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MALATTIE APPARATO RESPIRATORIO
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MICROORGANISMI NELLE BIOTECNOLOGIE
NANOTECNOLOGIE NEUROSCIENZE
ONCOLOGIA SVILUPPO E DIFFERENZIAMENTO

LIBRO

degli

ABSTRACT



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Area della Ricerca di Palermo Via Ugo La Malfa 153

assessed by western blot. Finally, we have performed ChIP experiments whose results strongly support the hypothesis that this new factor can bind to the sns5 insulator.

- [1] Srivastava S et al. 2015 Available online
- [2] Matharu NK et al. 2010 JMB 400 (3): 434-447
- [3] Fuda NJ et al. 2015. PLoS Genet 11(3): 100-108
- [4] Melfi R et Al. 2001 JMB (1); 304:753-63

SD8

The nucleic acid-binding protein *PcCNBP* is transcriptionally regulated during the immune response in red swamp crayfish *Procambarus clarkii*

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Cellular nucleic acid binding proteins (CNBPs) represent a highly conserved protein family among vertebrates; they harbour seven tandem zinc finger repeats CCHC type and have been described as transcriptional and translational regulator. To date, there is little characterisation of CNBP in invertebrates since its structure and function have been analyzed solely in *Drosophila melanogaster*. However no CNBP has been investigated in other arthropod systems. In an effort to isolate immune-related genes in *Procambarus clarkii*, a partial mRNA coding a zinc finger containing protein was found to be up-regulated during the response to white spot syndrome virus (WSSV) infection. The red swamp crayfish *P. clarkii*, represents an attractive animal model because of its tolerance to extreme environmental conditions and resistance to diseases. Thus it has become an important crustacean model organism for virological studies. In this study, a CNBP homolog from the red swamp crayfish *Procambarus clarkii* was characterised. The full-length cDNA of *PcCNBP* was of 1257 bp with a 5'-untranslated region (UTR) of 63 bp and a 3'-UTR of 331 bp with a poly (A) tail, and an open reading frame (ORF) of 864 bp encoding a polypeptide of 287 amino acids with the predicted molecular weight of about 33 kDa. The predicted protein possesses 7 tandem repeats of 14 amino acids containing the CCHC zinc finger consensus sequence, two RGG-rich single-stranded RNA-binding domain and a Nuclear localization signal, strongly suggesting that *PcCNBP* was a homolog of vertebrate CNBP. Analyses of transcriptional expression profile showed that *PcCNBP* was constitutively expressed among different tissues from the adult crayfish, under normal physiological conditions. Moreover, qRT-PCR assays indicate that the transcriptional expression of *PcCNBP* responds to bacterial and viral stimulations.

SD9

The analysis of the HSA20/21 Syntenic Association in Cercopithecini allows a Discussion on Neocentromeres Scattering in Primate Genomes

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In spite of many expectations there is not any room for the concept that mammalian genomes have a default chromosome rearrangement rate, and that sister taxa have an intelligible and predictable chromosome organization. A part from the initial distress, these evidences resulted very stimulating for researchers. *In situ* hybridization studies conveyed to a series of proposed “Ancestral Karyotypes”, and to the consequent discussion about, for example, the “conservativeness” of Carnivora, the rapid chromosomal evolution in Perissodactyla or in Rodentia and Primates (Supraprimates/Euarchontoglires). Chromosome painting and BACs FISH identified a series of apomorphic syntenic association in primates. Cercopithecini Tribe (Anthropoidea, Cercopithecoidea) is characterized by an apomorphic HSA20/21 syntenic association. This association demonstrates a high rate of polymorphism. We analyzed several species in the wide distributed African tribe of tree-dwellers, often identifying the 20/21 association as an heteromorphic pair in the