TABLE 82-2 SELECTED EXAMPLES OF DISEASES CAUSED BY MUTATIONS AND REARRANGEMENTS IN TRANSCRIPTION FACTOR CLASSES

Transcription Factor Class	Example	Associated Disorder
Nuclear receptors	Androgen receptor	Complete or partial androgen insensitivity (recessive missense mutations)
		Spinobulbar muscular atrophy (CAG repeat expansion)
Zinc finger proteins	WT1	WAGR syndrome: *W*ilms' tumor, *a*niridia, *g*enitourinary malformations, mental *r*etardation
Basic helix-loop-helix	MITF	Waardenburg's syndrome type 2A
Homeobox	IPF1	Maturity onset of diabetes mellitus type 4 (heterozygous mutation/haploinsufficiency)
		Pancreatic agenesis (homozygous mutation)
Leucine zipper	Retina leucine zipper (NRL)	Autosomal dominant retinitis pigmentosa
High mobility group (HMG) proteins	SRY	Sex reversal
Forkhead	HNF4α, HNF1α, HNF1β	Maturity onset of diabetes mellitus types 1, 3, 5
Paired box	PAX3	Waardenburg's syndrome types 1 and 3
T-box	TBX5	Holt-Oram syndrome (thumb anomalies, atrial or ventricular septum defects, phocomelia)
Cell cycle control proteins	P53	Li-Fraumeni syndrome, other cancers
Co-activators	CREB binding protein (CBP)	Rubinstein-Taybi syndrome
General transcription factors	TATA-binding protein (TBP)	Spinocerebellar ataxia 17 (CAG expansion)
Transcription elongation factor	VHL	von Hippel–Lindau syndrome (renal cell carcinoma, pheochromocytoma, pancreatic tumors, hemangioblastomas)
		Autosomal dominant inheritance, somatic inactivation of second allele (Knudson two-hit model)
Runt	CBFA2	Familial thrombocytopenia with propensity to acute myelogenous leukemia
Chimeric proteins due to translocations	PML-RAR	Acute promyelocytic leukemia t(15;17)(q22;q11.2-q12) translocation

Abbreviations: CREB, cAMP responsive element–binding protein; HNF, hepatocyte nuclear factor; PML, promyelocytic leukemia; RAR, retinoic acid receptor; SRY, sex-determining region Y; VHL, von Hippel–Lindau.

In patients with isolated renal resistance to parathyroid hormone (pseudohypoparathyroidism type IB), defective imprinting of the *GNAS1* gene results in decreased Gsα expression in the proximal renal tubules. Rett's syndrome is an X-linked dominant disorder resulting in developmental regression and stereotypic hand movements in affected girls. It is caused by mutations in the *MECP2* gene, which encodes a methyl-binding protein. The ensuing aberrant methylation results in abnormal gene expression in neurons, which are otherwise normally developed.

Remarkably, epigenetic differences also occur among monozygotic twins. Although twins are epigenetically indistinguishable during the early years of life, older monozygotic twins exhibit differences in the overall content and genomic distribution of DNA methylation and histone acetylation, which would be expected to alter gene expression in various tissues.

In cancer, the epigenome is characterized by simultaneous losses and gains of DNA methylation in different genomic regions, as well as repressive histone modifications. Hyper- and hypomethylation are associated with mutations in genes that control DNA methylation. Hypomethylation is thought to remove normal control mechanisms that prevent expression of repressed DNA regions. It is also associated with genomic instability. Hypermethylation, in contrast, results in the silencing of CpG islands in promoter regions of genes, including tumor-suppressor genes. Epigenetic alterations are considered to be more easily reversible compared to genetic changes, and modification of the epigenome with demethylating agents and histone deacetylases is being explored in clinical trials.

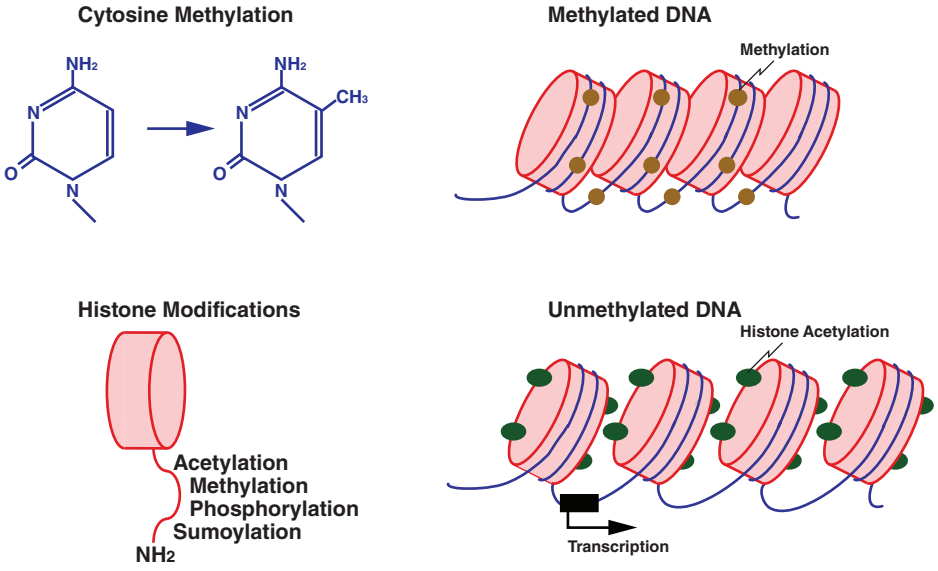

FIGURE 82-7 Epigenetic modifications of DNA and histones. Methylation of cytosine residues is associated with gene silencing. Methylation of certain genomic regions is inherited (imprinting), and it is involved in the silencing of one of the two X chromosomes in females (X-inactivation). Alterations in methylation can also be acquired, e.g., in cancer cells. Covalent posttranslational modifications of histones play an important role in altering DNA accessibility and chromatin structure and hence in regulating transcription. Histones can be reversibly modified in their amino-terminal tails, which protrude from the nucleosome core particle, by acetylation of lysine, phosphorylation of serine, methylation of lysine and arginine residues, and sumoylation. Acetylation of histones by histone acetylases (HATs), e.g., leads to unwinding of chromatin and accessibility to transcription factors. Conversely, deacetylation by histone deacetylases (HDACs) results in a compact chromatin structure and silencing of transcription.

MODELS OF GENETIC DISEASE

Several organisms have been studied extensively as genetic models, including *M. musculus* (mouse), *D. melanogaster* (fruit fly), *C. elegans* (nematode), *S. cerevisiae* (baker's yeast), and *E. coli* (colonic bacterium). The ability to use these evolutionarily distant organisms as genetic models that are relevant