAAATGTTTA TCACCTCTTC  
~~~~~  
5041 GTTCAGATAT TGAAAAAAT GTTTTTGATA TATTATGTGT AAGAGAATTA ACAGGTGGAA TTTATTTTGG TGAACCTAAA
~~~~~  
5121 GGCTTTGTAA ATAAAAACAA TACTAAATAT GCTTTTGATA CAGAAATTTA TCATGAGTAT GAAATTATCC GTATTGCTCA  
~~~~~  
5201 TTTAGCTTTT AAATTGGCAC GATCTAAGAA GAAGAAAGTC TGTTCTATAG ATAAATCAAA TGTTCTTCGA AGTTCTATTT
~~~~~  
5281 TATGGGGAAA AGTAGTTGAA AGTGTTTCTA AAAAAATACC AGATGTTTCT TTATCTCATT TATATATTGA TAATGCTGCT  
~~~~~  
5361 ATGCAATAA TTAAAGATCC TAATCAGTTT GATGTATTAT TATGCTCAAA TCTTTTTGGA GATATTATTT CTGATGAATG
~~~~~  
5441 TGCTACAATT ACAGGTTCOA TTGGGATGTT ACCATCAGCA AGTTTAAATG AAAAAAATTT TGGATTATAT GAGCCGGCAG  
~~~~~

5521 GCGGATCAGC ACCTGATATT GAAGGTAAAA ATATTGCTAA TCCGATTGCT CAAATACTTT CACTTTCTAT GTTAGTTAGA
~~~~~  
5601 TATGGCATGA ATTTAAATCA GATAGCAGAT AAAATTGATA AAGCTGTTAA TAATGTATTA AAAAAAGGTT ATAGAACTTC  
RBS 5  
~~~~~  
5681 AGATATATCT CATGATAATA ATTTTPTAAA AACAGATGAA ATGGGTGATC TTATTGTTGA TTCTTTAATT AATGGTAAAT
leuC (5764 - 7179)
~~~~~  
5761 GACATGAAGA AACATTATA CGATAAAATA TATGATTCAC ATATTGTTTA TGAAGAGAAA AATAATACAT CTCTTTTATA  
~~~~~  
5841 TATAGATTTA CATTACTTC ATGAGGTTAC ATCACCTCAA GCCTTTGATT CATTACGAGA TAAAAATCGA AAGGTTAGAC
~~~~~  
5921 AGCCTAAAAA AACTTTTGCT ACAATGGATC ATAATGTTTC GACAAC TAGT CAAGATATTA ATGCTTCAGG TTCTATGGCA  
~~~~~  
6001 AAGGTACAAA TGCAAGAATT AATTAATAAT TGTTCCGAGT TTAATATATC ATTATATGAT ATAAAAAATC CTAATCAAGG
~~~~~  
6081 GATTGTTTAT GTTATTAGTC CTGAAAAAGG GATGACTTTG CCGGGTGTGA CTATTGTATG TGGTGACTCA CATACTCGA  
~~~~~  
6161 CGCATGGCGC ATTTGGAGCA TTATCTTTTG GTATTGATAC TTCAGAAGTT GAACATGTTC TTGCAACTCA AACATTAATA
~~~~~  
6241 CAACAGCGTT TTAATAATAT GAAAATAGAA ATTACAGGAG AAATCAAAA ATTTGTCACT GCTAAAGATT TGATTTTGTT  
~~~~~  
6321 TATTATTGGA AAATTAGGAT CATCTGGAGG TGCAGGATAT ATAATTGAAT TTTGTGGTAA TGTGATTGAA AAAATGAGCA
~~~~~  
6401 TGGAAGAAAG GATGACAATT TGTAATATGG CAATTGAAAT AGGTGCAAAG TCAGGTTTGA TAGCACCAGA TGAAGTGACA  
Term. 6  
~~~~~  
6481 TTTTCTTATC TGAAAAATAA AATGTATGCA CCACGTGGTG TTTTGTGGAA AAAAGCATA AATTTTGGGA AGAATTTGAA
~~~~~  
6561 ATCTGATAAA AATGCTTTTT TTGATAAAGT TGTGAATATA AATATTTCTG ATCTCTCGCC ACAAATTACC TGGGGGACAA  
~~~~~  
6641 ATCCTGATCA GGTGATCTCA ATCGATCAAA AAATACCTGA TTTTAGTAGT TTTGATAATT TAATAAAGAA AGATTTAGCC
~~~~~  
6721 AAATCTGCAT GTAAATATAT GGGTTTAAAA ATAGTACTT ATTTAACTAA TATTACTGTT GATGAAGTTT TTATTGGATC  
~~~~~  
6801 TTGTAATAAT GGAAGAATAG AAGATTTAAG AGCTGCCTCA AAGATACTTA AAGATAAAAA AATTGCTAAT AATGTTAAAG
~~~~~  
6881 CTATTGTGTG TCCTGGATCA AGTTCAAGTA AGAGAGAAGC TGAAAATGAA GGTTTAGATA AAATATTTAT TAATGCAGGA  
~~~~~  
6961 TTCGAATGGC GTTTACCTGG TTGTTCTATG TGTTAGGTA TGAATAAAGA TAGATTAAAT GATGGTGAAC GTTGTGCGTC
~~~~~  
7041 TACTAGCAAT CGAAATTTTG AGGGTCGCCA GGGGAGAGGG GGGCGAACAC ATTTAGTAAG TCCTATTATG GCGGCTGCAG  
RBS 6  
~~~~~  
leuD (7182 - 7805)
7121 CTGCTGTATA CGGTAAATTT GTTGATGTTA GAAAATTATA TAATGGTGAG AATAATTAAA TATGTTTAAA TTTACTGGAC
~~~~~  
7201 ATGCTGGTAT CGTTGTTCCT TTAGATATAT CTAATATAGA TACAGATATT ATTATTCCGA AGCAATTTTT GAAAAGAGTA  
~~~~~  
7281 AACAAAATG GATTTGGTAA ATATTTATTT CATGACTGGC GTTTTATTGA TGCAAATCAA TTAGTAAAAA ATGAGGATTT
~~~~~  
7361 TATACTCAAT AAAAAAATTT ATAAAAACGC AAGTATTTTA TTAAGTAGAG AGAATTTTGG TTGCGGCTCA TCGAGAGAAC  
~~~~~

7441 ATGCTGTTTG GTCTCTAGTA GACTATGGAT TCAAAGTAAT AATTGCACCT AGTTTGTCTG ATATTTTTTA TAATAATAGT
~~~~~  
7521 TTAAACAATA AGCTTCTTTT AATCACTTTA AGTTCGAGTG AAATTACTTT TTTATTTGAT ATGTAAAAA ATAATATAGG  
~~~~~  
7601 TATTACTTTT GATGTAAGTT TAGTCGAAAA AACGGTACT GTAAATAAGG AAGTATTTTC ATTTGAATTA GATGATTTTC
~~~~~  
7681 ATTACTTTTG TTTGTTAAAT GATTTAGATA ATATTGATT GACTATGAAG CATTATCAG AAATAAAATC TTATGAAAGT  
~~~~~  
7761 CGTATATCTG ATTTTTTATT AGAAAGAAGA GATTCCAAT CTTAA

Figure S3. Comparative evolutionary analysis of pLeu promoters in the Aphididae family.

The analysis was performed on ten aphid species belonging to two tribes of the Aphididae family which diverged more than 50 Myr ago: the Macrosiphini (*Acyrtosiphon pisum*, *Aulacorthum solani*, *Macrosiphum rosae*, *Metopolophium dirhodum*, *Uroleucon sonchi* and *Diuraphis noxia*) and the Aphidini (*Schizaphis graminum*, *Rhopalosiphum cerasifoliae*, *Rhopalosiphum insertum* and *Rhopalosiphum padi*). We were able to locate: (i) the *repA2* promoter in 9/10 species (mean LDF \pm SE = -12.0 ± 1.6); we identified however the *M. rosae* boxes by visual homology, the negative BPRM resulting from a one-base pair difference thresholding effect; (ii) the *leuA* promoter in 10/10 species (mean LDF \pm SE = -9.6 ± 0.44); (iii) the *yqhA* and *repA1* promoters in 4/4 species (mean LDF \pm SE being -16.2 ± 3.0 for *yqhA* and -14.2 ± 0.9 for *repA1*); and (iv) for *leuB*: the alternate promoter signal was located as a conserved internal signal to *leuA* cds for two *Macrosiphini* species, whilst only one potential signal was found for the *Aphidini* species, immediately upstream of the *leuB* cds in *R. padi*. All these *leuB* signals were the weakest found with BPRM, whether included, or not, in coding regions (LDF = -6.2 ± 1.0).

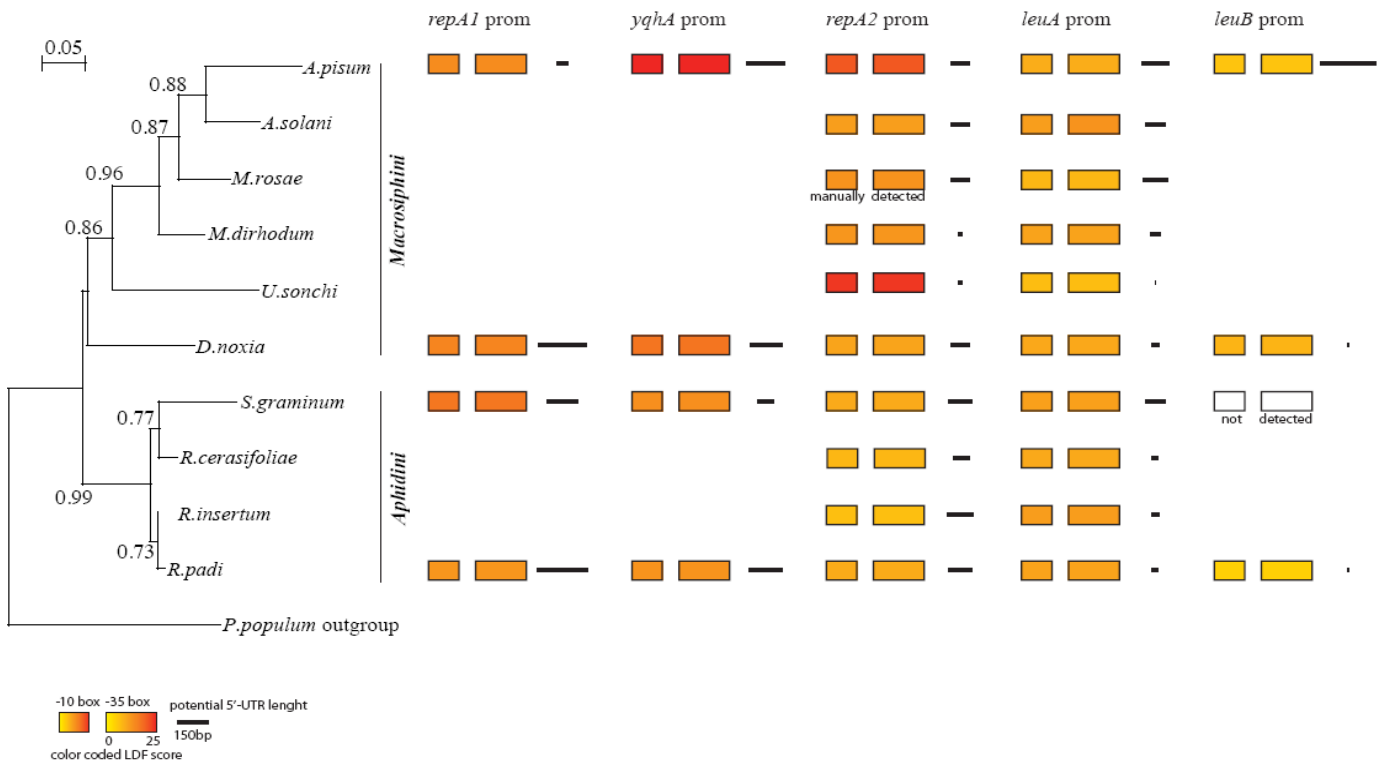


Table S1. Neosynthesis of amino acids from the carbons of sucrose in the symbiotic pea aphid reared on diets with leucine concentrations ranging from 0 to 80 mM.

Values (means \pm SE, n = 5) are expressed in sucrose equivalent (nmoles) per unit of aphid fresh weight (mg).

Amino acid	Dietary leucine concentration					P-value *
	0 mM	20 mM	40 mM	60 mM	80 mM	
Aspartic acid	9.1 \pm 0.6	9.9 \pm 0.5	10.1 \pm 0.3	10.1 \pm 0.4	10.2 \pm 0.4	0.49
Threonine	2.4 \pm 0.4^a	2.8 \pm 0.2^a	3.6 \pm 0.2^b	4.3 \pm 0.2^b	3.9 \pm 0.3^b	< 0.001
Serine	5.7 \pm 0.3	5.9 \pm 0.1	6.3 \pm 0.3	6.8 \pm 0.3	6.4 \pm 0.5	0.22
Glutamic acid	18.8 \pm 0.9	17.8 \pm 0.7	18.3 \pm 0.6	17.5 \pm 1.0	18.5 \pm 0.5	0.77
Proline	10.4 \pm 0.2	12.0 \pm 0.4	11.8 \pm 0.5	11.6 \pm 0.5	12.3 \pm 0.6	0.14
Glycine	4.2 \pm 0.2	3.9 \pm 0.1	3.9 \pm 0.3	4.1 \pm 0.2	4.1 \pm 0.1	0.77
Alanine	13.6 \pm 0.9	13.9 \pm 0.5	14.5 \pm 0.5	14.8 \pm 1.1	15.8 \pm 0.2	0.21
Valine	5.6 \pm 0.2^a	6.8 \pm 0.2^b	8.2 \pm 0.2^c	8.9 \pm 0.6^c	9.0 \pm 0.7^c	< 0.001
Cystine	0.7 \pm 0.1^a	0.7 \pm 0.1^a	0.3 \pm 0.05^b	0.5 \pm 0.05^{ab}	0.5 \pm 0.1^{ab}	0.02
Methionine	0.6 \pm 0.1	0.5 \pm 0.1	0.5 \pm 0.2	0.8 \pm 0.1	0.6 \pm 0.1	0.25
Isoleucine	5.9 \pm 0.4	4.4 \pm 0.2	5.3 \pm 0.3	5.4 \pm 0.6	5.1 \pm 0.3	0.14
Leucine	19.7 \pm 1.4^a	6.7 \pm 0.6^b	4.8 \pm 0.3^c	3.3 \pm 0.4^{cd}	2.4 \pm 0.3^d	< 0.001
Tyrosine	3.4 \pm 0.3^a	3.2 \pm 0.3^a	5.0 \pm 0.3^b	5.2 \pm 0.2^b	5.2 \pm 0.7^b	0.002
Phenylalanine	6.4 \pm 0.3	6.2 \pm 0.2	7.0 \pm 0.2	7.0 \pm 0.5	7.4 \pm 0.5	0.12
Lysine	3.8 \pm 0.4^a	3.4 \pm 0.2^a	4.8 \pm 0.2^b	4.9 \pm 0.6^b	5.4 \pm 0.4^b	0.006
Histidine	nd [†]	nd	nd	nd	nd	
Arginine	nd	nd	nd	nd	nd	

* P-values of ANOVA (diet effect) performed for each amino acid. When the diet effect was significant (bold values, F-test P-value < 0.05), means were further compared with Student-Newman-Keuls test; columns with different letters are significantly different.

† nd = null value or below the detection threshold.

Table S2. Sequence information on primers used for real-time quantitative PCR and operon validation experiments.

For each couple of primers, sequences, lengths, annealing temperature and amplicon length are specified.

Gene	Primer	Sequence primer 5'- 3'	Primer length (in bp)	Primer Ta (in °C)	Amplicon length (in bp)
<i>atpA</i>	atpA-For	AAATGATTTTATTGCCTAA	19	47.1	99
	atpA-Rev	CAGAAATATGAATATAGGGA	20		
<i>ilvH</i>	ilvH-For	GAATCAGGTGCACTATCAAG	20	46.8	90
	ilvH-Rev	AGGATCTTCAGTAGGTGCTA	20		
<i>ilvI</i>	ilvI-For	TCTTTAATGGGATTAGGTAG	20	47.5	183
	ilvI-Rev	AACAATCGCATTTGG	15		
<i>leuA</i>	leuA-For	GATATACTGTACCCAACGAA	20	46.8	178
	leuA-Rev	ATTCCGTTTATAGTCCCT	18		
<i>leuB</i>	leuB-For	TTGCCAAAACTACATTGC	19	47.1	93
	leuB-Rev	TTCTACTGGAAGGTTATCCC	20		
<i>leuC</i>	leuC-For	AGCCTTTGATTCATTACGAG	20	47.4	127
	leuC-Rev	TACCTTTGCCATAGAACCT	19		
<i>leuD</i>	leuD-For	ACATGCTGGTATCGTTGTTC	20	44.6	125
	leuD-Rev	AACGCCAGTCATGAA	15		
<i>leuABCD</i>	ABCD-For	TAAACGGAATTGGCGAAAGA	20	50.8	3697
	ABCD-Rev	GATGAGCCGCAACCAAA	17		
<i>repA1</i>	repA1-For	ATGGGTTTTGTTACTTGC	18	46.4	154
	repA1-Rev	TATTGATCCACCCTAATTGT	20		
<i>repA2</i>	repA2-For	ATTATATCGCAATTAGATGA	20	43.6	105
	repA2-Rev	TAAACCCTTCGGACCT	16		
<i>rplX</i>	rplX-For	AAAAAGAAGCACCTATTCAT	20	44.4	93
	rplX-Rev	TCCCTTCTTCAAACCTAA	18		
<i>rpmC</i>	rpmC-For	GGCATTGGTAGAATTTAGAA	20	46.8	184
	rpmC-Rev	CTCTTCCTTTGAATCTAGCA	20		
<i>yqhA</i>	yqhA-For	TTATCATGCCAGATATTGTG	20	47	174
	yqhA-Rev	CCATCCACCCTAATCTTT	18		

Table S3. Descriptive statistics from the BestKeeper software of the three candidates for data normalization, the *atpA*, *rplX* and *rpmC* genes.

On the three tested genes, only *atpA* and *rplX* met the criteria imposed by the Bestkeeper analysis: standard deviation ≤ 1 CP between the three tested conditions at each time point.

Abbreviations: n: number of samples; geo Mean [CP]: the geometric mean of CP; ar Mean [CP]: the arithmetic mean of CP; Min [CP] and Max [CP]: the extreme values of CP; std dev [\pm CP]: the standard deviation of the CP; CV [% CP]: the coefficient of variance expressed as a percentage on the CP level. Conditions showing significant gene variation (Cp \gg 1) are in red.

	12 hours			1 day			2 days			3 days			7 days		
	<i>atpA</i>	<i>rplX</i>	<i>rpmC</i>	<i>atpA</i>	<i>rplX</i>	<i>rpmC</i>	<i>atpA</i>	<i>rplX</i>	<i>rpmC</i>	<i>atpA</i>	<i>rplX</i>	<i>rpmC</i>	<i>atpA</i>	<i>rplX</i>	<i>rpmC</i>
n	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
geo Mean [CP]	25.90	26.30	26.27	24.64	24.41	24.86	24.88	21.44	25.65	24.65	21.68	24.83	25.92	23.54	23.64
ar Mean [CP]	25.92	26.32	26.46	24.65	24.43	24.90	24.91	21.47	25.76	24.67	21.71	24.94	25.94	23.54	23.65
min [CP]	24.77	24.8	23.68	23.78	23.33	22.77	23.5	19.94	22.68	22.74	20.31	21.33	24.7	22.77	22.81
max [CP]	27.55	28.04	31.44	25.72	26.41	26.67	26.49	23.62	28.34	25.75	23.45	27.17	27.9	24.27	24.65
std dev [\pm CP]	1.01	0.98	3.02	0.67	1.07	1.22	0.99	0.89	2.07	1.05	0.98	2.13	0.92	0.49	0.58
CV [% CP]	3.89	3.73	11.42	2.70	4.37	4.90	3.97	4.15	8.03	4.25	4.53	8.54	3.56	2.09	2.43

Table S4. Overall transcriptional response of *B. aphidicola* to variations of leucine concentration in the aphid diet.

CP values are indicated for each gene and for each sample. A sample is one of the three independent biological replicates for each condition (0, 20 or 60 mM leucine) and at each time point (12 h, 1, 2, 3 or 7 days) used in this experiment. For each sample, total RNA was extracted independently and 1 µg of it was retro-transcribed and then used for the quantitative PCR reaction. For each gene, the PCR efficiency represents the mean of all the reaction efficiencies obtained in this study.

Gene		<i>atpA</i>	<i>rplX</i>	<i>rpmC</i>	<i>ilvI</i>	<i>ilvH</i>	<i>leuA</i>	<i>leuB</i>	<i>leuC</i>	<i>leuD</i>	<i>repA1</i>	<i>repA2</i>	<i>yqhA</i>	
PCR efficiency		1.78	1.99	1.86	1.93	1.92	1.85	2.00	1.98	1.82	1.76	1.81	1.73	
12h	20 mM	Sample A1	25.64	25.75	23.87	19.83	20.90	25.25	23.81	21.78	23.55	28.05	29.84	27.69
		Sample A2	25.95	26.66	24.77	20.13	20.25	25.88	24.50	20.99	23.27	29.43	29.67	26.14
		Sample A3	24.83	24.80	24.34	19.49	20.50	25.72	22.18	21.50	22.94	27.56	29.79	29.23
	0 mM	Sample B1	24.93	27.68	24.08	18.96	21.76	24.02	22.01	19.45	21.96	28.67	27.95	23.78
		Sample B2	24.77	27.31	24.43	18.17	20.73	24.23	22.27	19.71	22.33	29.23	27.85	24.43
		Sample B3	24.92	28.04	23.68	19.01	20.44	24.26	21.46	19.57	22.43	28.06	27.76	23.13
	60 mM	Sample C1	27.34	25.53	31.01	26.30	22.86	29.97	27.87	25.41	26.88	37.23	34.65	30.92
		Sample C2	27.55	25.51	30.53	26.59	22.81	29.13	26.91	24.49	26.80	35.21	35.28	32.50
		Sample C3	27.41	25.59	31.44	28.06	23.00	29.38	26.79	24.78	26.91	36.20	33.98	29.33
D1	20 mM	Sample A4	25.72	23.33	26.67	24.67	23.56	26.84	24.54	23.69	24.80	31.36	28.34	26.00
		Sample A5	25.52	23.68	26.43	24.53	23.67	27.36	24.57	23.65	25.08	30.97	29.43	25.96
		Sample A6	25.65	24.02	26.19	24.77	23.62	27.26	24.58	23.49	25.17	31.71	30.94	25.91
	0 mM	Sample B4	23.78	26.41	22.77	17.69	20.13	22.25	20.42	18.95	21.97	25.89	25.29	19.91
		Sample B5	24.01	26.01	23.62	17.11	19.04	22.65	20.32	19.20	21.17	26.30	25.52	18.95
		Sample B6	24.71	25.69	22.83	17.49	19.84	22.89	20.39	18.79	21.21	25.43	25.69	19.70
	60 mM	Sample C4	24.03	23.59	25.33	26.68	26.54	26.90	24.31	22.66	24.12	33.93	34.05	26.49
		Sample C5	24.23	23.65	25.21	27.96	26.93	27.89	25.12	23.28	24.83	33.32	33.63	26.58
		Sample C6	24.20	23.53	25.08	27.02	26.68	28.94	23.45	22.30	24.93	33.30	34.42	26.48
D2	20 mM	Sample A7	25.98	22.09	28.34	22.41	21.86	28.23	22.84	21.17	24.90	31.83	31.49	34.33
		Sample A8	26.49	21.90	28.33	21.05	22.47	28.27	22.57	21.92	24.66	31.06	31.28	34.94
		Sample A9	26.46	22.23	28.28	23.73	22.47	28.05	22.73	21.55	24.93	31.47	31.65	33.71
	0 mM	Sample B7	23.50	23.62	22.68	16.31	18.47	21.38	20.85	18.63	21.10	25.88	23.68	19.00
		Sample B8	23.72	21.43	22.81	16.75	18.16	21.68	20.53	19.29	21.53	25.81	24.67	19.40
		Sample B9	24.06	21.53	22.80	17.67	18.44	21.67	20.73	18.54	21.31	26.48	24.75	19.79
	60 mM	Sample C7	24.52	20.46	25.42	21.68	20.64	25.93	22.30	21.58	23.22	28.11	30.25	24.04
		Sample C8	24.28	19.94	26.83	21.58	20.94	26.54	23.59	22.07	22.96	28.27	31.19	23.45
		Sample C9	25.15	20.04	26.31	21.74	20.92	26.69	23.00	21.58	23.39	28.59	29.92	22.88
D3	20 mM	Sample A10	25.26	21.84	26.18	23.65	21.97	26.07	24.72	21.85	24.59	28.91	28.03	28.80
		Sample A11	25.51	21.36	26.65	22.73	22.88	26.76	25.12	21.90	25.00	28.20	28.64	27.91
		Sample A12	25.64	20.83	25.70	23.73	22.58	26.61	25.47	22.90	24.80	29.58	28.66	29.69
	0 mM	Sample B10	23.13	23.15	21.33	18.16	18.78	22.46	24.07	19.35	21.58	26.21	26.15	20.80
		Sample B11	23.43	22.81	22.14	18.31	18.90	23.06	22.21	19.80	21.82	26.23	27.17	19.89
		Sample B12	22.74	23.45	21.76	20.20	19.21	23.21	22.46	19.53	22.17	26.20	26.89	20.03
	60 mM	Sample C10	25.13	20.31	26.94	22.85	22.44	27.74	23.64	23.23	24.43	29.62	31.12	24.13
		Sample C11	25.75	20.94	26.56	22.45	22.31	27.99	23.67	23.10	24.78	29.98	31.35	24.38
		Sample C12	25.46	20.67	27.17	22.38	22.54	28.79	23.79	23.33	24.63	30.28	31.30	24.17
D7	20 mM	Sample A13	25.71	23.64	23.57	23.36	24.34	24.09	24.59	24.14	24.16	25.66	26.02	23.85
		Sample A14	25.62	23.62	23.56	23.58	24.50	24.13	23.86	24.11	24.13	25.84	26.05	23.98
		Sample A15	25.99	23.49	23.73	23.56	24.45	24.21	24.22	24.10	24.06	26.06	25.77	24.32
	0 mM	Sample B13	24.70	22.77	22.81	22.89	23.95	23.55	23.64	23.58	23.66	25.02	25.28	23.71
		Sample B14	24.78	22.81	22.84	22.84	23.99	23.53	23.30	23.64	23.58	25.00	25.32	23.45
		Sample B15	24.74	22.89	22.87	22.92	23.92	23.62	23.15	23.56	23.62	25.07	25.32	23.33
	60 mM	Sample C13	26.76	24.19	24.51	24.50	25.06	24.71	25.22	24.56	24.70	26.45	26.38	24.89
		Sample C14	27.26	24.20	24.65	24.13	25.03	24.88	25.07	24.73	24.66	26.51	26.22	25.32
		Sample C15	27.90	24.27	24.29	24.52	25.02	24.91	24.86	24.87	24.54	26.66	26.36	25.28