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Research Paper

Multiple checkpoints of protein clearance machinery are modulated by a common microRNA, miR-4813-3p, through its putative target genes: Studies employing transgenic *C. elegans* model

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ABSTRACT

In order to maintain cellular homeostasis and a healthy state, aberrant and aggregated proteins are to be recognized and rapidly cleared from cells. Parkinson's disease, known to be associated with multiple factors; presents with impaired clearance of aggregated alpha synuclein as a key factor. We endeavored to study microRNA molecules with potential role on regulating multiple checkpoints of protein quality control within cells. Carrying out global miRNA profiling in a transgenic *C. elegans* model that expresses human alpha synuclein, we identified novel miRNA, miR-4813-3p, as a significantly downregulated molecule. Further studying its putative downstream target genes, we were able to mechanistically characterize six genes *gbf-1, vha-5, cup-5, cpd-2, acs-1* and C27A12.7, which relate to endpoints associated with alpha synuclein expression, oxidative stress, locomotory behavior, autophagy and apoptotic pathways. Our study reveals the novel role of miR-4813-3p and provides potential functional characterization of its putative target genes, in regulating the various pathways associated with PQC network. miR-4813-3p modulates ER^{UPR}, MT^{UPR}, autophagosome-lysosomal-pathway and the ubiquitin-proteasomal-system, making this molecule an interesting target for further studies towards therapeutically addressing multifactorial aspect of Parkinson's disease.

1. Introduction

It is a widely accepted fact that accumulation of protein aggregates is one of the most crucial factors associated with disease progression and outcome of multifactorial neurodegenerative diseases (NDs). Structural stability and molecular partnerships of misfolded proteins are altered because of their exposure to internal domains and hence form toxic aggregates in Alzheimer's disease (AD; aggregation of amyloid beta) and Parkinson's disease (PD; aggregation of α-synuclein) [1].

To check, regulate and prevent protein accumulation, cells employ their own protein quality control system (PQC). Inside the cell via its quality control (QC) pathways, cells invariably check the protein molecules for occasional damage or errors. PQC machinery recognizes the aberrant protein and either corrects it or degrades it rapidly to maintain cellular homoeostasis [2,3]. Within the neuron internally, PQC occurs in almost every cellular compartment, which is a necessity to identify a wide range of defects in the protein molecule from mislocalization to misfolding. The errors in recognizing such targets by quality control manifest in the unwanted accumulation of faulty stock that may aggregate further and create deleterious consequences. On the other hand, over sensitive or unregulated recognition may unreasonably target the functional proteins for degradation, draining the key resource of the cell. Therefore, very high precision in PQC is required within the cell, and knowing what goes wrong during PD, can aid in better understanding of the disease and in developing effective therapeutic strategies against it [4–6].

Elimination of protein aggregates within the cell is broadly affected by the ubiquitin-proteasome system, chaperone-mediated autophagy, lysosomal associated autophagy, and unfolded protein response (UPR) pathway of the endoplasmic reticulum and mitochondria. Therefore, identifying a potential common trigger that can regulate the major degradation pathways of PQC, may aid in bettering the outcome of protein clearance, thus ameliorating disease related effects. Among discrete mechanistic triggers for protein expression, the miRNA molecules are considered mechanistically critical as these molecules regulate expression of multiple genes. miRNAs are evolutionarily conserved

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nucleotides with a length of 20–25 base pairs; they block protein synthesis either by inhibiting the translation of mRNA or by degrading the mRNA itself. However, there are some reports which show they can even regulate gene expression at the transcription level [7,8].

In mammals, miRNAs play a crucial role in brain development, neuronal function, specification, and even in repair of maintenance system [9–11]. miRNAs also regulate most of the genes that are required for cellular identity, emphasizing their essential role in the maturation of cells, tissue, and organs [12,13]. Uncoordinated variations either in biogenesis or functioning of miRNAs have been found associated to manifest diverse ailments which includes neurodegenerative disease, cardiovascular disease, diabetes mellitus and cancer [14–16].

miRNAs have a discrete expression pattern, which not only varies from healthy to diseased individual but also from organ to organ within a particular organism. In present studies, we report a comparison of global miRNA profile of transgenic *C. elegans* strain expressing human α-synuclein (NL5901) in comparison to wild type strain (N2). We have successfully identified novel miRNA molecules that were not previously known to be associated with NDs. We further carried out in silico studies towards identifying their downstream predicted targets followed by their functional characterization and validation, having an association with the essential pathways of protein quality control. We suggest that if we can enhance the fidelity of PQC machinery by overexpressing crucial targets either genetically or pharmacologically, the clearance of aberrant and aggregating proteins could be a significant step towards slowing down the progression of NDs. Our studies present a considerable step towards identifying novel modulators of PQC machinery, which could be studied further for a targeted cure via bettering protein clearance in aberrant conditions.

2. Results

2.1. Potential miRNA molecules identified by global miRNA profiling in transgenic C. elegans model

We performed miRNA profiling of transgenic *C. elegans* model for PD, NL5901 (which expresses human α-synuclein protein tagged with YFP) in comparison to wild type strain (N2) employing Next Generation Sequencing (NGS) method. We have successfully identified novel miRNA molecules; among these, we found that miR-4813-3p is the most down-regulated molecule (>15-fold) and miR-8188-5p is the most upregulated molecule (>100 folds) as shown in Fig. 1A. The intriguing differential expression pattern of these two miRNAs was further validated by TaqMan assay, where miR-4813-3p was observed to exhibit 40-fold downregulation whereas miR-8188-5p exhibited a 9-fold upregulation (Fig. 1B). The 40-fold downregulation of miR-4813-3p inferred the importance of this molecule thus making it prudent to study it further in the context of PQC machinery.

In our preliminary studies, we prepared a dataset of predicted downstream mRNA targets of miR-4813-3p by using the miRbase towards getting its mature sequence and by using RNA22 tool to get the predicted targets; we identified 266 relevant targets (shown in Supplementary Table 2; excel sheet). Selective filters like (at least 60 % homology with the human counterparts, regulatory role in protein quality control or neuronal expressions based on existing literature mining) were applied to the dataset, and we ended up with 20 predicted downstream targets of miR-4813-3p, for which RNAi assays were available in the Ahringer library, as shown Table 1.

2.2. α-Synuclein expression gets modulated after knockdown of putative downstream targets of miR-4813-3p in transgenic C. elegans

Expression of α-synuclein followed by its accumulation being a key feature of PD [17,18], we studied the identified predicted downstream effector molecules of miR-4813-3p, for their role in accrual of α-synuclein NL5901 strain of *C. elegans*. We observed that from the 20 identified genes, RNAi of 12 *(acs-1, lgc-47, vha-5, B0361.6,* C27A12.7, D2030.2*, T09E8.3, cpd-2, gbf-1, nuo-5,* C05D11.9 and *cup-5*) significantly increases the accrual of α-synuclein and RNAi of 2 (*gpx-6* and *unc-11)* decreases accrual of α-synuclein, whereas RNAi of 6 genes (*cua-1, glr-1, egl-45,* C14C11.4*, lon-3, hke-1)* have been found to have no significant effect on accrual of α-synuclein, as shown in Fig. 2A and B. RNAi of *asc-1, cpd-2, cup-5* and *glr-1* induced a developmental delay as the worms were observed to attain L4 stage post 75 h of embryo isolation as shown in Fig. 3A and supplementary fig. 4.

2.3. Putative downstream targets of miR-4813-3p modulate multiple factors including α-synuclein accrual

The studies on α-synuclein accrual by knockdown of predicted targets of miR-4813-3p and further in silico interaction studies (using Gene Mania and STRING) revealed involvement of these predicted downstream targets in PD associated endpoints. We figured that the identified molecules may modulate multiple factors regulating biochemical pathways inside the cell like the protein quality control machinery, mitochondrial energy balance, muscle contraction, fatty acid metabolism, cytoskeletal dynamics, and calcium homeostasis (shown in Table 2) affecting other endpoints including α-synuclein accrual. These observations indicate, miR-4813-3p can regulate multiple pathways and probably can emerge as a common trigger for endpoints associated with PD. Based on our categorization and observed results, we observed that miR-4813-3p has six putative downstream targets (out of the 12, whose RNAi has increased the α-synuclein accrual) that can directly modulate the protein quality control machinery. To check further whether the expression pattern of these six PQC genes gets modulated by miR-4813-3p, we employed a knock out strain of miR-4813 (MLC425) and found there is significant increase in the mRNA levels of PQC genes shown in supplementary fig. 1 and supplementary table A. Hence, the six identified genetic modulators (*gbf-1, vha-5, cup-5, cpd-2, acs-1* & C27A12.7), presence of which seem to be critical for maintaining efficient protein quality control along with associated functions, were chosen for further functional characterization (reported function of PQC genes is described in Section 2.9 and Table 1).

We performed phenotypic studies in MLC425 (knock out strain of miR-4813) like body morphometry, fat content, locomotory and odorant response and behavioral assays which provide certain cues suggesting that miR-4813 might act upstream of PQC gene targets regulating α-synuclein accrual. We have observed, at all developmental stages that MLC425 shows a significant increase in its size as compared to wild type worms (N2) (supplementary fig. 3A), this might be probably because of marked increase in the fat content as observed under the knock out background of miR-4813 (supplementary fig. 3D). We further observed that in the absence of miR-4813, worms exhibit a significant increase in the locomotory behavior and quick response to both attractive and repellent odorant as compared to wild type (supplementary fig. 3B and Fig. 3C). Low fat deposition was previously reported to be associated with PD. It is known that the downregulated locomotory and odorant response time behavior is usually the phenotypic manifestation of distorted signaling of nigrostriatal pathway because of α-synuclein accumulation in the neurons.

2.4. Distorted dopamine signaling and locomotory behavior is observed after knockdown of putative downstream targets of miR-4813–3p

Death of nigrostriatal dopaminergic (DAergic) neurons is the dominant pathology of PD, resulting in a severe decrease of striatal dopamine levels. As age-associated functional decline is attributed to the failure of protein homeostasis in neurons [19–21], to know whether the knockdown of PQC genes impacts dopaminergic neuronal function, we carried out quantification of the dopamine levels by LC-MS in the transgenic strain of *C. elegans* NL5901. Interestingly, we observed a significant decrease in total dopamine content levels after the knockdown of PQC

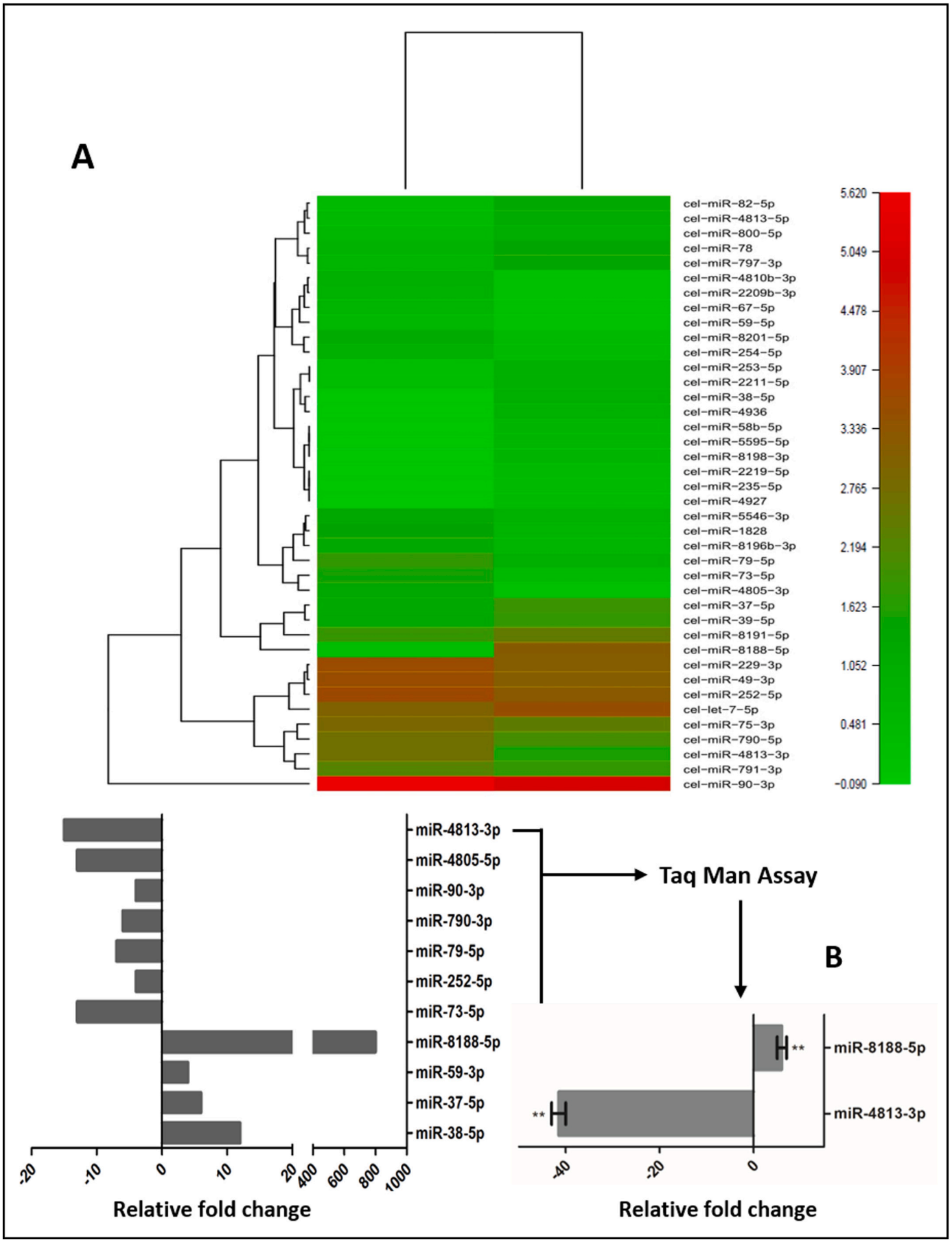

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Fig. 1. Identification of specific miRNA from global miRNA profiling in NL5901: (A); The figure describes the NGS miRNA profile of transgenic *C. elegans* (NL5901) expressing human α-Synuclein in comparison to N2 wild type strain; expression profile is depicted in the heatmap, and fold-change of miRNAs plotted with the help of R-package where we have identified miR-8188-5p is the most upregulated one and miR-4813-3p is the most down-regulated one (B); Shows miRNAs fold change, studied through Taq man real-time PCR in NL5901. Graphical representation of miRNA fold change in a transgenic strain expressing human α-synuclein (NL5901) over wild type train (N2 Quantified by and non-parametric independent *t*-test (Mean ± SEM; $*p < 0.05$, $**p < 0.005$, $***p < 0.0005$ & ns: non-significant).

genes as shown in Fig. 3B and supplementary table B.

In both vertebrate and invertebrate various findings suggest that dopaminergic neurons play a very critical role in various adaptive behaviours for the survival. Dopaminergic neurons integrate sensory information in their earning behavior which helps them to make decisions. PD is also associated with defects in motor neuronal signaling which leads to motor behavior defects [22–25]. Along with the observed decline in the dopamine levels after RNAi of PQC genes, we studied the locomotory behavior in worms as total number of thrashes per minute, after silencing of PQC downstream targets. We observed a decrease in the mean thrashing count after knockdown of PQC genes (Fig. 3C and supplementary table C). It is known that in Parkinson's disease, the dopamine transporter (DAT-1) can be reduced by upto 50–70 %; therefore, the dopamine transporter alone can be a critical determinant of the dopamine availability in PD [26]. We studied the effect on dopamine transporter (DAT-1) after knockdown of predicted PQC downstream targets by employing a transgenic strain of *C. elegans* BZ555 (which expresses GFP under dat-1 promoter in all eight of its dopaminergic neurons). We observed a non-significant variation in DAT-1 expression levels after RNAi of predicted downstream targets (Fig. 3D) even though there were significantly low dopamine levels. This observation indicates that RNAi of PQC genes distorts dopamine signaling and locomotory behavior by decreasing the total dopamine content which reflects as reduced number of thrashing counts in the worm.

Table 1
List of predicted downstream targets of miR-4813-3p after applying selective filters.

S. No.	Common gene name	Sequence name	Role in *C. elegans*
1.	*vha-5*	F55H10.4	Encodes an orthologue of subunit a of the membrane-bound (V0) domain of vacuolar proton-translocating ATPase (V-ATPase).
2.	*hke-4.1*	T28F3.3	Predicted to have metal ion transmembrane transporter activity, and it is expressed in nervous system
3.	C27A12.7	C27A12.7	Predicted to have ubiquitin-protein transferase activity, based on protein domain information.
4.	D2030.2	D2030.2	involved in nematode larval development, receptor-mediated endocytosis and striated muscle myosin thick filament assembly.
5.	*acs-1*	F46E10.1	involved in apoptotic process, embryo development, growth, lipid storage, locomotion, nematode larval development and reproduction.
6.	T09E8.3	T09E8.3	cni-1 is expressed in the nervous system; cni-1 is localized to the endoplasmic reticulum and the synapse.
7.	*cua-1*	Y76A2A.2	When mutated leads to Hailey-Hailey disease; loss of cua-1 activity via RNAi results in a number of defects, including slow growth, uncoordinated or no locomotion, adult and larval lethality, and axon guidance abnormalities.
8.	*cpd-2*	T27A8.1	Have peptidases activity
9.	*lgc-47*	F47A4.1	Ion channel in neuron
10.	B0361.6	B0361.6	Receptor mediated endocytosis and it is expressed in nervous system
11.	*glr-1*	C06E1.4	Glutamate receptor and it is involved in memory function.
12.	*gbf-1*	C24H11.7	Involve in apoptotic process
13.	*egl-45*	C27D11.1	egl-45 is predicted to have translation regulator activity, based on sequence information; egl-45 is expressed in the nervous system.
14.	*cup-5*	R13A5.1	Required for normal degradation of lysosome
15.	C05D11.9	C05D11.9	Code for pop-1, a riboendonuclease in mitochondria, that cleave mitochondrial RNA
16.	*gpx-6*	T09A12.2	Glutathione peroxidase in neuron
17.	*unc-11*	C32E8.10	Regulates neurotransmitter release by controlling vesicle trafficking and fusion
18.	C14C11.4	C14C11.4	Involve in apoptotic process
19.	*nuo-5*	Y45G12B.1	NADH-Ubiquinone Oxidoreductase Fe—S PROTEIN 1, which when mutated leads to mitochondrial complex I deficiency.
20.	*lon-3*	ZK836.1	Acetyl choline esterase

Source: Worm base version: WS275.

2.5. Expression of autophagy and apoptotic genes gets altered after knockdown of predicted PQC targets of miR-4813-3p

The clearance of protein aggregates and damaged organelles are mainly associated with autophagy. Mutations and downregulation of autophagy related genes are well known to be correlated with PD [27–32]. In order to study whether these putative PQC targets have any involvement in autophagy (the main protein clearance machinery of the cell) we studied known autophagy marker genes (*bec-1, lgg-1, atg-5 & vps-34*) using the quantitative real-time PCR (qPCR) method under the knockdown condition of PQC genes. We observed that RNAi of each PQC target leads to the downregulation of marker genes, as shown in Fig. 4A and supplementary table D and E. *bec-1* plays an essential role in the functioning of class III PI3 kinase LET-512; it is a crucial protein required for autophagy, endocytosis, and membrane trafficking. *lgg-1* encodes the ortholog of mammalian MAP-LC3 required for degradation of cellular components. *atg-5* is involved in autophagosome assembly during the autophagy process. *vps-34* encodes an ortholog of the phosphoinositide 3-kinase and is required for vesicular trafficking, including autophagy and apoptotic cell clearance [33–35].

As we observed a significant decrease in the mRNA expression pattern of autophagy-related gene *lgg-1* after RNAi of predicted PQC downstream targets, we have further studied autophagosome vesicle formation employing a transgenic strain DA2123 (LGG-1::GFP) in which decrease in the GFP puncta represents a declined flux in the autophagosome formation [36]. We observed a significant decrease in the number of puncta (thus validating findings from qPCR experiments) after RNAi of PQC genes (Fig. 5A and supplementary table F).

Neurodegenerative diseases, including Parkinson's and Alzheimer's, are characterized by neuronal cell death. It has been observed that certain transcription factors can link major molecular machinery together like FOXO3 (which can interlink autophagy and apoptotic machinery). These act as surveillance systems in the cell to monitor perturbations in the autophagy process and finally negotiate apoptotic process when the clutter is not cleared by autophagy. We executed quantitative-PCR of the few previously reported apoptotic genes (*cep-1, ced-4, jnk-1, jkk-1* and *nsy-1*) after RNAi of PQC genes to investigate whether the knockdown of PQC genes which create an imbalance in the autophagic process, do have any impact in the cell death process by impacting apoptotic pathway [37–40]. *cep-1* encodes an ortholog of human tumor suppressor p53 that promotes DNA damage induced-apoptosis [41]. *jnk-1* encodes a serine/threonine kinase and its direct activator *jkk-1* are members of C-Jun N-terminal kinases (JNKs) involved in apoptotic signaling in both intrinsic and extrinsic pathways [42,43]. NSY-1, is the ortholog of the mammalian apoptosis signal-

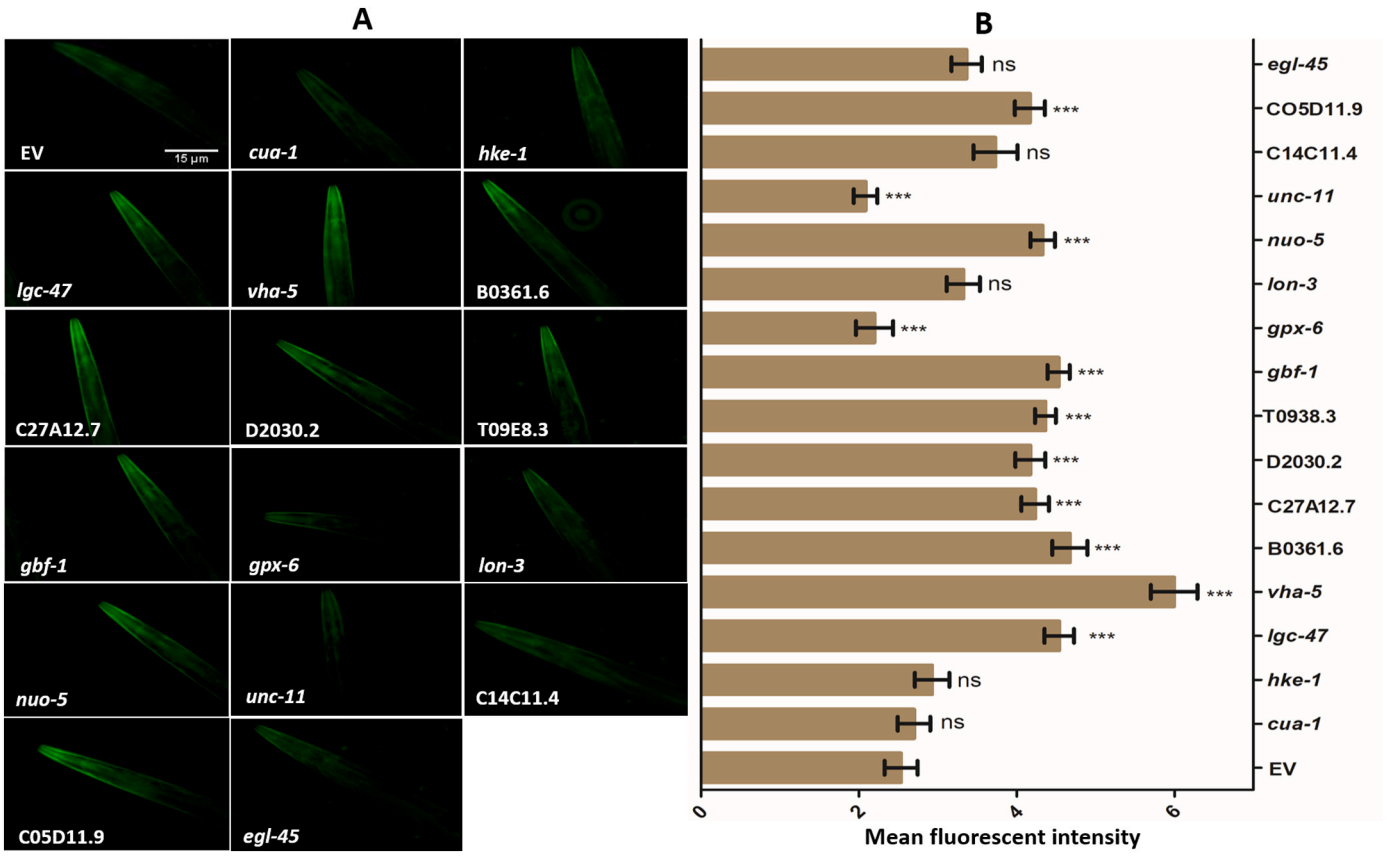

Fig. 2. Expression pattern of α-synuclein expression and accumulation in transgenic *C. elegans* strain NL5901 after knockdown of predicted downstream target genes of miR-4813-3p: (A); Shows α-synuclein accumulation in NL5901 after RNAi silencing *of cua-1, hke-4.1, lgc-47, vha-5,* B0361.6, C27A12.7, D2030.2, T09E8.3, *gbf-1, gpx-6, lon-3, nuo-5, unc-11,* C14C11.4, C05D11.9 *and egl-45* (B); Shows graphical representation of the fluorescence intensity as quantified by Image J analysis and non-parametric independent *t*-test (Mean ± SEM; $*p < 0.05$, $**p < 0.005$, $***p < 0.0005$ & ns: non-significant).

regulating kinase (ASK) family responsible for regulating the viability of animals in anoxia [39].

We observed that knockdown of PQC genes leads to downregulation of most of the apoptotic marker genes, as shown in Fig. 4B and supplementary table G and H. These observations show that knockdown of PQC genes downregulates both autophagy and apoptotic pathways, which might be the reason for augmented α-synuclein accrual and cellular stress.

2.6. Altered expressions of studied genes were observed in transgenic *C. elegans* strains having deletion mutation of autophagy and apoptotic markers

The experimental evidence gathered thus far shows that silencing of PQC genes modulates the expression of autophagy and apoptotic markers. To further explore the association of PQC genes with autophagy and apoptotic pathways, we checked their expression levels in transgenic *C. elegans* strains where autophagy and apoptotic pathways are compromised as they have deletion mutation of autophagy and apoptotic marker genes, VC8: *jnk-1* (deletion mutants), KU2: *jkk-1* (deletion mutants),VC172: *cep-1* (deletion mutants) and VC424: *bec-1* (deletion mutants). Interestingly, we observed the down regulation of the PQC genes in the deletion mutant background of *C. elegans* as shown in figure (Fig. 6A and B and supplementary table I). Under *jnk-1* and *bec-1* deletion background, we have observed a significant decrease in the mRNA fold change of six PQC genes. Under *jkk-1* deletion background, except for *gbf-1* we observed a significant decrease in the mRNA fold change of PQC genes. Under *cep-1* deletion background, except for *gbf-1, vha-5* and *cup-5* background, we observed a significant decrease in the mRNA fold change of other PQC genes. These observations in the deletion background of specific autophagy and apoptotic markers, reveal that there is a downregulation of most PQC genes indicating an interdependence between PQC genes and autophagy-apoptotic pathways.

2.7. PQC predicted targets of miR-4813-3p get modulated after inhibition of autophagy and proteasomal pathways

Our data suggests an interdependent co-expression pattern between PQC genes with autophagy and apoptotic pathways. As it is well known that there are two major proteolytic pathways by which proteins are degraded inside the cell, the autophagosome-lysosomal-pathway (ALP) and the ubiquitin-proteasomal-system (UPS), we went on to explore the impact of shutdown of these machineries on PQC gene expression pattern. For that, we have pharmacologically inhibited autophagy and proteasomal pathways, which is validated by the downregulation of autophagy markers (Fig. 4D) and proteasomal subunits (Fig. 4E) along with elevated α-synuclein expression levels (Fig. 4C). We observed that in case of autophagy inhibition, expression of PQC genes (barring C27A12.7) has been found to be significantly down-regulated, whereas after proteasomal inhibition (except for *cpd-2* and *acs-1)* other PQC genes have shown down-regulation (Fig. 4F and supplementary table. J & K). This observation reflects the involvement of PQC genes in the regulation of two major protein degrading machineries, autophagosome-lysosomal-pathway and ubiquitin-proteasomal-system, responsible for the clearance of unwanted aggregated proteins.

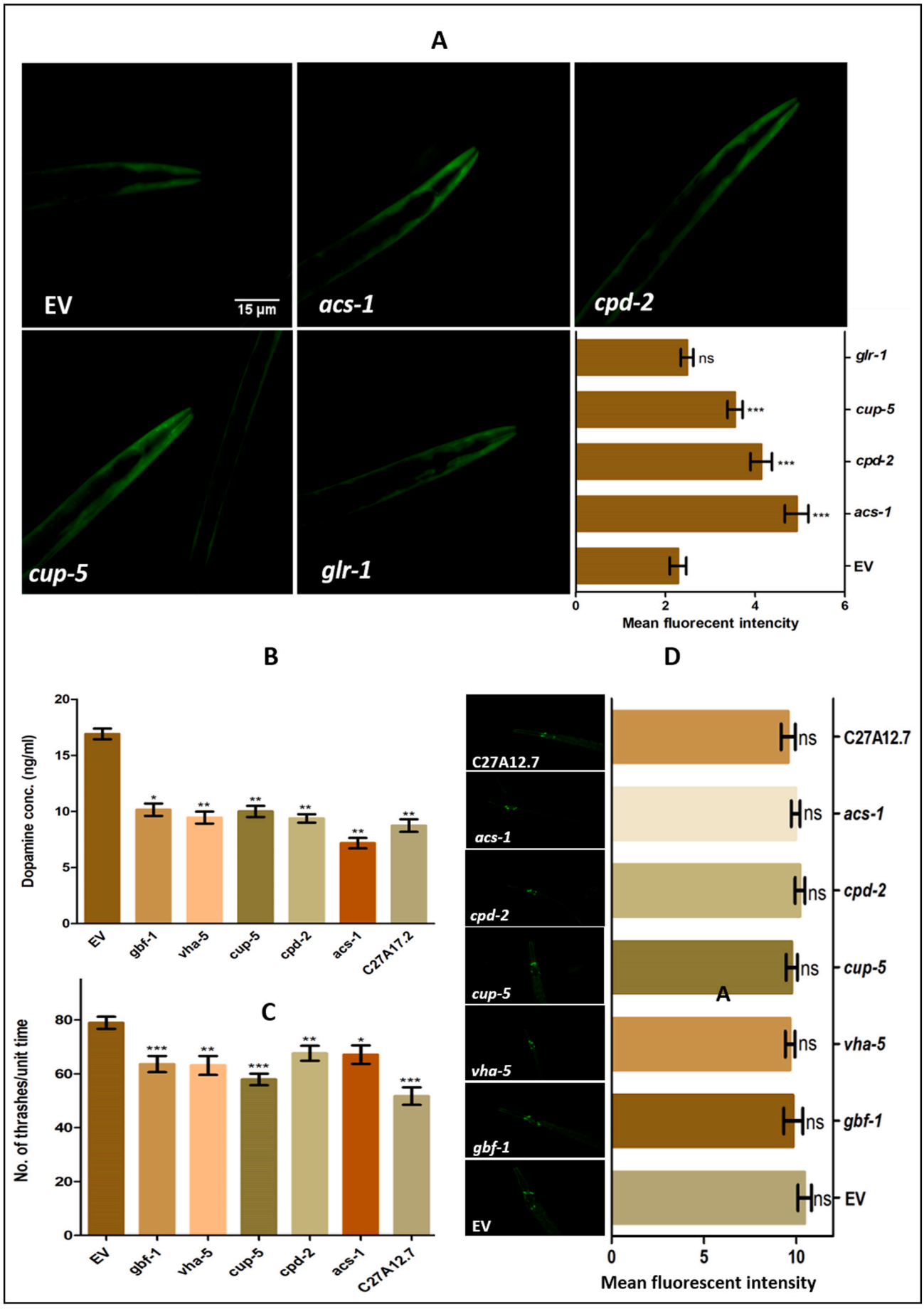

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Fig. 3. Attenuated dopamine signaling and locomotory behavior is observed after knockdown predicted PQC targets of miR-4813-3p: (A); Shows α-synuclein accrual in NL5901 after RNAi silencing *acs-1, cpd-2, cup-5 & glr-1* post 75 h. The graphical representation shows the fluorescence intensity as quantified by Image J analysis and non-parametric independent t-test (*p < 0.05, **p < 0.005, ***p < 0.0005 & ns: non-significant) (B); Quantification of dopamine levels in transgenic *C. elegans* strain NL5901 after RNAi of PQC genes *(gbf-1, vha-5, cup-5, cpd-2, acs-1* & C27A12. 7). The graphical representation shows the fluorescence intensity as quantified by Image J analysis and non-parametric independent t-test (*p < 0.05, **p < 0.005, ***p < 0.0005 & ns: non-significant) (C); Quantification of the number of thrashes per unit time in transgenic *C. elegans* strain NL5901 after RNAi silencing of six PQC genes and (D); Expression pattern of DAT-1:: GFP in transgenic *C. elegans* strain BZ555 after RNAi silencing of six PQC genes. The fluorescence intensity was quantified by Image J analysis and non-parametric independent *t*-test are used to analyze the quantified fluorescent images, no. of thrashes and dopamine content (Mean ± SEM; *$p < 0.05$, **$p < 0.005$& ***$p < 0.0005$).

2.8. Elevated ROS levels and reduced longevity were observed after knockdown of PQC genes

Quality control (QC) pathways are aimed to identify and remove damaged proteins and organelles mainly by the autophagic pathway, which is crucial for post-mitotic cells such as neurons, to maintain homeostasis. Our experiments suggest that the silencing of PQC genes interferes in the autophagic pathway which could lead to oxidative stress due to accumulated defective mitochondrial proteins or by the damaged mitochondria [44–49]. To determine whether the putative PQC targets modulate ROS levels, we quantified the ROS levels under the knockdown condition of PQC targets in wild type worms. There was a significant increase in the fold change of ROS levels after knockdown of PQC genes (Fig. 5B and supplementary table L).

Reactive oxygen species can cause genotoxic and physiological damage when produced in excess amounts. Such accumulated oxidative stress leads to various cellular insults like DNA damage, modulating various signaling cascades, gene expression profile, peroxidation of lipids, and finally, protein homeostasis. Excessive oxidative stress can accelerate aging and could trigger neurodegeneration as well [46,50]. Therefore, we have performed the life span assay to check the effect on longevity after the silencing of PQC genes. Interestingly we observed a decrease in the life span of NL5901 strain after silencing of putative PQC downstream targets of miR-4813–3p. The median survival of NL5901 is 11, 10, 10, 10, 10 & 13 after knockdown of studied PQC genes, whereas the median survival of control was found to be 16 days (Fig. 5C).

2.9. Identification of possible pathways in which putative PQC downstream genes of miR-4813–3p are involved in causing neurodegenerative disease

After finding the strong association of predicted target genes of miR-4813–3p with quality control machinery mainly with autophagy and proteasomal clearance system, we further carried out studies towards identifying the possible pathways in which the identified PQC genes are involved as their down-regulation leads to the manifestation of PD pathological systems.

In the case of *gbf-1*, the literature suggests that *gbf-1* is involved in ER-Organization, endosomal transport, Mt-Organization and secretion [51–53]; therefore, we checked the expression levels of marker genes related to ER^{UPR} and MT^{UPR} systems. We found the results to be in concurrence with RNAi condition of *gbf-1* where we observed significant down regulation of most of the makers of both ER^{UPR} and MT^{UPR} pathways. In case of ER^{UPR}, we observed significant downregulation of *ire-1*, *hsp-6 and hsp-60*. In case of MT^{UPR}, we observed considerable downregulation of *hsp-6, hsp-60, clpp-1 and atfs-1* (Fig. 7A and supplementary table M).

vha-5 encodes a membrane-bound subunit of V0 domain associated with vacuolar proton translocating ATPase (V-ATPase) in the lysosome involved in regulating the acidic pH of lysosomal lumen; therefore, we checked the expression levels of lysosomal associated enzymes related to PD like *gana-1* and *gba-1* which are the human orthologues of α-galactosidase-A and β-glucosyl ceramidase, respectively [54–58]. We also checked the expression levels of marker genes (*hsp-1* and *imp-2*) associated with one of the lysosome-based autophagy pathways, i.e., chaperone-mediated autophagy (CMA) [59,60]. Significant down regulation of *hsp-1, imp-2*, *gana-1*, and *gba-1* was observed after RNAi of *vha-5* in NL5901 (Fig. 7B and supplementary table N).

The *cup-5* gene encodes an ortholog of the human mucolipin 1 gene; *cup-5* is required for viability, *endo*-lysosomal transport and the normal degradation of lysosomes [61–63]. Therefore, we checked the expression pattern of lysosomal enzymes associated with PD; *gba-1* and *catp-5*, *ctp-6* & *catp-7* which are the orthologues of human gene ATP_{13A2}. *This gene*, also known as *PARK9, responsible for the transport of polyamines in the cell, regulates lysosomal activity in cellular digestion and recycling. Mutation or lack of activity in ATP_{13A2} increases* genetic and environmental risk factors for Parkinson's [64,65]**.** We observed significant down-regulation of *gba-1, catp-5, ctp-6* & *catp-7* as a result of *cup-5* RNAi in NL5901 (Fig. 7C and supplementary table.O).

cpd-2 encodes a putative metallocarboxy peptidase orthologous to the human AEBP1 gene. We performed in silico studies and found genetic interaction between *cpd-2* and *imp-2* (supplementary fig. 2A), which is one of the markers of chaperone mediated autophagy; therefore, we further checked the expression levels of marker genes (*hsp-1* and *imp-2*) associated with CMA. We observed significant down regulation of all the marker genes *hsp-1* and *imp-2* as an effect of *cpd-2* RNAi in NL5901(Fig. 7D and supplementary table.P).

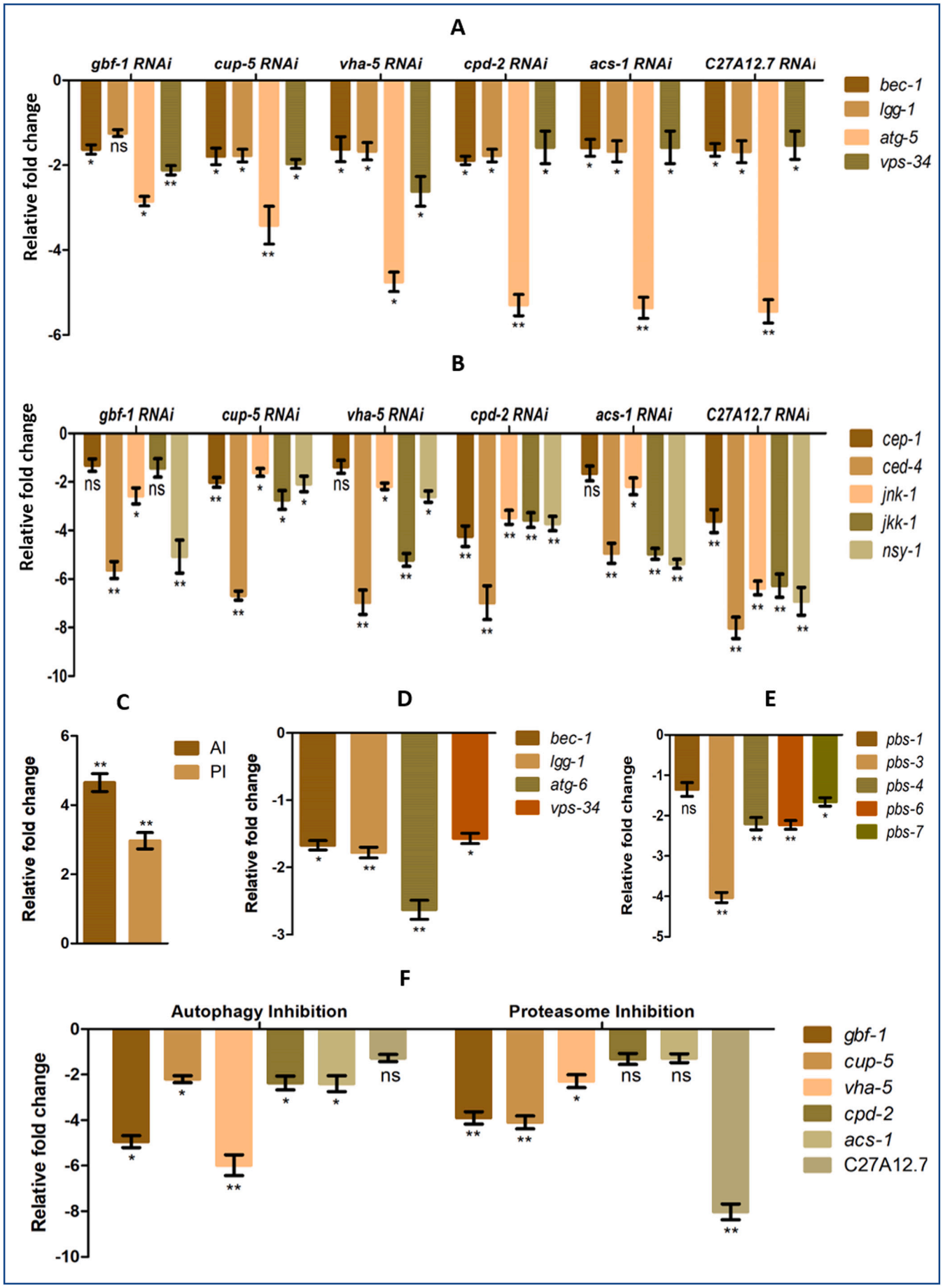
acs-1, an ortholog of human ACSF2 (acyl-CoA synthetase family member 2), is expressed in neurons and is involved in fatty acid metabolism [66,67]. With in silico studies we observed genetic correlations of *acs-1* with *daf-2* (via *itr-1*; *acs-1* is involved in IP3 signaling via *itr-1 receptor*) and with *bas-1* (supplementary fig. 2B and 2C) (which are involved in the biosynthesis of dopamine from tyrosine). We studied the expression levels of *itr-1*, *daf-16, cat-2*, and *bas-1* and found significant down regulations of these after RNAi of *acs-1* except for *daf-2* showing non-significant change in expression levels (Fig. 7E and supplementary table.Q).

C27A12.7 is an ortholog of human ARIH1 (Ariadne RBR E3 ubiquitin-protein ligase 1); we carried out in silico studies and found its correlation with *ubc-18* (which encodes for an E2 ubiquitin enzyme similar to human UBCH7), which has further associations with proteasome beta subunits (*pbs-1, pbs-3, pbs-4, pbs-6* & *pbs-7*) supplementary fig. 2D. We further investigated the expression levels of these genes after RNAi of C27A12.7 in NL5901 and observed that these are significantly downregulated (Fig. 7F and supplementary table R). The reported functional aspect of these studied genes, is summarised in supplementary table S.

Table 2
miR-4813-3p via its predicted downstream targets modulates α-synuclein accrual in transgenic *C. elegans*:

Downstream targets of miR-4813-3p	Pathway Involved
acs-1	Protein Quality control
vha-5	
C27A12.7	
cpd-2	
gbf-1	
cup-5	
nuo-5	Mitochondrial bioenergetics
C05D11.9	
D2030.2	
lgc-47	Ion channel
T09E8.3	Synaptic transmission
B0361.6	Predicted to have methyltransferase activity

*Source: Worm base version: WS275.



(caption on next page)

Fig. 4. Modulation of autophagy, apoptotic and PQC genes in NL5901 strain:(A); Quantitative PCR patterns of autophagy markers *bec-1, lgg-1, atg-5 & vps-34* (B); Quantitative PCR patterns of apoptotic markers *cep-1, ced-4, jnk-1, jkk-1* and *nsy-1* in transgenic *C. elegans* strain NL5901 after RNAi silencing of predicted PQC downstream genes *gbf-1, vha-5, cup-5, cpd-2, acs-1* & C27A12.7. (C); Quantitative PCR patterns of α-synuclein expression levels in transgenic *C. elegans* strain NL5901 after pharmacological inhibition of Proteasome and Autophagy (D); Quantitative PCR patterns of autophagy markers *bec-1, lgg-1, atg-5 & vps-34* (E); Quantitative PCR patterns of proteasome subunits *pbs-1, pbs-3, pbs-4, pbs-6&pbs-7,* (F); Quantitative PCR patterns of PQC genes (*gbf-1, vha-5, cup-5, cpd-2, acs-1* & C27A12.7) in transgenic *C. elegans* strain NL5901 after inhibition of Autophagy machinery, quantitative PCR patterns of PQC genes (*gbf-1, vha-5, cup-5, cpd-2, acs-1* & C27A12.7) in transgenic *C. elegans* strain NL5901 after inhibition of Proteasome machinery. Fold change are quantified using non-parametric independent *t*-test (Mean ± SEM; $*p < 0.05$, $**p < 0.005$, $***p < 0.0005$ & ns: non-significant). Actin (*act-1*) is used as an endogenous control with which ct values of each gene is normalized. AI: Autophagy Inhibition and PI: Proteasomal Inhibition.

3. Discussion

The build-up of aberrant and malformed proteins is known to be the key cause of effects linked with age-associated neurodegenerative diseases. In a healthy state, the clearance of such noxious accumulations is maintained via an efficient protein clearance system involving the autophagic–lysosomal network, ubiquitin-proteasome system or by chaperone mediated autophagy [68]. Considering the multiple factors that govern various checkpoints of these pathways, we endeavored to identify a common trigger behind these phenomena. Since single miRNA molecules are known to regulate multiple genes [69], we carried out miRNA profiling and identified miR-4813-3p that was significantly downregulated in *C. elegans* strain expressing human α-synuclein. Interestingly, we observed strong functional association of this miRNA molecule despite its low abundance. This phenomenon has also been previously observed in context of colon tumor wherein low abundance miR-206 was reported to regulate cell fate [70]. Our studies further led to the identification of six predicted downstream targets of miR-4813-3p namely *gbf-1, vha-5, cup-5, cpd-2, acs-1* and C27A12.7, which are directly related to the protein quality control system.

3.1. Modulation of α-syn accumulation by PQC genes

Elevated levels of α-syn as a result of its accumulation within tissues are well documented in PD [71,72]. This fact prompted us to study the effect of PQC gene silencing in association with α-syn accrual. We observed a significant increase in the α-syn accrual after silencing of identified PQC genes. *gbf-1* is reported to be involved in the endoplasmic reticulum and mitochondrial organization. We observed that knockdown of *gbf-1* significantly downregulates ER^{UPR} and MT^{UPR} markers. Such a compromised UPR pathway may be the possible reason for α-synuclein accumulation [73,74]. Lysosomal associated autophagy is the main pathway for the clearance of highly unfolded and aggregated proteins inside the cell. Compromising the lysosomal pH by knockdown of *vha-5* (lysosomal V-ATPases) will not only alter the proper functioning of lysosomal hydrolytic enzymes but also, we observed downregulation of associated lysosomal enzymes related to PD [75–77]. These findings suggest that *vha-5* is necessary for the clearance of aggregated α-syn. *cup-5* is being reported to be involved in normal lysosomal viability, degradation and calcium ion homeostasis. Our experimental results also complement the above findings as knockdown of *cup-5* has downregulated not only lysosomal associated enzymes related to PD but also a lysosomal P-type ATPase that has involvement in

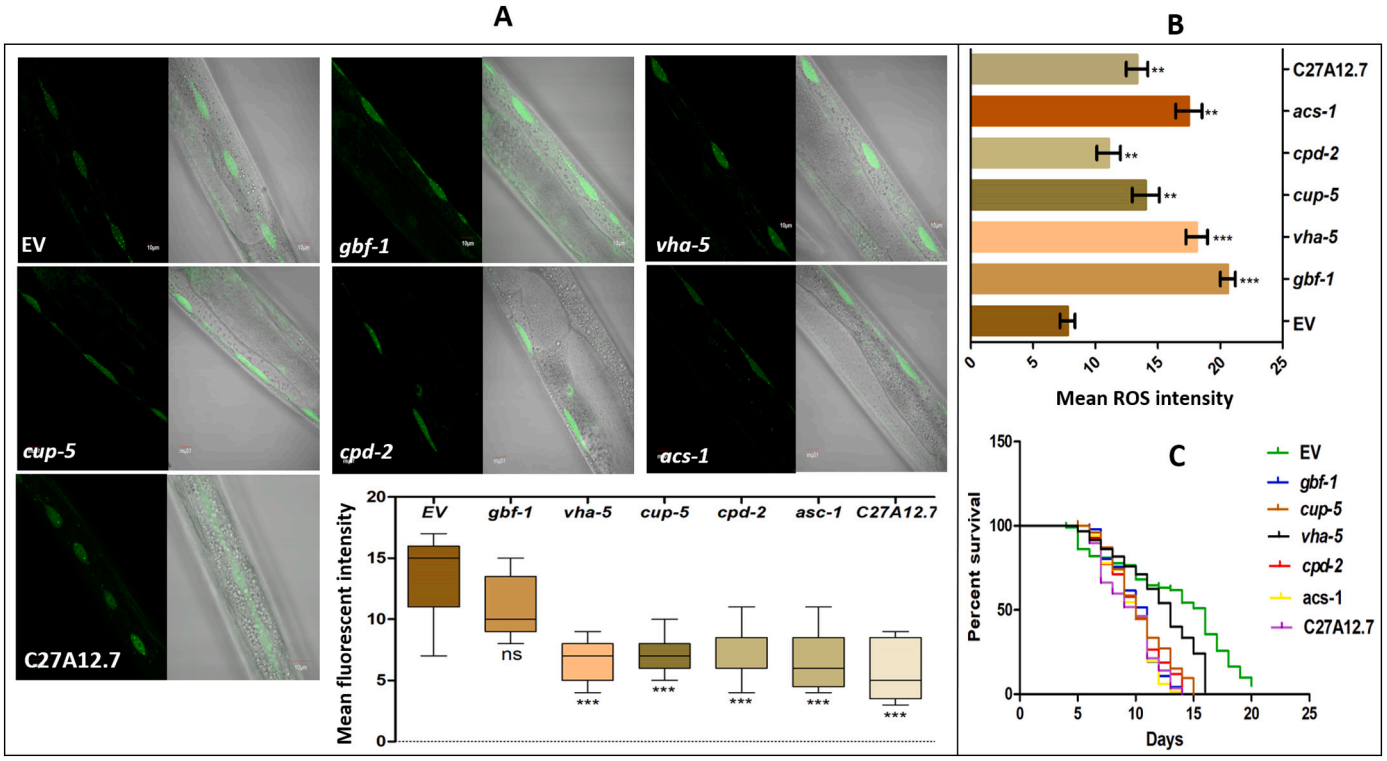


Fig. 5. Modulation of major PD associated endpoints (LGG-1, ROS & longevity) after RNAi of PQC genes (*gbf-1, vha-5, cup-5, cpd-2, acs-1* & *C27A12. 7*): (A); Expression pattern of LGG-1: GFP in transgenic *C. elegans* strain after RNAi silencing of six PQC genes in DA2123 strain. (B); Quantification of ROS in wild-type *C. elegans* strain N2 after RNAi knockdown of six PQC genes. (C); Survival curve of NL5901 after RNAi silencing of PQC genes. The fluorescence dots were quantified by Image J analysis and a non-parametric independent t-test was used to analyzed quantified fluorescent images and ROS values (Mean ± SEM; $*p < 0.05$, $**p < 0.005$& $***p < 0.0005$). For life span, Data was analyzed by Kaplan Meier survival curve.

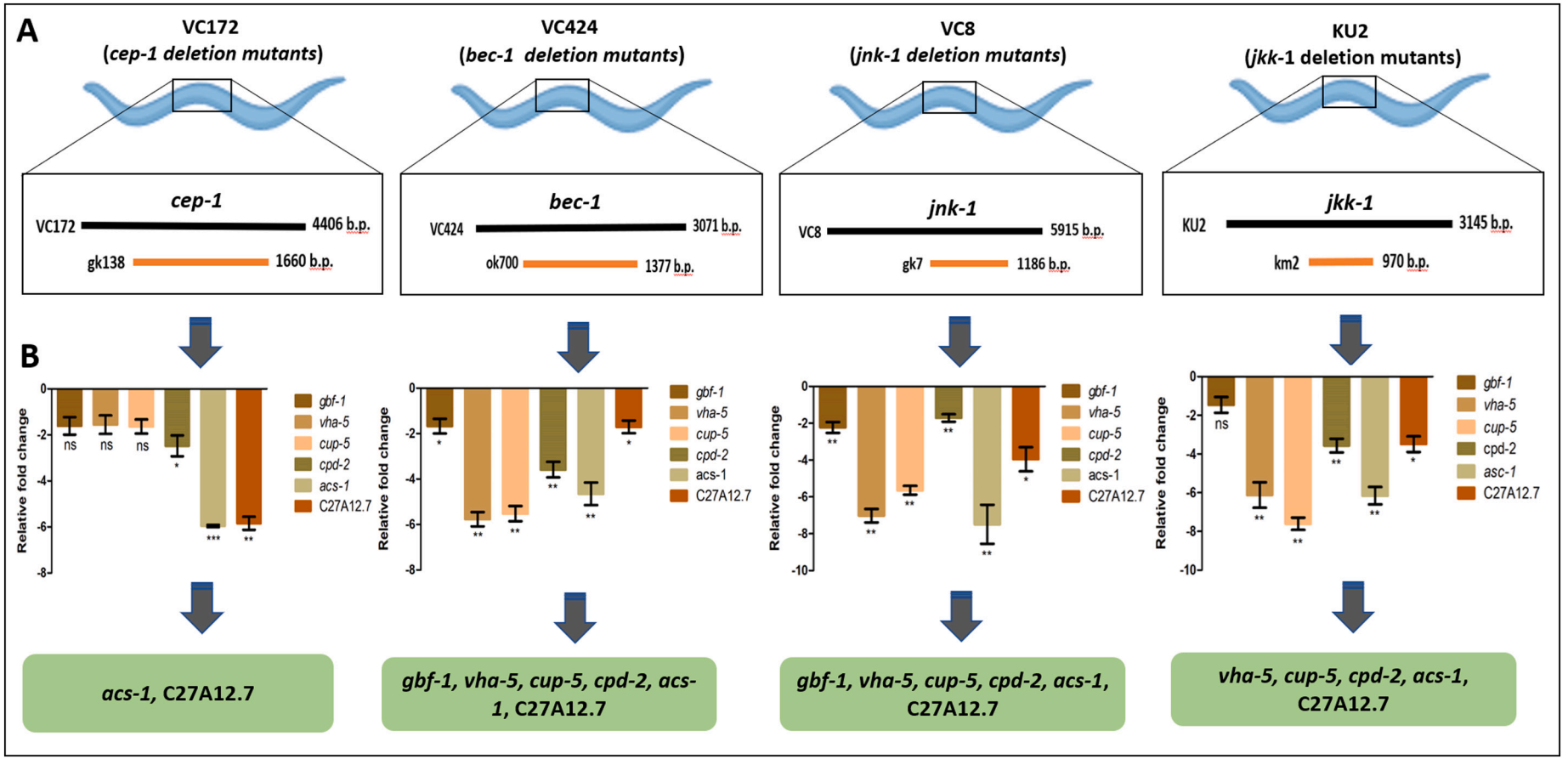


Fig. 6. Modulation of PQC genes under deletion background of autophagy and apoptotic deletion mutants: (A); Transgenic *C. elegans* strains having deletion mutation of autophagy and apoptotic makers, VC172: *cep-1* (deletion mutants), VC424: *bec-1*(deletion mutants), VC8: *jnk-1*(deletion mutants) and KU2: *jkk-1* (deletion mutants), (B); Quantitative PCR expression patterns of PQC genes (*gbf-1, vha-5, cup-5, cpd-2, acs-1 & C27A12.7*) in transgenic *C. elegans* strain VC8, KU2, VC172 & VC424. Fold change are quantified using and non-parametric independent *t*-test (Mean ± SEM; $*p < 0.05$, $**p < 0.005$, $***p < 0.0005$ & ns: non-significant). Actin (*act-1*) is used as an endogenous control with which ct values of each gene is normalized.

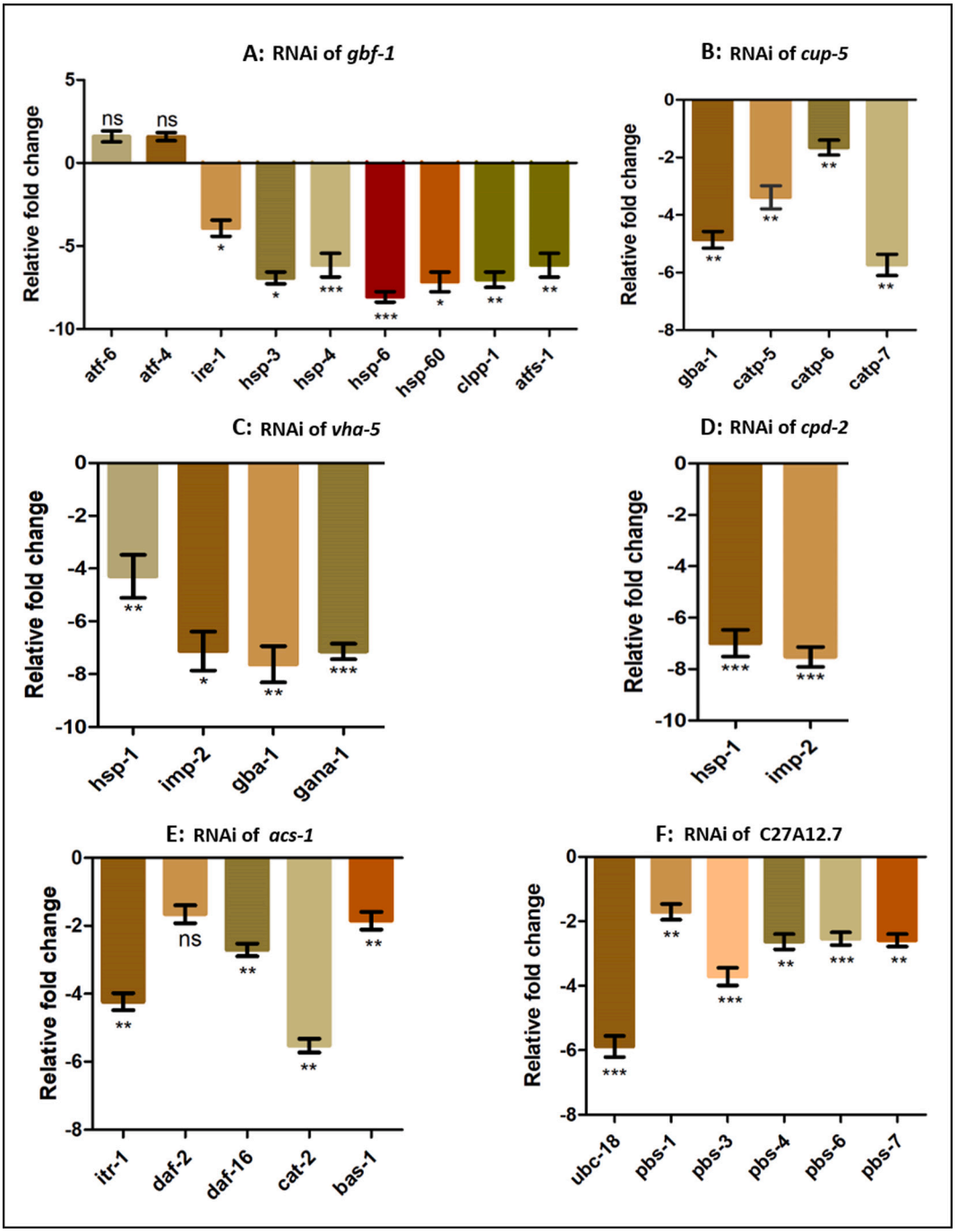


Fig. 7. Modulation of major marker genes of various pathways after RNAi of PQC genes (*gbf-1, vha-5, cup-5, cpd-2, acs-1&C27A12.7*): (A); Quantitative PCR patterns of ER^{UPR} marker genes (*atf-6, atf-4, ire-1, hsp-3, hsp-4 and hsp-4*) and MT^{UPR} marker genes (*hsp-6, hsp-60, clpp-1* and *atfs-1*) after silencing of *gbf-1* gene (B); qPCR expression patterns of *catp-5, ctp-6 &catp-7* and lysosomal associated enzymes *gba-1* after silencing of *cup-5* gene (C); qPCR expression patterns of chaperone mediated autophagy marker genes (*hsp-1 & imp-2*) along with lysosomal associated enzymes like *gaba-1* and *gba-1* related to PD after silencing of *vha-5* gene (D); qPCR time expression patterns of chaperone mediated autophagy marker genes (*hsp-1 & imp-2*) after silencing of *cpd-2* gene (E); qPCR expression patterns of *itr-1, daf-2, daf-16, cat-2* and *bas-1* after silencing of *acs-1* gene (F); qPCR expression patterns of *ubc-18*& proteasomal beta subunits *ubc-18, pbs-1, pbs-3, pbs-4, pbs-6&pbs-7*after silencing of *acs-1* gene. All the above mRNA expression levels were observed in transgenic *C. elegans* strain NL5901. Quantified by and non-parametric independent t-test (Mean ± SEM; *p < 0.05, **p < 0.005). Actin (*act-1*) is used as an endogenous control with which ct values of each gene is normalized.

calcium ion homeostasis. Therefore, altering the normal turnover of lysosomes with unregulated Ca^{+2} homeostasis could be the possible reason for elevated α-syn accrual [78,79]. *cpd-2* is a metallo carboxy peptidase; we observed in the in silico studies that *cpd-2* has genetic interactions with markers of chaperone-mediated autophagy (CMA) and RNAi of *cpd-2* led to downregulation of the markers of CMA (*hsp-1* and *imp-2*) which is one of the dedicated events responsible for the partial clearance of redundant soluble cytoplasmic proteins in PD [80,81]. Our findings also substantiate with one of the studies where *imp-2* inhibition leads to compromised proteasomal activity and chaperone-mediated autophagy clearance pathway in context of glucotoxicity in *C. elegans* [82] .This could be one of the possible reasons for the upsurge in α-syn accrual after the silencing of *cpd-2*. RNAi of *acs-1,* which is expressed neuronally and is involved in fatty acid metabolism, down-regulated

daf-16 transcription factor and the enzymes involved in dopamine synthesis from tyrosine (based on the clues from in silico genetic interaction). Existing literature shows that loss of *daf-16* and reduced dopamine levels are one of the major factors in PD ailments by augmenting the α-syn aggregation [28,83]. Possibly this could be a reason for increased α-syn accrual after silencing of *acs-1*. Based on existing literature, C27A12.7 is predicted to have ubiquitin-protein transferase activity, and we have validated the down-regulation of proteasome beta subunits after silencing of C27A12.7. Earlier reports suggest reduced proteasomal activity in substantia nigra of PD patients [84–86]. Therefore, it is likely that the silencing of C27A12.7 can lead to α-syn accrual associated with proteasome dysfunction.

3.2. Involvement of PQC genes in redox homeostasis

Oxidative stress is an essential factor that is associated with PD, along with α-syn [87–89]. Therefore, we studied the ROS levels after the silencing of identified PQC genes, and interestingly we observed elevated ROS levels after knockdown of each of the identified genes. Apart from vesicular transport *gbf-1* (GTPase ARF) is involved in mitochondrial homeostasis. Such a similar pattern of defects was also observed in mammalian and yeast cells [53]. Therefore, knockdown of *gbf-1* leads to impaired mitochondrial functioning manifesting elevated ROS levels inside the cell. *vha-5* is a component of lysosomal V-ATPases. It is reported that disturbance in the lysosomal functional composition leads to a decrease in the cardiolipin content (as a cross-talk signaling between lysosome and mitochondria), which leads to mitochondrial fission accompanied by deregulation in mitochondrial function and ROS generation [90]. This substantiates the observation of elevated ROS production after the silencing of *vha-5*. *cup-5* is an ortholog of human mucolopin1 (MCOLN1), also known as TRPML1, a vital calcium ion channel on the membrane of the lysosome. Activation of TRPML1 is well reported to maintain the homeostasis inside the cell by maintaining the clearance of damaged mitochondria and excess ROS by activating the autophagy process; therefore, knockdown of *cup-5* has shown elevated ROS within the cells [91]. Silencing of *cpd-2*, an ortholog of human carboxypeptidase (CPM), led to elevated ROS levels; previously, it has been reported that upregulation of protective genes including CPM, led to antioxidant effects in a patient who was at the risk of developing anemia thus substantiating the observed correlation [92]. From in silico studies, we found genetic correlations of *acs-1* with *itr-1* (*acs-1* has been reported for the optimal IP3 signaling, and *itr-1* encodes for inositol 1,4,5-trisphosphate receptor (IP3R)). Recent studies have shown that cell lines devoid of IP3R (DT40 cell lines) have higher ROS levels with downregulated glutathione and superoxide dismutase 2 (SOD2) as compared to wild type. This supports our evidence of elevated ROS levels after the silencing of *asc-1* in NL5901 [93]. C27A12.7 is an ortholog of human ARIH1 (Ariadne RBR E3 ubiquitin-protein ligase 1). ARIH1 polyubiquitinates damaged mitochondria and direct them for degradation by autophagy [94]. Therefore, after knocking down of C27A12.7 we observed elevated ROS levels probably because its knockdown perturbs the damaged mitochondrial removal in the cell.

3.3. Amelioration of dopamine levels and locomotory behaviour

Impairment of specific neuronal populations inside the brain is one of the features of PD. The dopaminergic neurons of substantia nigra pars compacta are the most susceptible ones as the disease progresses [95]. Therefore, we investigated the dopamine levels after the silencing of identified PQC genes, and strikingly we observed downregulated dopamine levels after knockdown of each PQC gene. *gbf-1* is predicted to have ARF guanyl-nucleotide exchange factor activity; existing literature supports the fact that ARF-GTPase like gene products alleviate neurodegeneration by improving the protein trafficking towards lysosome. Other findings suggest that ARF guanyl-nucleotide exchange factor activity interacts with neuronal calcium sensor-1 in the calcium signaling pathway, determining the *C. elegans* locomotion at elevated temperature [96,97]. Therefore, it seems likely that the silencing of *gbf-1* is not neuroprotective for dopaminergic neurons. Lysosomal acidification is necessary for the proper functioning of hydrolyzing enzymes in it. One of the findings suggests that compromising lysosomal acidification by tumor necrosis factor-α can lead to the accumulation of α-syn in the dopaminergic neurons leading to cell death [90]. Impaired lysosomal acidification by knockdown of *vha-5* in present studies, could be the possible cause of dopaminergic neuronal damage. It is well reported that Ca^{+2} homeostasis disruption in neuronal cells can lead to impaired neuronal functions, which progressively can lead to neurodegenerative diseases such as PD. Dopaminergic neuronal death has been reported either by knockdown of TRPC1 (transient receptor potential (TRP) channel superfamily, which includes mucolipin) or the addition of TRPC channel blockers. Therefore, knockdown of *cup-5* (orthologue of human mucolipin) may be involved in dopaminergic neurodegeneration by disrupting the Ca^{+2} homeostasis inside the neuron [98]. Carboxy Peptidase E (CPE) plays an important role in the nervous system. It is required for proper neuronal structure (dendrite patterning), neuronal survival (hippocampal neurons) & proper cognitive function. *cpd-2*, an ortholog of human CPM, shares around 65 % homology with CPE. Therefore, possibly the role that CPE is playing in the hippocampal neurons, *cpd-2* might play for the dopaminergic neurons in the substantia nigra, though further investigation is required for analyzing such specific role [99]. In recent studies, overexpression of mutated α-synuclein has been shown to lead to the accumulation of triacyl glycerol (TAG) in dopaminergic neurons. Elevated neuronal TAG content was associated with increased activity of the Acyl-CoA synthetase [100,101]. *acs-1* is a human orthologue of acyl-CoA synthetase family member 2; therefore, knockdown of *acs-1* is probably hampering the lipid metabolism inside the dopaminergic neurons making these further vulnerable. C27A12.7 is an ortholog of human E3 ubiquitin-protein ligase 1. It has been reported that endogenous PARKIN plays an essential role in dopaminergic neuronal protection from mitochondrial stress [102]. Therefore, the silencing of C27A12.7 makes dopaminergic neurons more susceptible to elevated mitochondrial stress. In PD the dopamine transporter (DAT-1) can be a critical factor for maintaining of the dopamine concentration [26]. But after knockdown of identified putative PQC downstream targets, we observed that there is a non-significant variation in DAT-1 expression levels even though we observed significantly reduced levels of dopamine. It is known that locomotory deficits in case of PD are associated with decline in dopamine levels, [103,104] hence the observed effect on locomotory behavior, vis studying thrashing of worms, could be because of reduced neurotransmitter dopamine levels following silencing of predicted PQC downstream targets.

Autophagy is a highly conserved evolutionary cellular process that plays a crucial role not only in maintaining the cellular homeostasis (by degrading misfolded proteins and damaged organelles) during stress situations but also takes part in remodeling during the developmental process [28,105]. As neurons are the most long-lived post-mitotic cells, brain becomes one of the most vulnerable organs for the mutations involved in autophagic pathways and lysosomal disorders, which leads to the pathobiological feature of many neurodegenerative disorders. We observed that the silencing of identified PQC genes down-regulates the autophagy markers (*bec-1, lgg-1, atg-5* and *vps-34*) significantly. BEC-1 plays an essential role in the functioning of class III PI3 kinase; it is an important protein required for autophagy, endocytosis, and membrane trafficking [33]. On the other hand, interestingly, we have observed down-regulation of PQC genes in the *bec-1* deletion mutant background of *C. elegans*, which indicates a strong association between *bec-1* and PQC gene expressions. *vps-34* encodes an ortholog of the phosphoinositide 3-kinase and is required for vesicular trafficking, including autophagy and apoptotic cell clearance. *lgg-1* encodes the ortholog of mammalian MAP-LC3 required for the degradation of cellular components [34,35]. We further validated LGG-1 expression levels with a

decrease in the GFP puncta, which imitates curtailment in the autophagosome formation in DA2123 transgenic strain of *C. elegans* after silencing of PQC genes. Even after impeding the autophagy and proteasome machinery pharmacologically, we observed downregulation of most of the PQC genes, which shows a substantial alliance of PQC genes with the protein clearance system.

3.4. Alteration of autophagy and apoptotic process

Among diverse cell death pathways involved in PD pathogenesis, apoptosis plays a critical role. It is not only necessary for building a decisive neuronal network in the developing brain but also plays an important role in eradicating the damaged neurons as the aging progresses. Although excessive, uncontrolled apoptosis has been reported to accelerate the disease progression in PD [106], we observed that silencing of identified PQC genes down-regulates the apoptotic markers (*cep-1, ced-4, jnk-1, jkk-1* and *nsy-4*) significantly. *cep-1* encodes an ortholog of human tumor suppressor p53 that promotes DNA damage induced-apoptosis. Programmed cell death is initiated by *ced-4*, which activates *ced-3* and in turn encodes the caspase required for the execution of apoptosis [41]. *jnk-1* encodes a serine/threonine kinase and its direct activator, *jkk-1* are members of C-Jun N-terminal kinases (JNKs), which belongs to the MAP-kinase superfamily. Both are expressed in most of the neurons and mediate apoptotic signaling in both intrinsic and extrinsic pathways [42,43]. NSY-1, is the ortholog of mammalian apoptosis signal-regulating kinase (ASK) family of MAP kinase (MAPK) kinase kinases (MAP3Ks) responsible for regulating the viability of animals in anoxia [39]. We also observed that most of the PQC genes were down-regulated *under cep-1, jnk-1 & jkk-1* deletion mutant background, which shows a relevant involvement of PQC genes with the apoptosis process. Both autophagy and apoptosis protect the cell or the nearby cell during an adverse situation. Therefore, a balance between apoptosis and autophagy becomes crucial to maintain normal physiological function. Downregulation of apoptotic and autophagy markers under the knockdown condition of PQC genes and vice versa suggests their core involvement in both of the QC process. Though we have provided some probable mechanistic insight of PQC gene involvement in certain pathways (that can directly or indirectly affect the overall quality control network), still to get a clear picture of their regulatory role in autophagy and apoptosis needs further investigation.

Based on our experimental results we can say that we have identified six PQC genes (*gbf-1, vha-5, cup-5, cpd-2, acs-1 & C27A12. 7*) playing a vital role in PQC machinery therefore any mimetics or drugs that can over express the human orthologue (GBF-1, ATP6V0A 1/2, MCOLN 1/3, CPE/ CPN1, ACSF2 and ARIH1 respectively) of these six genes could possibly play a potential therapeutic target for drug development for the Parkinson's patients. The future implications of the present study would be regarding understanding the mechanistic aspects and regulation of PQC genes via miR-4813-3p, particularly in the context of aging, which could be achieved with efficiency via employing the various developmental stages of *C. elegans*.

4. Conclusion

Neurodegenrative PD exhibits impairment in clearance of toxic protein aggregates, which ultimately leads to neuronal cell death, decline in essential neurotransmitter levels and declined bodily functions. Employing transgenic *C. elegans* strain that expresses 'human' alpha synuclein, we report on the the novel role of micro RNA molecule miR-4813-3p in regulating the various pathways associated with proteostasis network via its predicted downstream targets (*gbf-1, vha-5, cup-5, cpd-2, acs-1* and C27A12.7). Our studies show that the absence of putative downstream targets of miR-4813-3p clutter the PQC network via α-syn accrual and its associated outcomes which further impact autophagy and apoptotic pathways. The studies propose miR-4813-3p as a common trigger for multiple factors associated with PD. The findings are a step towards exploring potential of this, and other, micro RNA molecules towards pharmacological manipulations in the interest of bettering mechanistic understanding to Parkinson's disease.

5. Methods

5.1. C. elegans culture and maintenance

For our studies, we have used an *Escherichia coli* stain (OP50) to deliver as a source of food. OP50 seeding was done to prepare bacterial lawn onto NGM plates. Nematode Growth Medium was prepared by adding 2.5 g Peptone (sigma),3 g NaCl (sigma),17 g agar (HIMEDIA). After the solution is autoclaved around 50 °C,1 ml cholesterol (5 mg/ml), 1 ml $MgSO_4$(1 M), 1 ml $CaCl_2$(1 M), 25 ml KH_2PO4(1 M pH 6.0) was added. Then the media was poured on 90 mm petri plates under sterile conditions and left till it solidify. After sterilizing the plates by U.V. treatment, plates are stored at 4 °C. The bacterial lawn was prepared by spreading 500 μl of OP50 on NGM plates with the help of a spreader under sterile conditions, which were incubated overnight at 22 °C. Subculturing of *C. elegans* strains were performed on these pre-seeded OP50-NGM plates and propagated further at 22 °C.

5.2. C. elegans embryo isolation

From previously chunked *C. elegans* grown on OP50 seeded NGM plates, gravid reproductively mature *C. elegans* population was harvested by using M9 buffer. Worms were settled down in a 15 ml conical centrifuge tube by centrifugation at 1300 rpm for 2 mins. Settled worms were resuspended in M9 buffer and washed thrice in order to remove any adhering bacteria on the surface of worms. Finally, to the worm pellet, 2 ml of sodium hypochlorite and 1 M sodium hydroxide solution hypochlorite (the axenizing solution) was added. To dissolve the worm body, the whole solution was gently mixed to release the embryos. The derived embryos were pelleted down via centrifugation for 5 mins at 1300 rpm. The pelleted embryos were then washed with M9 buffer thrice and was spread onto experimental treatment plates under sterile conditions.

5.3. C. elegans strains

Strains used in this study were N2; Bristol wild-type, NL5901; pkIs2386 [unc-54p::alpha-synuclein::YFP + unc-119(+)] [106](**97**), DA2123; adIs2122 [lgg-1p::GFPC rol-6(su1006)] and BZ555; egIs1 [dat-1p::GFP]. From *Caenorhabditis* Genetics Center (University of Minnesota, Minneapolis, MN) entire strains were received. All the strains are propagated at 22 °C either on OP50 or on RNAi treatment plates.

5.4. RNAi-induced gene silencing

RNAi-Induced feeding protocol was used for the silencing of specific genes. Bacterial clone expressing dsRNA (source Ahringer library) targeted for *C. elegans* was first cultured for 6–8 h in Luria Bertani Broth media containing ampicillin (50 μg/ml). When the culture attains its active log phase,500 μl of this bacterial culture was seeded onto NGM plates (having 5 mM IPTG and carbenicillin; 25 mg/L) incubated overnight at 22 °C. Under sterile conditions, embryos of the desired strain were transferred to these treatment plates.

5.5. Image acquisition

Synchronized worms were washed thrice with M9 buffer to remove adhering bacteria from the treatment plates and immobilized with 100 mM sodium azide (Sigma, Cat No. 71289). Immobilized worms were mounted on a clean glass slide with the help of a coverslip. Finally, the images of the worms were captured using Carl Zeiss Axio ImagerM3 for α-synuclein protein expression/accumulation experiment and a

multiphoton confocal microscope to capture the images of transgenic *C. elegans* strains NL5901 and DA2123, respectively. ZEN2010 image acquiring software was used for image acquisition, and images are finally quantified through Image J software (Image J, National Institutes of Health, Bethesda, MD).

5.6. Estimation of Reactive Oxygen Species (ROS)

ROS estimation was done by using 2,7-dichlorodihydrofluorescein diacetate (H_2DCFDA). Both control and RNAi silenced groups of worms were washed three times with M9 buffer and two times with phosphate buffer saline (PBS). Each group (of around 100 worms/100 ml assay solution) was analyzed in triplicates and finally transferred to assay wells (OptiPlate-96 F; PerkinElmer). 100 μl H_2DCFDA (Cat. No. D399, Invitrogen) from 100 mM stock prepared in ethanol was added to each well. Quantification of the fluorescence intensity from each well was taken at three discrete time intervals, (i); before the dye was added (ii); instantly after the addition of dye and (iii); 1-hour post-incubation after the dye was added. Multimode plate reader (Perkin Elmer, VICTOR X3) was used to measure the fluorescence intensity having an excitation wavelength of 485 nm and an emission wavelength of 520 nm. The difference in the fluorescence was determined by subtracting the initial reading (before the addition of dye) from the readings of the immediate addition of dye, which was finally subtracted from the reading of post 1 h incubation of dye. Finally, fluorescence intensity per worm was plotted as its mean value. Statistical significance was evaluated as by student's *t*-test using GraphPad Prism software. For ROS estimation in N2 strain, we have performed the experiment in three replicates and in each experiment, we have taken 100 worms for each group.

5.7. Estimation of neurotransmitter dopamine levels using LC-MS/MS

Using LC-MS/MS, dopamine content of both control and treatment worms were measured. Age synchronized adult worms (L4 stage) were washed thrice with M9 buffer to remove adhering bacteria on it. Worm pellet was flash frozen using liquid nitrogen. The lysis of worms is carried out by using the sonicator (at 30 % amplitude for 5 min (pulse rate 2 s on/off) using 300 μl Tris buffer (pH = 8). Lysate samples were centrifuged for 10 min at 13000 rpm in 4 °C, and the supernatant was collected (the extracted protein sample) which is quantified by the Bradford method. The LC consists of Delta 600 binary pump WATERS (Manchester, UK) linked with 2707 autosampler and in-line AF degasser equipped with API 3200 triple, quadruple mass spectrometer (ABI SCIEX, ON, Canada). Using a basic protein precipitation technique, using acetonitrile (1:3) samples were processed; centrifuged for 20 min at 14,000 rpm and supernatant (20 μl) was injected into LC-MS/MS. The separation was accomplished using 150 × 4.6 mm, 2.6 μm Thermo Fischer scientific Accucore AQ column having an acetonitrile's mobile phase (with a 0.1 % formic acid (35:65) having a flow rate of 0.6 ml/min. For the sample, the total run time was 4.00 min. The ionization of dopamine was achieved in MRM positive mode with the transition of 154.00/137.2. Integration of Analytical data was performed by Analyst software version 1.6 (AB SCIEX, ON, Canada). For each group, 7000 worms were taken for estimation and dopamine concentration was achieved in ng/ml.

5.8. Assay for motility of worms

Worms motility is estimated by thrashing assay where the number of thrashes is counted in per unit time. One thrash means; one-way complete bending of the body to the extreme angle and return to the initial position. In our study, worms harvested from the treatment plates were washed three times with M9 buffer to remove the bacteria's adhering bacteria. On a drop of M9 buffer, a single worm was placed and the total number of thrashes in 30 s was counted using a timer under Sterio zoom microscope (Leica). Ten worms were counted for each group in a separate experiment (in duplicate). For each group randomly, ten worms were selected for thrashing count.

5.9. Total RNA isolation and cDNA synthesis

Age synchronized worms were washed thrice with M9 buffer and then twice with diethylpyrocarbonate (DEPC; Sigma Cat. No. D5758) treated water to discard adhering bacteria. To isolate the total RNA from all the different strains of *C. elegans* used in our study, we have used RNAzol® RT (Sigma, Cat. No. R4533) method as per the manufacturer's protocol. The RNA concentration was determined by using the UV spectrophotometer Nanodrop (Quawell-UV–Visible Spectrophotometer, Thermo-Q5000). One ng of total isolated RNA was used for preparing cDNA by using cDNA synthesis kit (Thermo Fisher-Verso cDNA Synthesis Kit; Cat no: AB1453B) according to the manufacturer's protocol. Finally, cDNA concentration is measured by using a nanodrop spectrophotometer in ng/μl. For RNA isolation, we have taken 2000 worms at L4 stage for each group and the experiment and repeated it three times.

5.10. Quantitative real-time PCR assay

Amplified cDNA quantitative assessment was done by using SYBR Green dye (Thermo Scientific Cat. No. K0251) and according to the manual protocol by the manufacturer, all qPCR experiments were performed by the manufacturer. Briefly, 100 ng of cDNA was amplified using a thermal cycler detection system (Agilent Technologies-MX3005P). The amplification conditions were: pre-incubation cycle (Total 1 cycle for 2 min at 50 °C and for 10 min at 95 °C) which is followed by 40 amplification cycles o (for 30 s at 95 °C, for 30 s at 55 °C, and for 30 s at 60 °C) and to generate melting curve (95 °C for 5 s, 65 °C for 1 min). Each q-PCR experiment was performed at least twice in replicates. We have normalized the ct values of each gene with actin (*act-1*) as an endogenous control.

5.11. Lifespan assay

Isolated embryos of desired *C. elegans* strains were applied on both treated and control plates to obtain age-synchronized worms. After 48 h, onto freshly prepared feeding plates of treatment control and groups, under stereo zoom microscope, one hundred adult worms (L4 stage) were picked and transferred respectively. From that day onwards, daily scoring of live, dead, and censored worms was performed; two plates for each group is used for scoring. A censored set of data was recorded based on the total number of missing worms or the desiccated worms near the plates' edge. Based on the feedback response to gentle prodding on the head of worms, live, and dead worms were identified. The worm was considered dead if no response is observed. On a daily basis for 20 days, the nematodes were transferred onto fresh feeding plates which were maintained at 22 °C using BOD incubators that we employ for rearing of the worms. The scoring of worms was performed from egg till its death, and data was analyzed by Kaplan Meier survival curve.

5.12. Gene network analysis

We used GeneMANIA (Gene Multiple Association Network Integration Algorithm), a free accessible and user-friendly web tool for the retrieval of interacting genes/proteins (http://www.genemania.org, Application version: 3.1.2.8). Genes were represented as “node”, while the interactions between the genes were represented as an “edge”. Based on query gene, it shows results for an interactive functional associative network according to their; Genetic and Physical interaction data derived from BioGRID.

5.13. Autophagy and proteasome inhibition

For Autophagy inhibition, we have used 10 mM of 3-Methyl Adenine

(3-MA), and for proteasome inhibition, we have used 50 μM of MG132. The inhibitors are seeded with the culture overnight at 22 °C at BOD and used in the next day to put isolated embryos on it.

5.14. Statistical method and control for the experiments

For microscopy-based quantification assays, we have carried out at least two independent experiments treating and studying over 100 worms for each group. Whereas the fluorescence intensity of worms is observed for the entire set of slides, the representative images are grabbed for $n = 10$ within each individual experiment. Wherever two independent experiments are conducted, we end up studying the fluorescence pattern in 100–200 worms and record images for at least $n = 20$. These images are then processed for quantification of intensity using Image J analysis.

To analyze statistically quantified fluorescent images, ROS values from luminometer, Number of thrashes of worms and dopamine content and the ct values obtained from qPCR methods we have followed non-parametric independent 't' test using Prism 5 software, where *p*-value is represented as; $*p < 0.05$, $**p < 0.005$ $***p < 0.0005$ & ns: non-significant.

Across all experiments, we have used adult worms at L4 stage. For the control groups, we have used an empty vector (EV) with respect to which we have accessed the phenotypic, behavioral or genetic modulations in the *C. elegans.*

5.15. Isolation of small non-coding RNAs using mirVana™ miRNA isolation kit

The standard protocol was employed for the extraction of small non-coding RNAs; briefly, 0.2 % diethylpyrocarbonate (DEPC-Sigma, Cat. No.-D5758) treated water was used to remove adhering bacteria from age synchronized control and treated groups. The mirVana™miRNA isolation kit (Ambion P/N AM1561) was used for the isolation of miRNAs. According to protocol 250 μl lysis/binding buffer was added worms were homogenized in lysis buffer followed by the addition of 1/10 miRNA homogenate additive; the solution was mixed gently and kept on ice for 10 mins. After this step, to the lysate, an equal amount of Acid-phenol: chloroform was added and centrifuged for 5 mins at 10,000*g. After centrifugation, the aqueous phase was removed and 1.25 times the volume of absolute ethanol was added after this step, filtration was done by passing through the filter cartridge, washing and elution.

5.16. Reverse transcriptase reaction

cDNA was prepared from isolated non-coding small RNAs using MicroRNA Reverse Transcription TaqMan® kit (Applied Biosystem cat no. P/N 4366596). For reaction, 10 ng noncoding RNA (template), 1 μl multiscribe RT enzyme (50 U/μl), 1.5 μl 10X RT buffer, 0.19 μl RNase inhibitor (20 U/μl), 3 μl specific miRNA primer were added into PCR microcentrifuge tube. Gently vortexed the reaction mixture and processed using Agilent sure Cycler 8800 at 16 °C for 30 min, at 42 °C for 30 min, at 85 °C 5 min and then held at 4 °C.

5.17. TaqMan miRNA assay

miRNA quantification was carried out using Universal Master MixII TaqMan® MixII (Applied Biosystem cat no. 4440040). 100 ng cDNA template and 1X TaqMan® Universal Master MixII were mixed together to prepare the reaction mixture. The amplification program was 95 °C for 10 min (for1 cycle), then by 95 °C for 15 s and finally 60 °C for 1 min (for 40 cycles) run into 3005P-Agilent. The experiment was carried out in triplicate sets for each sample. Fold change of all the samples were evaluated using comparative $2^{-\Delta\Delta CT}$ [99,100,107,108]. For normalization of miRNA expression U18 was used as an endogenous control.

5.18. Non-coding small RNA library preparation for next-generation sequencing (NGS)

1 μg of total RNA was used as the starting material and 3′ adaptors were ligated to the specific 3'OH group of miRNAs followed by 5′ adaptor ligation. Superscript III Reverse transcriptase was used for the reverse transcription of miRNA ligated products by priming with Reverse transcriptase primers. The cDNA was enriched and barcoded by PCR (15 cycles) and cleaned using Poly-acrylamide gel. 140–160 bp range of size was selected for the library followed by overnight gel elution. Salt was precipitated using Glycogen, 3 M Sodium Acetate and Absolute Ethanol and re-suspended in Nuclease-free water. The prepared library was quantified using Qubit Fluorometer and validated for quality by running an aliquot on a High Sensitivity Bioanalyzer Chip (Agilent).

5.19. Analysis of miRNAome data

Srna-workbenchV3.0_ALPHA was used to trim the Trueseq adapter sequences and perform length range filtering [109]. Sequence length of >16 bp and <36 bp were appraised for further analysis. *C. elegans* GRCh38 genome build used for the sequence alignment and Aligned reads were extracted and checked for ncRNA (rRNA, tRNA, snRNA and snoRNA) contamination. The unaligned reads in ncRNAs were considered as known miRNAs. Reads were made unique and hence read count profile was generated. *C. elegans*mature miRNA sequences retrieved from miRbase-21 [110] and miRNAs homology search were done by NCBI -blast-2.2.30+ [111]. Sequence-matched reported for known miRNAs and showing no hits with known miRNAs were predicted as novel miRNAs, done by Mireap_0.2. Differential Gene Expression (DGE) analysis was carried out using DESeq [112] tool and for reference, *C. elegans* genome sequence was used.

Abbreviations

PD	Parkinson's Disease
PQC	Protein Quality Control
ROS	Reactive Oxygen Species
NDs	Neurodegenerative Diseases
UPR	Unfolded Protein Response
AD	Alzheimer's disease
ISF	interstitial fluid
CSF	Cerebrospinal fluid
qPCR	Quantitative Polymerase Chain Reaction
SOD2	Super Oxide Dismutase 2
ALP	autophagosome-lysosomal-pathway
UPS	Ubiquitin Proteasomal System
CPM	carboxypeptidase
NCS-1	Neuronal calcium Sensor-1
TNF	Tumor Necrosis Factor
CPE	Carboxy Peptidase E
TRP	Transient Receptor Potential
TAG	Triacyl Glycerol
ASK	apoptosis signal-regulating kinase
MAPK	MAP kinase
(ko)	Knock Out
ER^{UPR}	Endoplasmic reticulum unfolded protein response
MT^{UPR}	Mitochondrial unfolded protein response
BOD	Biological Oxygen Demand
Alpha-synuclein	α-synuclein
micro RNA	miRNA

Supplementary data to this article can be found online at https://doi.org/10.1016/j.bbamcr.2022.119342.

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CRediT authorship contribution statement

AS conducted the experiments, analyzed data, wrote the manuscript, RH, S and LK contributed in conducting some of the experiments and towards analyzing data; AN conceived the study, provided infrastructure and reagents, analyzed the data and edited the manuscript.

Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declaration of competing interest

All authors read the manuscript and agreed its content before the submission. The authors declare no competing interest.

Data availability

Data will be made available on request.

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