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COMPUTATIONAL PREDICTION OF POTENTIAL GENES: INVOLVE IN DIFFERENT HUMAN DISEASES FIND OUT WITH THE HELP OF C. ELEGANCE NUCLEOTIDES

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ABSTRACT

Micro RNAs of C.*elegans* are small, non-coding regulatory RNAs. The *C. elegans* genome encodes hundreds of miRNAs. Computational prediction and systematic cloning of miRNA reveals that hundreds of genes encoding miRNAs exist in the genome of *C.elegance*. In the present study, we describe a computational procedure to identify miRNA genes conserved in more than one genome. Applying this program, known as DINA, together with molecular identification and validation methods. Many of these miRNA conserved in other organism. We identified 610 genes from C. elegance miRNAs and these identified genes play a very important role in human genomic functions.

Keywords:miRNA, ***C. elegans*** , Genomic function.

INTRODUCTION

MicroRNA is a family of small non-coding RNAs that regulate gene expression in a sequence-specific manner. (1) Small non-coding RNAs that regulate gene expression in a sequence-specific manner (2) miRNAs are a family of 19 to 25 small nucleotide RNAs (3) Most noncoding RNAs are characterized by a specific secondary structures that determine their function. miRNAs are well conserved in both plants and animals, and are thought tobe a vital and evolutionarily ancient component of genetic regulation. Extensive studies have revealed critical rolesformiRNAs in human genomics.(4)

C. elegans is a free-living, non-parasitic nematode, with a life cycle of 3.5 day and a lifespan of about 2–3 weeks under suitable living conditions. The adult is about 1 mm in length and 80 µm in diameter. It feeds on bacteria such as Escherichia coli in liquid medium or on agar plates and can be easily cultivated in large numbers.C. elegans has emerged as a powerful experimental system to study the molecular and cellular aspects of human disease in vivo. It has been estimated that about 42% of the human disease genes have an ortholog in the genome of C. elegans, including those genes which associated with Alzheimer's disease (AD), juvenile Parkinson's disease (PD), spinal muscular atrophy (SMA), hereditary nonpolyposis colon cancer, and many others age-related disorders (6–7).

Because of its short lifespan and well-known biology, coupled with a completely sequenced genome that shares extensive homology with that of mammals, Caenorhabditiselegans is one of the most versatile and powerful model organisms. Research in C. elegans has been instrumental for the elucidation of molecular pathways implicated in many human diseases.

The nematode holds promise of providing clear leads towards the identification of potential targets for the development of new therapeutic interventions against human diseases. (8)

METHODOLOGY

Sequences are fetched from miRBase are precursor of *C.elegance* and miRNA (mirbase@manchester.ac.uk) of *C.elegance.* Then thermodynamic study with minimum free energy of fetched precursor sequences for potential miRNA of *C. elegance*.Then we select potential miRNA on behalf of precursor thermodynamics ratings and miRBase high-confidence sequences of c.elegances. Now miRNA selected and submitted to Diana Tv3.0 and results were analyzed for targeted genes of human.

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Table 1 : Selected miRNAs(miRBase- ID) for identification of genes in humans

S.No	miRNA (mirbase) ID	Name of gene Identified
1	>cel-miR-35-3p	WDR90, C17orf62
2	>cel-miR-795-5p	FIGN, LIN28B, IGF2BP1,ONECUT2, ARID3B, NR6A1,CLCN5, FOXP2, HIC2, IGF1R,BACH1, TRIM71, FBN1, YOD1, C14orf28, CPEB2, CCND2, PKN2, BZW1, ZNF512B, PAPPA, FNDC3A, TGFBR1, PTPRD, DUSP16,GALNT1, PBX2, HOXA1, SMARCAD1, TTLL4, PTCH1, CPEB1, NAP1L1, ABCC5, IGF2BP2, CPEB3, ACVR2A,PBX3, PPP1R15B, PPARGC1B, POU2F1, CPEB4,MACF1, ACVR1C, GDF6, INSR, UTRN, DLC1, NAT12,FNDC3B, GATM, COL1A2, MIB1, PGM2L1, ABL2, COL27A1, C1oorf64, WDFY4, ADAMTS8, DMD, ZFYVE26,
3	>cel-miR-37-5p	FOXI2, RSPO4, FGFR1, MEF2D, C8orf13, FOXP4, UCK1, SYNGR1, TCF21, HIVEP3, TSPAN18, PCNT, SDC3, PVRL1, ZMIZ1, KLF13,SCN3B, SPNS2, KIAA1324, TTYH3, SPN, ATXN1, SGIP1,
4	>cel-let-7-5p	FIGN, IGF2BP1, LIN28B, NR6A1, ONECUT2, ARID3B, FBN1, BACH1, CLCN5, YOD1, HIC2, IGF1R, FOXP2, PBX3, TRIM71, CCND2, PKN2, MAP4K3, CDV3,COL1A2, IGF2BP3, PAPPA, CPEB2, NAP1L1, C14orf28, PPP1R15B, PTPRD, RAPGEF6, FNIP1, GALNT1, SOCS4, DUSP16, TGFBR1, HOXA1, ARHGAP28, MAP3K1, LRIG2, UHRF2, LRIG3, BPTF, GAS7, CCNJ, B3GNT7, ABL2, CPEB3, ACVR2A, ABCC5, BCAT1, RANBP2, PCDH19, GAN, MAPK8, COL3A1, PPARGC1B, BZW1, POU2F1, CPEB4, FNDC3A, HDX, DLC1, NAT12, IDE
5	>cel-miR-2208b-5p	TNPO1, GLIS3, WDR35, ANKRD57, SLC12A2, ST6GALNAC3, DLG2, BICD2, IVNS1ABP, RNF38, NFIB, TP53INP1, C6orf89, IL6ST,EIF5, FIGN
6	>cel-miR-80-3p	LUZP4, ZC3H12C, KIAA1853,CLIC2, GFOD1, NLRC3, CARD8, C4orf15, CRX,PSMB2, UBE2R2, S100A7A, OPHN1, RNF144B, EXOSC6,C3orf64, KIAA0408, METTL7A, C20orf117
7	>cel-miR-42-5p	FOXI2, RSPO4, FGFR1, SYNGR1, PVRL1, ZMIZ1, FOXP4, C1orf21,PPARD, ATP11A, KLF13, SCN3B, TRDMT1, NPLOC4, MAML1, HAPLN4,PCNT, PRKCA, ADCY1, MECP2, TCF21, TSPAN18,C10orf105,
8	>cel-lin-4-5p	SMEK1, FAM120A, TRIM71, MXD4, ATXN7, RYBP, KIAA0174, OSBPL9, PAFAH1B1, KIAA1522, DAAM1, RAPGEF5, ZSWIM6,AEBP2, KLF13, PSCD1, BAK1, BCL2L7P1, MYT1, C11orf57, ST8SIA4, SEMA4D, ABHD6, ZSWIM5, MFHAS1, ARID3B, ADAM9, LRRC8B, SLC39A9, TAF9B, SH3TC2, LIN28, ANPEP, CDC37L1, IRF4, ZSCAN29, MACF1, ENPP1, GGA2, TMEM77, MLF2, CDR2L, TBC1D1, ZNF385, ANKRD50,NIPA1, SUV39H1, TGOLN2, STARD13, NUP210, KPNA6, SGPL1, ESRRA, FUT4, SCN2B, ACHE, ALPK3, SLC35A4, TSEN54, NCAN, GALNT14, TRIAP1, MSI1, BMF, UBE2R2, FAM78A, CDH5, IER3IP1, LFNG, PCTP, NPL, MCL1, DIRAS1, HCN3, C14orf43, SUV420H2, C10orf105, KLHL6
9	>cel-miR-79-5p	ONECUT2, POU2F1, MLL, FOXP2, CPEB2, LIN28B, POU2F2, CNOT6L, VPS13B,NR5A2, DST, FBN1, KIF13A, FOXP1, LDLRAP1, EPB41L3,PRDM6, SRGAP3, PRDM1, PCNP, STC1, KCNA1
10	>cel-miR-239a-3p	ST8SIA3, MACF1, MECP2, NTRK3, ZNF395, IGF1R, MYO1D, MDN1, ULBP1
11	>cel-miR-74-5p	KIAA1045, MACF1, HPS1, FAM86C, ADM2, AFF2, DST, ATP2B3, KIAA1529, CECR6,ZNF783, PLEKHF1, ARC, RAB43, ISY1, LARP1, H6PD,BMP1, SLC12A5, LYNX1, IKZF1, ZNF135
12L	>cel-miR-355-5p	TNRC6B, ONECUT2, GK5, ELOVL6, ELAVL4, DST, ZNF462, MACF1, LAMP2, GABRA4, AMMECR1, VGLL3,XKR6,
13	>cel-miR-791-5p	POU2F1, CRB1, DST, ADAM22, ANKRD15, ST13, FAM10A6, ST13P7
14	>cel-miR-50-5p	GPR123, BACH2, KPNA5, DDEF2, MYO5A, PSD3, KIAA2018, NEUROD1, EXT1, RPS6KA3, STK38L, IKZF2, ERG, TNRC6A, BCL11A, SMAD2, KLHDC5, C12orf5, OSBPL6, PCDH17, MOBKL1A, AMMECR1, ANKRD34, FOXP2, RNF144B, PHF20L1,

S.No	miRNA (mirbase) ID	Name of gene Identified
15	>cel-miR-5545-3p	BNC2, MYEF2, POU2F1, CRB1, MACF1, NTRK3, NFIB,PROS1, HS2ST1, CCDC144B,SASH1, DIAPH2, PDE10A, SMAD2, ZBTB41, NOVA1, KIAA0430, PAG1, PHF16, ELOVL6, ACADSB, IPO9, CLIC4, GAD2, TTN, MLL, USP6, CNTNAP2, ANKRD30B, SETD7, CCDC93,ARGFX, GDA, ZNF587,
16	>cel-miR-4805-5p	No data could be retrieved from the database
17	>cel-miR-61-5p	KIAA1853, ADH6, CNOT6L, USP47, PTPRT, ARCN1,
18	>cel-miR-786-3p	KIAA1609, NFIB, DST, NUFIP2, GPR92, SGTB, KIAA1239, WDR37, ZNF644,KIAA1147, VGLL3, MLL5, EPC1, KCNJ2, ANKRD28, CLCN6, DCP2, DOCK4, USP48, KIR3DX1, ANKS6, SH3PXD2A, EPAS1, IL1RAP, TMEM164, PIK3R3, HDAC9, EHF, ZNRF1, NR3C2, ARRDC3, ACVR1, RIT1, KCNA1, UBR4, DTNA, APOL6, ARF3, TRHDE, LAMP2, NSL1, RGS9BP, ENAH, TBCEL, PCDH15, ADCY1
19	>cel-miR-231-3p	DLGAP2, MDN1
20	>cel-miR-45-5p	GSG1L, CLDN19, PRKCA, C18orf1, KIAA0226, C1orf141, SMAD2, KLHL21, C1orf116, SS18L1, CRAMP1L, HN1L, RERE, C1orf21, XRRA1, UBR2, ACACB, VGLL3, CHL1, TMEM125, KLF12, ARC,AFAP1, BNC2, DNMBP, UBR4, TRIOBP, LPAL2, MEGF6, URB1, CDH23, TEAD1, SARM1, NCOA6
21	>cel-miR-53-5p	BAZ2A, CDH23, NMT1, TRIB2, SLC25A16, ADCY1, MBNL1, KBTBD8, FZD8, AGO2, FZD5, GIYD1, GIYD2, ITGB1, HS3ST2, FGFR3, MTMR3, HS3ST3B1, LRRC8B
22	>cel-miR-794-3p	GABRA4, NTRK3, KITLG, MYO5A, COL19A1, ATP9A, RAB3IP, NHS, POU2F1, PRPF4B, QSER1, BCL2, PSME3, YTHDF3, SFMBT2, DCX, KIAA1600, FGF2, SNTB2, C5orf21, SUDS3,KLHDC5, SOCS4, NFAT5,ADH1B, ADH1C, DTWD2, AKAP11, MAP3K7IP3, DLGAP2, XYLT1, TEAD1, PTEN, PTENP1, BTBD7, PCGF3
23	>cel-miR-2208b-3p	TNRC6B, RAB11FIP2, MBNL2, ZNF264, HSPA12A, RAB3IP, MLL, ERBB4, ZFAND5, NFIB, LUZP1, DST,NAV1, FBXW2, AFF2, OSBPL3, BCL7B, GRIN2A, NCOA1, MAFB, CPSF6, F11R,GAS7, CCDC6, C6orf103, CCDC140, PSD3, MAMDC2,CAMK2G, C18orf1, RC3H1, PARK2, C10orf63, TMEM47, SPATA13, IYD, ITGB1, FAM91A1, KIAA2026, SRSF1, PTGFRN, TTN,MACF1
24	>cel-miR-54-3p	TRIB2, MBNL1, KBTBD8, HOXA1, ZZEF1, SLC25A16, NTRK3, C4orf16, CTDSPL, PPP3CA, SMARCA5, LRRC8B,THAP2, CLDN11, EPDR1, ICMT, LIF, BAZ2A, ADCY1, FZD8, EIF2C2, FZD5, CAMTA1, MTMR3, ST6GALNAC4, FRAP2, PRDM1, PPP1CB, C1orf121, INSM1, AMMECR1, BMPR2,CDC25A, SETD1B, TMEM30A, RAC1, CYP26B1, ZNRF2, FIGN, TRIB1, PPFIA3, SMARCD1, ZBTB7A, CCDC21, ST5, RAVER2, PI15, JMJD3
25	>cel-miR-55-5p	SV2B, NOTCH2, KIAA1147, SSR2, JARID1A, GRIN2A,C9orf7, ASB1, KRT84, SMU1, GCC1, TNRC6B, MMD, CCND2, FRAS1, RUNX1, HEMK1, C22orf29, WDTC1, SMAD2, G6PC, TOLLIP, UST, ATP9A, PVR, E2F2, FOSL2, FOXK1, XYLT1, GRM4, TBC1D13, ZDHHC8, CYP8B1, CHST3, RNF216,
26	>cel-miR-236-3p	ZEB2, FIGN, GPM6A, FBXW7, KIAA1432, RPS6KB1, TSGA14, RAP1B, LRP1B, JHDM1D, NFIB, MAP2, C16orf72, YWHAG, RAP2C, PAPD5, NEGR1, RANBP10, TRIM33, PCTK2, MSN, NOVA1, CRKL, EPS8, CDYL, WIPF1, SYNJ1, SESN1, WAPL, LCORL, PKN2, ELAVL2, MEX3B, CTDSPL2, KIAA0355, RANBP9, BNC2, ESRRG, ERRFI1, AKAP2, PALM2, SCAMP1, CCNJ, MED13

Table 1 Explains: This table explains selected miRNAs of C.elegans from miRBase as also explains name of identified genes via miRNAs*C.elegans in humans*

RESULTS AND DISCUSSION

With the help of DINA-microT3.0 server we analyzed the identified genes of human via C. elegance miRNA. In present study we analyzed 610 potential genes of human beings. These potential genes are in table 1.

CONCLUSION

In present study we analysed 610 potential genes from miRNA of C. elegance. Out of 610

potential genes some are responsible for cause ofdifferent diseases like cancers, perkinson'sdisease, alzhiemer'sdisease etc. Finally we conclude that if we control its malfunctioning at its initial stage, we can control many diseases and present study may also be beneficial for new researchers in many ways.

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