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Cloning and Characterization of the *DMRT* Gene Homologue in the Sawfly, *Athalia rosae ruficornis* (Hymenoptera)*

Jae Min LEE[1], Daisuke S. YAMAMOTO[2] and Masatsugu HATAKEYAMA[1]

[1] *Developmental Mechanisms Laboratory, Developmental Biology Department, National Institute of Agrobiological Sciences, Owashi, Tsukuba, Ibaraki 305–8634, Japan*

[2] *Division of Bioscience, Graduate School of Science and Technology, Kobe University, Nada, Kobe, Hyogo 657–8501, Japan*

E-mail: sawfly@nias.affrc.go.jp (MH)

The system of sex-determination has been well studied in *Drosophila melanogaster.* The *doublesex* (*dsx*) gene functions at the downstream-most of the sex-determining cascade, and the female- and male-specific proteins (DSX^F, DSX^M) regulate expression of genes engaged in sexual differentiation such as yolk protein genes (Burtis and Barker, 1989; Schutt and Nothiger, 2000). The *dsx* homologues have been identified in many species other than *Drosophila: Bmdsx* from *Bombyx mori*, *mab-3* from *Caenorhabditis elegans*, *DMRTs* from human, and *Dmrts* from mouse and chicken (Shen and Hodgkin, 1988; Ohbayashi *et al.*, 2001; Ottolenghi *et al.*, 2002; Smith *et al.*, 2002). These *dsx* homologues were considered to regulate sexual differentiation and have been evolutionary conserved as the sex-determining genes (Raymond *et al.*, 1998). A common characteristic of these gene homlogues is the presence of a DNA binding domain termed the DM domain (Zhu *et al.*, 2000).

In the present study, we cloned and sequenced two *dsx* gene homologues from the sawfly, *Athalia rosae* (*ArDMRT1* and *ArDMRT2*). Reverse transcription PCR demonstrated that the *ArDMRT1* was expressed in embryos, larvae and pupae of both sexes, while the *ArDMRT2* was expressed only in embryos of both sexes. A molecular phylogenetic analysis demonstrated that *ArDMRT1* and *ArDMRT2* were more similar to homologous genes of vertebrates, rather to *dsx* of *D. melanogaster.* Recent progress of the genome research in the honey bee *Apis mellifera* revealed that there are some *dsx* homologues similar to that of *D. melanogaster.* Investigation of these genes in *A. rosae* is under way. We plan to analyze the function of these genes using the germline transformation system that we have recently established in *A. rosae* (Sumitani *et al.*, 2003).

References

Burtis, K.C. and B.S. Baker (1989) *Cell*, **56**, 997–1010.
Ohbayashi, F., M.G. Suzuki, K. Mita, K. Okano and T. Shimada (2001) *Comp. Biochem. Physiol.*, **B128**, 145–158.
Ottolenghi, C., M. Fellous, M. Barbieri and K. McElreavey (2002) *Genomics*, **79**, 333–343.
Raymond, C.S., C.E. Shamu, M.M. Shen, K.J. Seifert, B. Hirsch, J. Hodgkin and D. Zarkower (1998) *Nature*, **391**, 691–695.
Schutt, C. and R. Nothiger (2000) *Development*, **127**, 667–677.
Shen, M.M. and J. Hodgkin (1988) *Cell*, **54**, 1019–1031.
Smith, C.A., T.M. Hurley, P.J. McClive and A.H. Sinclair (2002) *Mech. Dev.*, **119S**, S73–S76.
Sumitani, M., D.S. Yamamoto, K. Oishi, J.M. Lee and M. Hatakeyama (2003) *Insect Biochem. Mol. Biol.*, **33**, 449–458.
Zhu, L., J. Wilken, N.B. Philips, U. Narendra, G. Chan, S.M. Stratton, S.B. Kent and M.A. Weiss (2000) *Genes Dev.*, **14**, 1750–1764.

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