Short communication

A POSSIBLE APPROACH TO STUDY AUTOPHAGY IN *DROSOPHILA**

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The process of autophagy, or bulk degradation of cellular proteins and organelles through an autophagosomic-lysosomal pathway constantly functions in all eukaryotic cells. Also a type of physiological cell death exists, which is best characterized with the strenghtening of the autophagic process, but no DNA degradation or caspase activation can be detected, in contrast to apoptosis [2].

Autophagy can be promoted in various ways: addiction of certain drugs (like vinblastine [6]), hormones (like 20-hidroxy-ecdysone [3]) or simply nutrition deprivation [5] leads to the increased amount of proteins degraded by lysosomal enzymes.

The isolation and cloning of yeast autophagy mutants gives an excellent opportunity to examine their putative homologs in *Drosophila melanogaster*. Fourteen genes have been identified in *Saccharomyces cerevisiae* required for autophagy [5], based on several mutant phenotypes, like the sorting problems of vacuolar enzymes such as carboxypeptidase Y or aminopeptidase I, or the less of viability and the inability of degrading cytosolic proteins like fatty acid synthase during starvation. Nine of them *(apg5, apg6, apg7, apg12, aut1, aut2, aut7, aut9, vps4)* appear to have clear homologs in the fly and human genome, using the BLAST tools at http://workbench.sdsc.edu, http://www.ncbi.nlm.nih.gov and http://www.fruitfly.org (BLASTN, TBLASTN services) for sequence similarity searches. The sequence alignment of the yeast, fly and human proteins can be seen in Figure 1.

The high degree of similarity suggests existing homology among these genes, although new and lost functions were identified in some cases [7]. Remarkably, *vps4* exists in two slightly different copies in human, and *aut7* exists in multiple different copies as well (two in *Drosophila* and three in *Homo*), suggesting different roles, or at least different regulation. As expected, fly and human genes are much more similar to each other than to the yeast homolog, promising that *Drosophila* experiments will better contribute to the understanding of the roles of these genes in detail in higher eukaryotes. The precise function of these genes is still unclear, however, molecu-

^{*}Dedicated to Professor János Kovács on the occasion of his 70th birthday.

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Fig. 1 Multiple sequence alignment (using the CLUSTALW program at http://workbench. sdsc.edu) of the nine yeast autophagy genes and their putative APG5 1 ---MNDIKOLL&NGELNVLVSIDPSFLMKGSDREIAV RIGDPRETYLVN MEDIWADISFLEFDPLTDSEK-YFERHEK. IP N. FVEDITC CLEGKSATFTSFENQVODVLTFL Sc 1 MARCHEVIENTNE, QUECTEQALREETVENTSELS------ CIECVICKIRAY-RYISA HQQGAVEEDF STELREASTST Y CLEHPEEDSTENCLIEFS------1 MTDEKINA DVNFGRIPTETLYQESITEREASFYYLELPEYS------YUT CIECKIR HUQKVMRQEDIS-EISTEYEETFEKERFESLESELS SS-SALFMIIVEEM-----Dm Hs Dm 108 -----KETEDMLVKLNSKELLESHYDSKLWERDVLKHRG-LEISANGEMEENNGLELGEVERKEEGEN VERLESPYGDLESEKNEELESHYDDVRLHVHPETDFEDQEGRTKEEFG Sc 209 --TSGTERISQPTIENTGVNPTLEDIEGDILEVKEGINGED------VM-ICQLEEIPWHMLEVDEVSKERSFEGFEVETKVEIKGGDKASSEL Dm 219 RENGRIIDTCAOSAGEGERIGALHA/LATGEREGEGKESSAPESRTPGLIGCRTHADDLHES COMMADAGE FLATELAVDYKDV-------HS 197 PRIOKLERPVAD OLH LGDLEEVCPSAIDED EKKNQ------VMICTEPMLE POLESSE ALADED FILL QPTD-----Sc - Saccharomyces cerevisiae Apg5 Dm - Drosophila melanogaster CG1643 Hs - Homo sapiens mRNA for apoptosis-specific protein (Y11588) APG6 1 MKCOTCHLPLOLDPSLEGLSLTORNLLLSTORIIITATNENVISNKGIE ADN GPO PKERLRRLGEION KONKOKLITDSFVF NHD DD A ITSNSREDORY NANGNDNKKA Sc Dm 1 ------MEGSKT SATE TO SATE AND SA Hs SC 121 NODTSDGTSTFRDHUEREQEATDEDENQQIQLNS TO TQVNAMTNVRN GOR TO TQVNAMTNVRN GOR TINQUCKNI INR KS YDDAIKER T AQFESKLESG KEISESNKEKQYSHNLSEKEN Dm 54 ASSEDHEVERYALT.SINGTGEM.V--SCRON KMEAAFYLKAELECCHENSELERED. A.SMEELM REIRIAD.W.V.BAYDDELECRAPP-----NVEALDKELDE HS 76 DGVSRREIFRAMMST SANSET IGEAEDGTMEN. RRLEVTGD.FIM.G.DV.H.LEETTILDQ.TQ.NVT.NECQN.ERC.EI.F.M.ED------DSEQ.QMELKE SC 241 FKERERLADQULRLAMTDDDDDGELVRLAEKKVQUENEKLAKLSDQNLMDLNNIQFNKNLQUKLYELALNALDNIUFRATAUAAL SUBSVAPAKAAAL Dm 164 KRSQQLISEKEKKEEQSINDALAEEQOREE HEQEESIWASITKHRIELMLEEDKRSISCIA KOSISTIPPEDALEITINAAHITTIAAH HS 188 ALEESSIQEEDVENRKIVAENEEKVAAARIDQEEAYQEISEKKQQLELDEKKVNMRAQTIIDIKKIVVIATTIPPAAH Sc 361 COLLELATINKNLKINLVDCELQEM SFSKIKKRWN CONNNSTINAPGDWLIEV VDENFNLERERKES COCKSLETT EIISEITROLSTIASSYSSQTLTTSODESSMNNAND

Sc 481 VENSTSILELPYIMNKDKINGLOV/LHGSOPNLE/CT/MFCLUCOV/RLARSONLLSKSITLSPTVNYNDKTISGN

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Sc - Saccharomyces cerevisiae Apg6 Dm - Drosophila melanogaster CG5429 Hs - Homo sapiens Bcl-2 interacting protein Beclin

homologs in Drosophila melanogaster and Homo sapiens. Light grey letters refer to identical, dark grey letters refer to similar amino acid residues

APG7 i MSSERVLSYARAFKSFLDTSFFØELSRLKLDVLKLDSTCQPLTVNLDLHNIPKSADQVPLFLTNESFEKHNNKRTNEVPLQGSLFNFWVLDEFKNLDKQLFLHQRALECNEDGI Dn 1 MSSERBIILQFAP-NESFVSFTFWHKLAELKLDHDRLSDSKRSTTOHYTNRNSGCLLEVDYTAXNRNAKPPKFSHSALG%LYNKWTIEFFKALDKUQLFLHQRALECNEDGI Hs 1 MAAAIGDPGLSKLQFAP-FSSALDV3FWHELAELKLDHDRLSDSKRSTG9YYTNBASGCLLEVDYTAXNRNAKPPKFSHSALG%LYNKWTIEFFKALDKLQFLADDCM Hs 1 MAAAIGDPGLSKLQFAP-FSSALDV3FWHELTQKKLNEYKLDEAEKDIKGYYYNODSAGLPARLTEFSAFDNSAPTPARCCFAIGFLYNNTUFFSFKTADKKLDEAGAANELWES-I	<pre>sc 115 KDINKCVSFULISFADLKKYREYYMLGVPCFQRESSTVLHVRDEPSLKGLESKCQKWFDVNYSKWYCILDADDELVNYDKCIIRKTKVLAIRDTST Dm 111 CSGGAARDPSLLFRFVLSFADFKCHSYTWRAFPDPLTFTLKLQGAVQKLRDLRUSSSYIMALKALPTE-SQNFFILYANVEKNIFEARSLSSLDDKNVEFCYFGFADPSE Hs 117 KSGTALENPVLANKFLLLFFADEKKYHFYTWFCYPALCLPESLPLIQGPVGLDQRFSLKQEADELBCAXDNLCQTEGVTALPFLIKYDENMVLVSLLKHYSDFFQGGGRTKITISVYDEN Hs 117 KSGTALENPVLANKFLLLFFADEKKYHFYTWFCYPALCLPESLPLIQGPVGLDQRFSLKQEADELBCAXDNLCQTEGVTALPFLIKYDENMVLVSLLKHYSDFFQGGGRTKITISVYDEN</pre>	Sc 211 MENVPSALTKNPLSVEQYDVP-DLIDFKLLIRQUBGSFALMATFASIDPQSSSSNPDMKVSGMERNVQGKLAPKVVDLSSLLDPLKIADQSVDEALKLMKWKLEFDIALDTIK Dm 222 YEH-PAMINENYAAFLLQQCP-SFVGKPIKFLG-LEHNQOMIDDSLWKVICTEACDLSQSSNIKFVGMELMKOKMGPRMVCMRDSMDPAKIAENSVNENLELMKUKLVPDEALLIN Hs 237 LAQYPGMPLAPRPLVLAARRUSSSPQSVEVVCFRDRTMQGARDVAHSIIFBVKLPRMA-FSPDCFXAVGMERKNQKGGMGPRMVULSECMDPKKIAESSVDEALKCWRLVPTLDLDKUVV	8c 324 NTKULLDAGTEGCVVSRALIAWGVKRITFUNGTVSYSNPVRQALNNEBCGKEKABLAASLKRIPPLNDATGVKLSIPMIGHKLVNEBAQHKDFDRLRALIKEHDIIFLL Dm 339 OTKOLLFGAGTEGGAVARMLLSKSFRHITLDOSGKOFSNPVRQMUTTADAVAGNRMKATTAAQRAKEINPSAFRAGYULEIPMPGHTIGESLLAQTKEHLKVIKKLVQDHDVIFLL Hs 355 SVKCLLLGAGTEGGAVARMLLSKSFRHTTPUDMAKISYSNPVRQMLXFBADAVAGNRMKATAAADRLQKIFFPGVNARGFNMSIPMFGHPVNFSSVTLEGARHDVBGLEQLIESHDVVFLL	5c 437 UDSRESRWLFSLLSNIENKTVINAALGFDSYLWRHGURD-EQSSKQLGCYFCHDWVAPPDSLTDRTLDQWCTWFHGWAMMASSLAVELMTSL Dm 457 TDSRESRWLPTLAGAAKRENTNIAALGFDSYLWRHGTTR-KEAGDDG0BIBGLKCINGQLGCYFCHDWDAFDSLTDRTLDQWCTWFHGWSNIASYAVELLVAL Hs 475 MDTRESRWLPAVIAASERKLVINAALGFDTFVYRHGLKKPKQQGGDDLCPNHPVASADLLGSSLFANIPGYKLGCYFCHDWVAPGDSTRDRTLDQQCTWFHGLAALAFDLAALAVELMVSV Hs 475 MDTRESRWLPAVIAASERKLVINAALGFDTFVYRHGLKKPKQQGGDDLCPNHPVASADLLGSSLFANIPGYKLGCYFCHDWVAPGDSTRDRTLDQQCTWFHGLAALAFDLAALAFDALAFLAASIAVELMVSV	Sc 530 LQTKYSGSETTVLGDIPHQIRGFLHNFSILKLEPPAYEHCPACSPEVIEAEPDLAMEFVEKALHHP-LYLREISGLSVIKQ3VBRLGNDVFBMDDE Dm 564 LQHPRKELAPAYYQSGRCRSEETEEKVPEGLLGILPHSIRGMLCNYENILPAYQKPACCIACSAAVLNEYKKBGHAFLFNTFFTA-KFLEDLIGGISEFKRLNSEIIDFDDEEFDBNSDSD HS 595 LQHPBGGYAIASSSDDRMNEPPTSLGUVPHQIRGFLSRFDNVLEVSLAPDKCTACSSKVLDQYEREFNEKKBSHFLEDLIGGISEFKRLMSEIIDFDDEEFDBNSDDE HS 595 LQHPBGGYAIASSSDDRMNEPPTSLGUVPHQIRGFLSRFDNVLEVSLAPDKCTACSSKVLDQYEREFNELAKVFNSSHSFLEDLIGGIFLLHQ3YBRLGNDSE HS 595 LQHPBGGYAIASSSDDRMNEPPTSLGUVPHQIRGFLSRFDNVLEVSLACCCCSSKVLDQYEREFNELAKVFNSSHSFLEDLIGGIFLLHQ3YBRLGNDSE HS 595 LQHPBGGYAIASSSDDRMNEPTSLGUVPHQIRGFLSRFDNVLEVSLACCCACSSKVLDQYEREFNELAKVFNSSHSFLEDLIGGIFLLHQ3YBRLGNDSE HS 595 LQHPBGGYAIASSSDDRMNEPTSLGUVPHQIRGFLSRFDNVLEVSLACCACSSKVLDQYEREFNELAKVFNSSHSFLEDLIGGIFLLHQ3YBRLGNDSE HS 595 LQHPBGGYAIASSSDDRMNEPTSLGUVPHQIRGFLSRFDNVLEVSLACCACSSKVLDQYEREFNELAKVFNSSHSFLEDLIGGYLLAQ3YBC HS 595 LQHPBGGYAIASSSDDRMNEPTSLGUVPHQIRGFLSRFDNVLEVSLACCACSSKVLDQYEREFNELAKVFNSHSFLEDLIGGYLLHQ3YBV HS 505 LQHP	Sc - Saccharomyces cerevisiae Apg7 Dm - Drosophila melanogaster CG5489 alt1 Hs - Homo sapiens El-like protein (only the sequences corresponding to the first 626 amino acids of Apg7 are shown)	APGI2 3c 1 MSRILESENBTESDESSIISTNNGTAMERSNANDELRSSPHTVONRLELFSRALSQLGLASD: SVDQOVEDSSSGTYEOEHTIKTNAQTSKQKSHKDEKNIQ1KFQFLGSLGQLKPS Dn 1 FULSQRLASDSSESSES 1 FULSQRLASDSSESSESSESSESSESSESSESSESSESSESSESSESS	Sc 121 UCKIENSOSFAMUILELERERLENEHVYCYINNEFAESPOONIGELMMOFKENDELIVSYCASVAFG Dn 44 TWTUDDNEFVGWIOTFIHKELKLDASEQIFLYNNQTFAPAPDQIIKULVKCHGYNGKLULVYCKNQAMO HS 70 KWAVERTERIQGLIDFIKKEELKLVASEQLFIYVNQSFAPSPDQEVETLYECFGSDGKLULHYCKSOAMG	Sc - Saccharomyces cerevisiae Apg12 Dm - Drosophila melanogaster CG10861 Hs - Homo sapiens cDNA clone AW085439	AUT1 Sc 1 MIRSTLSSMREYLFPITHKSTFLTGQITPEEFVQAGDYLCHMEPTWKMNEBSSDISYRDPLFKUKQFLIIKKPFCDKRAEQCVEVEGPDVIMKGFAEDG2DDVLSYIG Dn 1 MOSVLNTVKGTALAVAEYLFFULKSSKFRETGVLTPEEFVQAGDYLCHMEPTWKMREBSSDISYRDPLFKUKQFLIIKKPFCDKRAEQCVEVEGPDVIMKGFAEDG060WVBTHQLNDDGTF Dn 1 MOSVLNTVKGTALAVAEYLFFULKESKFRETGVLTPEEFVQAGDHLVHHCPFWQMAAG-DETKTKPYLPKDKQFLIIKKVPCCKRCKQMEYVGE-ETLVEEESGDG060WVBTHQLNDDGTF Hs 1 MONVINTVK0KAGEVAEDGVLTPEEFVAAGDHLVHHCPFWQMAAG-BELKVKAYLPTGKQFLUTKNVPCCKRCKQMEYSDELEATIEBDDG0606WVBTYHN-TGIT	Sc 111 SETERVQSTPAGG-TKDSSIDDIDELIQDMEIKEEDENDDTEETNAGGGLAKDMAQERYDENIANSTSYRVFXMIV95NSN Dm 119 QLEDKICELIMEETREEMHTPDSDKSAFGAGGAEDEDDDFAIDMODFEESKMALAUTTEKPEFEAKASPVAAASGDAEASGDSVLHTRTYDLHISYDKYVQTPRLMVV9VDEQ Hs 118 GITEAVKEITLEN-KDNIRLQDCSALCEEEEBEBGEGAEMESVERSSGLLEFTEATLDTKKIVERCKAKTDAGGEDAILQTHYVDLYITYDKYKYVQTPRLMVV9VDEQ Hs 118 GITEAVKEITLEN-KDNIRLQDCSALCEEEEBEBGEGAEMESVERSSGLLEFTEDTKKIVERCKAKTDAGGEDAILQTHYVDLYITYDKYVQTPRLMFJGYDEQ	Sc 193 GSPEGFBQMFBDFSADYRFKFAFIEKLPFYNNSULGVSTHPCKHANVMKTLLDKVRVVRQRRKELQEBQELDGVGDWBDLQDDTDBSLRVDQVLIVEHKPTESVF9SIGHDYFMEGM Dm 239 KKPEFVFBQMYEDDFACKTVTMESHPHLP-GPNDASVHPCRHADINKKIIQTVEEG	Sc - Saccharomyces cerevisiae Autl Dm - Drosophila melanogaster CG6877 Hs - Homo sapiens cDNA clone AL137515
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Fig. 1 (cont.)	AUT2 1 PDDFDSRIGUTYPOR-WLQDWKMDLVQKVSHGVFEGSSE PAALM-HUYTEUEV, PERDESGAEQCEQDCRYRGEAVSDGFLSSLFGREISSYTK_FLUPTSAVADAUTAPTREVERAL Sc 1 NLVGDDQLARIDESVFEAXLGPDSVLASAVQQAVGSGEPTIERRTTUP VERDESGAEQCEQDCRYRGEAVSDGFLSSLFGREISSYTK_FLUPTSAUA Dm 1 NLVGDDQLARIDESVFEAXLGPDSVLASAVQQAVGSGEPTIERRTTUP VERDESGAEQCEQDCRYRGEAVSDGFLSSLFGREISSYTK_FLUPTSAUA Hs 1 NLVGDDQLARIDESVFEAXLGPDSVLASAVGQAVGSGEPTIERRTUP VERDESGAEGCEQDCRYRGEAVSDGFLSSLFGREISE	Sc 119 RADDGPSPLSLNLLVRTNPLSTIEDYLANPDCEN IL CARALLET SLIGNALLET SLIGNALLET DE VNGNES-LERES FAWEN TPEAPFILLINFVSATTELSDER PREFERANTSLID Dm 87 EVQLTTTLLTTLLTTLLTTLLTTLLTTLLTTLL	Sc 238 QSHIYGEPECGIDDCI'SVSGGDIYENENEKFRA	<pre>sc 327 suppletentpletents.compStyleGtentpletentput Intigentpletentput Intigentput StatinularRMDDFDVS TMDDV StandardDV StandardDV Dm 264 DDTVTLLDETTTTTTTTTYPETTYRQK1-AA CAFTA CAFTA CAFTA CAFTA SEELLTKLEEV STATENDFDVS TMDDV STANDTTEDLDW TMPD Hs 271 BEDLINDERTTYPETTYRE-DESERCOFPECENSTATENETLEETLEVETTYPETLETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT</pre>	Sc 437 VIJGAIFPHTTNTEDVIDEYDCEOLIHCKKQKIVVMGNTHTVNANLTTYEVE VIVEKETVGIHSPIDEKC Dm 369 IUWPAGTADSUSFAIVEBSGRÜSUAGSGKKPSERAVISUAGSGKKPSERAVI	Sc - Saccharomyces cerevisiae Aut2 Dm - Drosophila melanogaster CG4428 Hs - Homo sapiens cDNA clone AL080168 (KIAA0943)	AUTT SC 1 INTURKISEY FREKASERIADREKNEIVICE ESDIPETER FALL VYV M P.K.I.T. DTL.I.A.LSALCKKK G. VT G. TFR-SC Dm1 1 INTURKISED NUDFERVER T YAL P.K.I.T. DTL.I.A.LSALCKKK G. VT G. TFR-SC Dm1 1 INTURKISED NUDFERVER T YAL P.K. TS.T. RQ- Dm2 1 INTURKISED NUDFERVER G. K A.K. FORMARK MAK Hs1 1 VIV F.F. VIV S E.F. IA.C. Hs2 1 VV F.F. VIV S E.F. IA.C. S LA.C. Hs2 1 VV F.F. VIV S E.F. IA.C. S LA.C. LA.C. S LA.C. LA.C. LA.C. S LA.C. LA.C	Sc - Saccharomyces cerevisiae Aut? Dml - Drosophila melanogaster CG12334 Dm2 - Drosophila melanogaster CG1534 altl Hsl - Homo sapiens GABA-receptor associated protein Hs2 - Homo sapiens cDNA clone AA476809 Hs3 - Homo sapiens Gef-2 protein (the last two amino acids [I,N] of Dm2 are not shown)	
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AUTS SC 301 BNLIFLQDVNNYLGNGYCILLERLENICILLEREVETVNGE DYSKEP SHRVSDIJD.CYSNSITGEKFELWMFYFFVILKIVOLYEDVGKLSELON KY Dm 92 EDESSESSMO.QXHHATVIVVDBM.QUEFGERWHLAFVMER REDVIEDDIHHRIEN.NYCYALANFILDERCENN WYTYLVVFIAAIYLGFRIERWYHITGYADIKRFANS Hs 1	SC I -PETTGFELQ SIDUTTOPEYTAYNGLD LMLLKSKN-PISTLYFE E. NENQ XH E'E ANA XS SAG GNGGNK I QEE D-NGGEDNY RG Dm I - RAYT LYALL VALLEY SAEDENNYRAEAA EG SEETTER LYEE FROM LY UN KG VIN HAAN SAEDEN AN SAEDEN AN SAEDEN AN SA HS1 I - MTSI SAEDEN AN SAEDEN A HS2 I MSSI SPN JYALL VALLEY SAEDEN AN SAE	Sc 118 ALSSELLS FORCES ENGINEERE LEVEL VEELLEVART KINKTS OF YET WELLER VEEL AND AN OVER MEREN PATER VEEL VEEL Dm 117 KLEDE VEERVOKENDALEAANDEREATUREERE LEVEL FOR VEEL VEEL VEEL VEEL AND KOURDERE VEEL AND VE VEEL AND VEEL AND	Sc 237 ITTTGGGGGB/STATTLYPEN TERS SQUVITENT TYQUESPIRETTRIFTEDDLANTTTEINUDE CITKELY T.GAMIERES. AVV KERANETTI Dm 237 MSR.SDDENDSVETTSELYREN SUTTENT STATESTATION OF THE DETENDENT TO DE LANTTENDE CITKELY T.GAMIERES. AVV KERANETTEN HS1 232 BOGBENDESERAFTER STANDARD NEUTENDENT STATESTATESTATESTATESTATESTATESTATESTA	SG 357 AFRENDYSEEDDETRKLERONSEGEDONLENS TITEATELKEDLIK FRAKKS REDVELLIQUEDTRENDEN VANN Dm 357 AFRENSKE PROHETENDELVERONDEN VANNEN SPELFERPERSKE KRENSE KERKEN DE SAME AFRENSE VAN DE SAME VAN DE SAME Hal 352 Afrenske Gebenniskmindeligtender Mennen frem seine Leiten Canter Krenske frem dat de Afrenske frem som Has 359 Afrenske Gebenniske Statementendere Mennen frem seine Leiten Canter Krenske frem dat de Afrenske frem so	Sc - Saccharomyces cerevisiae Vps4 Dm - Drosophila melanogaster CG6842 Hs1 - Homo sapiens Vps4 Hs2 - Homo sapiens Endl3
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lar and genetic studies are under way on yeast cells and cell lines of various organisms.

Holometabolic insects are promising model organisms, as massive autophagytype programmed cell death occurs in several organs during metamorphosis [1, 8], inevitable for the formation of adult organs. The known complete genome sequence and the broad variety of molecular and genetic tools make *Drosophila* a good choice to study autophagy. There are P-element mutants for two of the genes in Fig. 1.: l(3)00096 for CG5429 and EP(X)0362 for CG1534, making it possible to remobilize the P-element and gain null allele of the gene of interest. In the other cases, "knockout", or in other words, hypomorphic mutants can be generated by the RNAi (RNA interference) method [9], thus silencing the gene corresponding to the injected dsRNA (double-stranded RNA). During the RNAi reaction, both strands of the dsRNA are processed to RNA segments 21-23 nucleotides in length. Processing of the dsRNA to the small RNA fragments does not require the targeted mRNA. The mRNA is cleaved only within the region of identity with the dsRNA. The improved version of this method is the EIR (expressed inverted repeat) technique [4], when in vivo transcription of an inverted repeat transgene might also produce a dsRNA "hairpin" that is capable of triggering post-transcriptional gene silencing (PTGS). In vivo dsRNA formation can be promoted simply by keeping the stock at 29 °C, although it is not known yet which step is temperature-dependent: either dsRNA formation, or the enzymes participating in RNAi, or the Gal4-UAS system.

Drosophila experiments will hopefully help us better understand the molecular biology of autophagy.

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