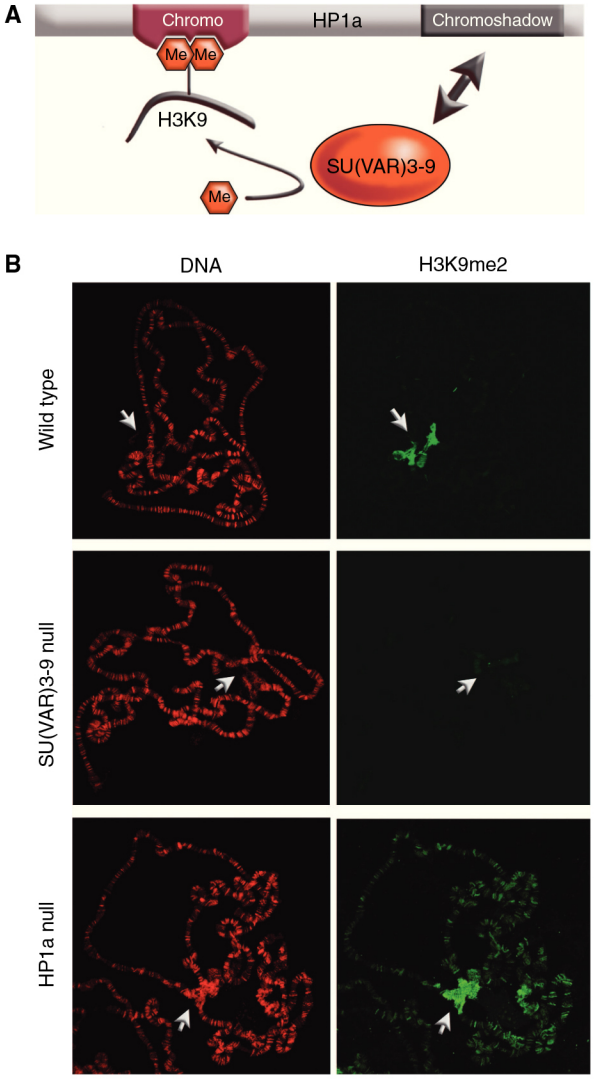

Figure 4. Interaction of SU(VAR)3-9 and HP1a in setting the distribution pattern of H3K9 methylation. (*A*) HP1a interacts with H3K9me2/3 through its chromodomain, and with SU(VAR)3-9 through its chromoshadow domain. By recognizing both the histone modification and the enzyme responsible for that modification, HP1a provides a mechanism for heterochromatin spreading and epigenetic inheritance. (*B*) SU(VAR)3-9 is responsible for much of the dimethylation of H3K9 (H3K9me2); loss of the enzyme results in loss of this modification in the pericentric heterochromatin, as shown by loss of antibody staining of the polytene chromosomes (compare *middle* panel with *top* panel). Loss of HP1a results in a loss of targeting of SU(VAR)3-9; high levels of H3K9me are consequently now seen throughout the chromosome arms (*bottom* panel).