

Z603 Characterization of Calreticulin (*crt-1*), a calcium binding protein, in *Caenorhabditis elegans*

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A *C. elegans* homologue of calreticulin has been cloned and sequenced previously (Smith, 1992). Calreticulin gene (*crt-1*) consists of three exons and encodes a protein of 395 amino acid residues. It contains a putative signal sequence at amino-terminus and a ER retention sequence (HDEL) at carboxy-terminus. The amino acid sequences show overall 61% identity to mouse calreticulin, where much higher (82%) identity in the proline-rich region.

In order to study expression pattern of *crt-1*, Northern analysis and *in situ* hybridization experiments were carried out. Developmental stage specific Northern analysis data revealed that the level of gene expression was very high during embryonic stages and was reduced but maintained during post embryonic stages. *In situ* data showed confirmed that during early embryonic stages the transcripts were the most abundant and during later stages the transcripts were restricted to intestinal precursor cells. At larval and adult stages, gene expression was only detected in intestinal cells.

C. elegans calreticulin over-expressed in *E. coli* was used to test calcium binding activity. Indeed calcium overlay with Ca^{45} and stains-all experiments showed that *C. elegans* calreticulin binds to calcium. Immuno-staining with polyclonal antibody against *C. elegans* calreticulin revealed that calreticulin may localize at endoplasmic reticulum of early blastomeres.

We speculate that *C. elegans* calreticulin may play an important role during embryogenesis and intestine cell development.

Z604 PCR-Based Polymorphisms for the Y Chromosomal Loci *DYS19* and *DXYS5Y* (47Z) in the Korean Population

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We examined Y chromosomal DNA polymorphisms at the *DYS19* and *DXYS5Y* loci in a total of 480 unrelated male samples from the Korean population. All five common alleles were identified at the tetranucleotide microsatellite locus *DYS19* in this study. The C allele was the most frequent (212/480), followed by the D (136/480), B (75/480), E (36/480) and A (21/480) allele. The frequency of Y2 allele at the *DXYS5Y* locus was found to be 4.6% (22/480). Combining the allelic variation at these two loci resulted in a total of 9 combination haplotypes. The mean combination haplotype diversity was 0.72. Based on results of these two loci, Korean and Japanese populations may share some common genetic structure that is rare or not present in the other ethnic groups. It is suggested that the genetic similarity between Korean and Japanese populations provides an evidence for the large infusion of Y chromosomes with the Yayoi migration starting 2,300 years ago from Korea to Japan.