demolition in the levels of MDA and HP in case co exposure of **G** with Par treated flies homogenate. The level of SOD and CAT were brought to near basal level in the homogenate of flies co exposed with **G** and Par. In negative geotaxis assay it was found that **G** was able to rescue the flies significantly from deteriorating locomotors dysfunctions. The extract **G** showed significant antibacterial property against tested strains.

References: Ravindra, P.S., S. Shashwat, and K. Suman 2004, JIACM 5: 218-225; Sittipunt, C., 2005, Respir. Care 50: 383-385; Suntres, Z.E, 2002, Toxicol. 180: 65-77; Smith, L., M.S. Rose, and I. Wyatt 1978, Ciba Found. Symp. 65: 321-341; Tapiwanashe, M, W. Melanie, R. Kumars, P.M. Michael, A.J. Robin, and L.P. Smith 2006, Mech. Age. Devpt. 127: 356-370.

Sequence variations in dosage compensation genes and histone deacetylases in *In(1)B^{M2}(reinverted)* of *Drosophila melanogaster.*

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The *Drosophila* strain *In(1)B^{M2}(reinverted)* arose in 1978 as a spontaneous re-inversion in *In(1)B^{M2}* (inversion break points 16A-20F) (Mazumdar *et al*., 1978). This re-inverted strain manifests a sex and chromosome specific alteration of the male X chromosome, which can either be induced through continuous rearing at 18 ± 1^{o}C (Mukherjee and Ghosh, 1986) or through a brief exposure to cold shock at 12 ± 1^{o}C for four hours (Kar *et al.,* 2000). The alteration in the structure of the male X chromosome is associated with a transient, male specific increase in the acetylation of histone H4 at lysine 16 (H4K16) (Kulkarni-Shukla *et al.,* 2008). This male specific acetylation is brought about by the gene *males absent on the first* (*mof*), a histone acetyltransferase that is a component of the multiprotein complex that brings about dosage compensation in *Drosophila melangoster* (Bone *et al.*, 1994). Due to the male sex specific phenotype and the observed hyperacetylation, we investigated whether the structural alteration of the male sex chromosome occurred due to mutations in the genes of the dosage compensation pathway (*i.e*., *mof*, *male- specific lethal 1*, *msl-1*; *male-specific lethal 2, msl-2; male-specific lethal 3*, *msl-3*; *maleless, mle*; *RNA on the X 1, roX1;* and *RNA on the X 2, roX2*) chromatin remodelling genes associated with dosage compensation (*Imitation SWI*, *Iswi*; *Trithorax-like*, *Trl*; *supercoiling factor*, *scf*; and *JIL-1*) or due to mutations perturbing the activity of histone deacetylases (HDAC) (*Rpd3, HDAC6, Histone deacetylase 3* [*Hdac3*], *HDAC4,* and *Sir2*).

The sequences of these sixteen genes were identified using FlyBase (Tweedie *et al.,* 2009), and primers were designed using Primer3 primer design programme (Rozen and Skaletsky, 2000). Amplifications and sequencing were carried out in triplicates. The gene sequence variations were determined by aligning them to the wild type sequences obtained from FlyBase using ClustalW2 with default settings (Larkin *et al.,* 2007). Coding sequences were translated using EMBOSS Transeq (http://www.ebi.ac.uk/Tools/ emboss/transeq / index), and the predicted protein sequences for each gene were aligned to that of the wild type using ClustalW. Nucleotide variations were categorized as synonymous, non-synonymous, conserved or semi conserved depending on the resultant amino acid change.

Of the sixteen genes only one, HDAC, *Rpd3* showed 100% homology to the wild type sequence reported in the FlyBase. Table 1 shows the variations reported for the other fifteen genes.

Table 1. Nucleotide variations in the sequenced genes of *In(1)B^{M2}(reinversion).*

Gene	Gene Size (bp)	Total changes observed	Unique variations	Type of variation	Gene	Gene Size (bp)	Total changes observed	Unique variations	Type of variation
mof	3017	9	7	3 synonymous 1 non-synonymous 3 non coding	*Iswi*	4011	31	31	6 non coding 25 synonymous
msl-1	5077	5	4	1 conserved 1 non-synonymous 2 non coding	*Trl*	13121	26	9	3 synonymous 6 non coding
msl-2	3899	51	4	2 synonymous 2 non coding	*scf*	1772	19	8	5 non coding 3 synonymous
msl-3	2314	36	22	10 non coding 6 conserved 2 semi conserved 3 synonymous 1 non-synonymous	*Rpd3*	2751	-	-	-
mle	6035	2	-	-	*HDAC6*	7401	4	4	3 non coding 1 non-synonymous
roX1	3792	2	2	2 non coding	*Hdac3*	1789	2	2	1 synonymous 1 non coding
roX2	1377	2	1	1 non coding	*HDAC4*	22433	45	40	34 non coding 6 synonymous
JIL-1	14391	11	4	4 non coding	*Sir2*	4001	8	8	5 non coding 2 synonymous 1 non-synonymous

Table 2. Non-synonymous changes in genes of *In(1)B^{M2}(reinversion).*

Gene	Position	Nucleotide change(s)	Amino acid Position	Amino acid Change
mof	2580	C→G	791	His→Pro
msl-1	2446-2448	3 bp deletion	672..673	Del of 2aa
msl-3	418	T→G	67	Val →Gly
HDAC6	5535	A→G	973	Glu→ Gly
Sir2	3023	G→T	802	Asn→Asp

There were 253 nucleotide changes which were not reported in either the FlyMine (Lyne *et al.*, 2007) or The FlySNP Project databases (http://flysnp.imp.ac.at/flysnpdb.php). After performing a BLAST search (Altschul *et al.*, 1990) for the variations, 107 variations found matching hits in the *Drosophila melanogaster* Nucleotide database of NCBI. Thus, there were 146 variations that were unique to *In(1)B^{M2}(reinverted)*. Of these, 21 were structural variations (insertions/deletions), 48 were synonymous variations, seven were conserved, two were semi-conserved, and 64 variations were in the non-coding regions. Only four single nucleotide variations were non-synonymous and were present within the coding regions of *mof*, *msl-3*, *HDAC6*, and *Sir2* genes (Table 2). Except for MSL-3, none of the amino acid substitutions were within the functional domains of the proteins. For MSL-3, the valine to glycine change observed at position 67 was within the chromo related domain (CRD) of this protein. Of the 21 structural changes, only one was present in the exonic region of *msl-1*. This change involved a 3bp deletion (TCA), resulting in the deletion of valine and asparagine at

672..673aa and addition of aspartic acid (Table 2). The mechanism by which the sequence variations of *In(1)B^{M2}(reinverted)* may affect the phenotype is being currently studied.

References: Altschul, S.F., W. Gish, W. Miller, E.W. Myers, and D.J. Lipman 1990, J. Mol. Biol. 215**:** 403-10; Bone, J.R., J. Lavender, R. Richman, M.J. Palmer, B.M. Turner, and M.I. Kuroda 1994, Genes Dev. 8**:** 96-104; Kar, A., S. Kulkarni-Shukla, I. Dey-Guha, and J.K. Pal 2000, Genet. Res. 76**:** 11-7; Kulkarni-Shukla, S., A.P. Barge, R.S. Vartak, and A. Kar 2008, J. Genet. 87**:** 235-40; Larkin, M.A., G. Blackshields, N.P. Brown, R. Chenna, P.A. McGettigan, H. McWilliam, F. Valentin, I.M. Wallace, A. Wilm, R. Lopez, J.D. Tompson, T.J. Gibson, and D.G. Higgins 2007, Bioinformatics 23**:** 2947-2948; Lyne, R., R. Smith, K. Rutherford, M. Wakeling, A. Varley, F. Guillier, H. Janssens, W. Ji, P. McLaren, P. North, D. Rana, T. Riley, J. Sullivan, X. Watkins, M. Woodbridge, K. Lilley, S. Russell, M. Ashburner, K. Mizuguchi, and G. Micklem 2007, Genome Biol. 8**:** R129; Mazumdar, D., M. Ghosh, M. Das, and A.S. Mukherjee 1978, Cell Chromosome News Letter 1**:** 8-12; Mukherjee, A.S., and M. Ghosh 1986, Genetical Research 48**:** 65-75; Rozen, S., and H. Skaletsky 2000, Methods Mol. Biol. 132**:** 365-86; Tweedie, S., M. Ashburner, K. Falls, P. Leyland, P. McQuilton, S. Marygold, G. Millburn, D. Osumi-Sutherland, A. Schroeder, R. Seal, and H. Zhang 2009, Nucleic Acids Res. 37**:** D555-9.

Circadian rhythm of locomotor behavior of *D. agumbensis* and *D. rajasekari* collected from Sakleshpur.

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Abstract

Circadian clock regulates physiological and behavioral processes in a wide variety of organisms ranging from unicellular organism to human beings. The present study is aimed to investigate circadian rhythm of locomotor behavior of *D. agumbensis* and *D. rajasekari* collected from Sakleshpur, Karnataka, India at 910m altitude. Locomotor activity behavior was assayed by using *Drosophila* activity monitor (Trikinetics IV) under laboratory conditions. Both the species exhibited unimodal activity. The range of activity was 126-851 in *D. agumbensis* and 114-964 in *D. rajasekari*. The period of activity of both the species was closer to 24h. Statistical analysis revealed that there is a significant difference in the locomotor behavior of the two species. Keywords: locomotor activity; *D. agumbensis*; *D. rajasekari.*

Introduction

Circadian rhythms characterize the physiological processes of organisms ranging from the unicellular dinoflagellate *Gonyaulax polyedra* (Hastings and Sweeney, 1958) to human beings (Wever, 1979; Aschoff, 1981; Brady, 1981). It is now reported that besides eukaryotes, even cynobacteria among eubacteria possess circadian clocks (Ouyang *et al.,* 1998). The ubiquitous occurrence of circadian clocks at various levels of organization and complexity suggests that they may be of adaptive value (Aschoff, 1994; Aschoff *et al.,* 1982; Hastings *et al.,* 1991; Pittendrigh, 1993; Sharma, 2003a). It is believed that circadian clocks benefit organisms by efficiently timing various behavioral and metabolic processes to appropriate times of the day in accordance with cyclic external and internal environments (Aschoff, 1964; Aschoff *et al.,* 1982; Hastings *et al.,* 1995;