



CDB SEMINAR

Date: Friday, March 4
Time: 15:00 P.M. - 17:00 P.M.
Place: 7F Conference Room of Building A

Speaker1: **Bruce P. May**
< Cold Spring Harbor Laboratory >

Title: **“Regulation of Centromeric Transcripts
and Chromatin in *Arabidopsis thaliana*”**

Summary:

Centromeres interact with the spindle apparatus to enable chromosome disjunction and typically contain thousands of tandemly arranged satellite repeats interspersed with retrotransposons (Choo 2001). While their role has been obscure, centromeric repeats are epigenetically modified and centromere specification has a strong epigenetic component (Karpen and Allshire 1997). In the yeast *Schizosaccharomyces pombe* pericentromeric repeats are transcribed and contribute to centromere function via RNA interference and consequent recruitment of histone H3 lysine-9 methylation (Volpe et al. 2002). We have found transcripts from a subset of centromeric repeats in the higher plant *Arabidopsis thaliana* (which, unlike yeast, has methylated DNA). The transcripts are strand-specific, appear to remain associated with heterochromatin, and are silenced by RNAi and histone modification. Another subset of 180 bp repeats are silenced on both strands by the canonical CG DNA methyltransferase MET1, the histone deacetylase HDA6/SIL1 and the chromatin remodeling ATPase DDM1. Centromeric transcripts of the first class are inherited epigenetically, but silencing of the second class is re-established in backcrosses with MET1 and SIL1, resembling retrotransposon LTRs which are partially responsible for their transcription. Small interfering RNAs (siRNA) from centromeric repeats are retained in *met1* and *sil1*, but not in *ddm1*, indicating a role in silencing. Histone H3 lysine-9 methylation is associated with both classes of repeats and depends on the RNAi gene ARGONAUTE (AGO1). We propose roles for transcribed repeats in centromere function and evolution.