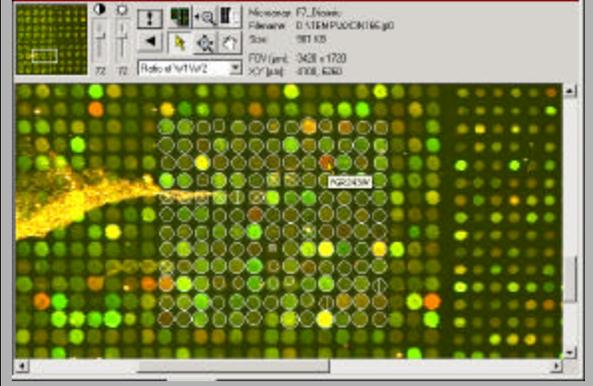


20 Epigenetics



<http://www.landesbioscience.com/journals/epigenetics/>

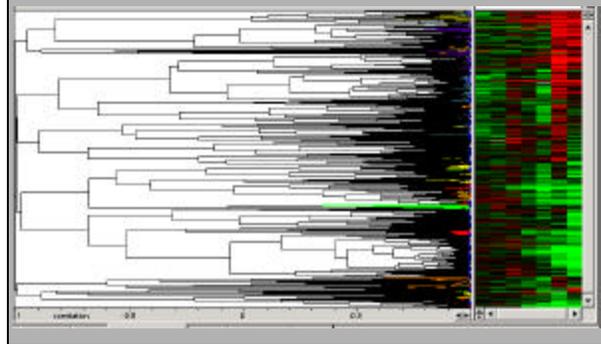
Microarray Hybridization for mRNA



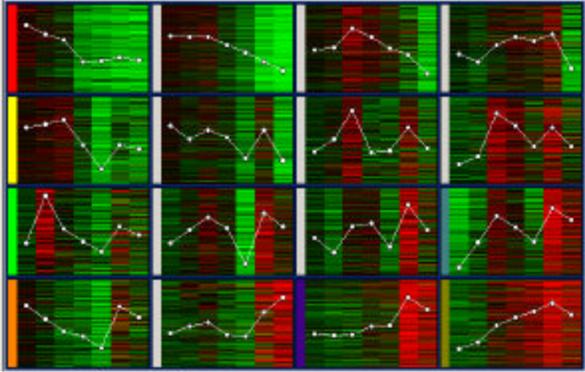
mRNA Identity ?

Substance	F1_Rn	F2_Crown	F3_Diamond	F4_Crystal	F5_Star	Protein	Function
VMR221C	1.198	1.195	1.095	1.073	1.1	VMR221C	alpha,alpha-trimethylcrotonate synthase C
VMR221C	1.202	1.197	1.044	1.045	1.2	VMR221C	alpha,alpha-trimethylcrotonate synthase C
VMR201C	0.909	0.832	0.910	1.049	1.1	VMR201C	alpha,alpha-trimethyl phosphate synthase C
VMR221C	1.136	1.183	1.085	1.082	1.1	VMR221C	malon synthase
VMR221C	0.450	0.891	0.840	0.791	1.2	VMR221C	malon synthase
VMR221C	0.226	0.162	0.816	0.442	1.2	VMR221C	1,4-alpha-glucan branching enzyme
VMR221C	0.946	0.882	1.095	0.974	1.1	VMR221C	1,2-beta-glucan synthase
VMR221C	0.927	1.132	1.412	1.552	1.3	VMR221C	1,2-beta-glucan synthase
VMR201C	1.017	0.834	1.079	0.834	1.3	VMR201C	1,2-beta-glucan synthase
VMR221C	0.900	1.147	1.505	1.143	1.4	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.138	1.192	1.222	1.336	1.2	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.037	0.891	1.095	1.183	1.1	VMR221C	nicotinic acidase
VMR221C	1.011	0.825	1.441	1.217	1.1	VMR221C	oxalate phosphate transferase
VMR221C	0.716	0.792	1.106	0.887	1.1	VMR221C	oxalate phosphate transferase
VMR221C	1.303	0.899	1.368	0.849	1.1	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	0.922	0.854	1.155	1.159	1.4	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.075	1.338	1.496	1.280	1.1	VMR221C	ATP phosphoribosyltransferase
VMR221C	0.972	0.707	1.150	0.974	1.1	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	0.266	0.799	1.066	1.246	1.2	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.126	0.811	0.893	0.845	1.1	VMR221C	oxalate phosphate transferase
VMR221C	1.144	1.497	1.095	1.135	1.2	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.120	1.122	0.962	0.897	1.1	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.140	1.848	1.300	1.287	1.1	VMR221C	beta-D-mannosyl phosphate transferase
VMR221C	0.915	0.392	0.866	0.740	1.2	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	0.814	0.849	1.185	0.883	1.1	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	0.768	1.395	1.367	1.285	1.1	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase
VMR221C	1.022	1.182	1.021	1.169	1.1	VMR221C	oxalate phosphate transferase
VMR221C	0.946	1.816	0.965	0.834	1.2	VMR221C	nicotinyl phosphate beta-D-mannosyltransferase

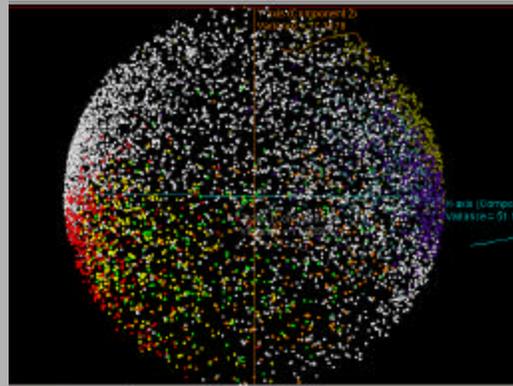
Cluster Analysis for functional groups



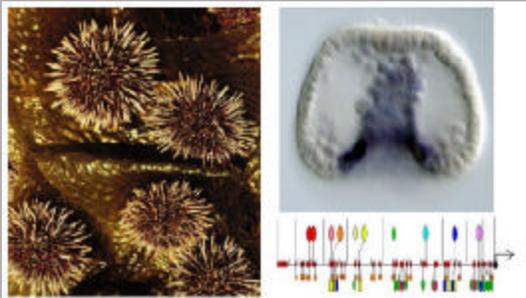
Group Expression Dynamics



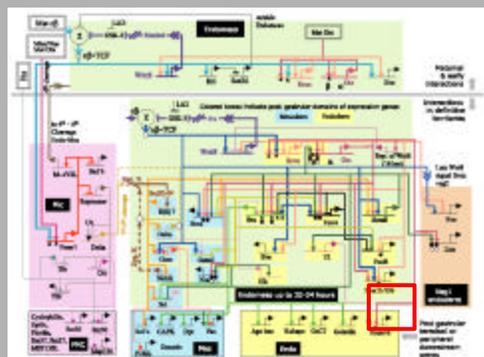
Genomic Network Structure



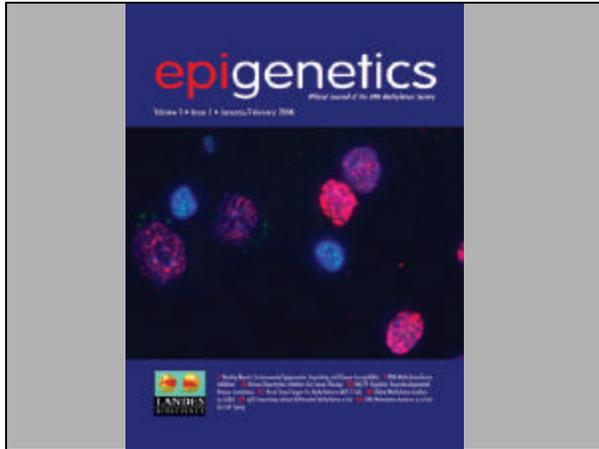
Development & Gene Expression Networks



Developmental Regulatory Network



Davidson et al., 2002, Science



Conrad H. Waddington (1905-1975),

- Conrad H. Waddington (1905-1975), developmental biologist known as the inventor of the term *epigenetics*
- Waddington suggested that *epigenesis* + *genetics* = *epigenetics*, referring to the debate on epigenesis versus "preformationism" in neoclassical embryology
- Trained as a geologist, he did not respect the traditional boundaries established between genetics, embryology, and evolutionary biology.

Epigenetics

- **What is epigenetics?**
Epigenetics, literally "on" genes, refers to all modifications to genes other than changes in the DNA sequence itself. Epigenetic modifications include addition of molecules, like methyl groups, to the DNA backbone. Adding these groups changes the appearance and structure of DNA, altering how a gene can interact with important interpreting (transcribing) molecules in the cell's nucleus.

Epigenetic Regulation: Covalent modifications of DNA to alter expressed phenotypes

Most plants, ~~animals and fungi~~ utilize:

- Acetylation
- Methylation

- Phosphorylation
- ADP-ribosylation

for control of gene expression

Covalent modifications of DNA:

1. Acetylation of histones

Acetylation/De-acetylation

- Hypoacetylation of *Lys* residues
 - Heterochromatin & Silenced euchromatic genes
- Hyperacetylation of *Lys* residues
 - Euchromatin and Inducible genes
 - HS regions

Covalent modifications of DNA:

2. Methylation of histones

H3 methylation at Lysine 9 (H3-mLys9)

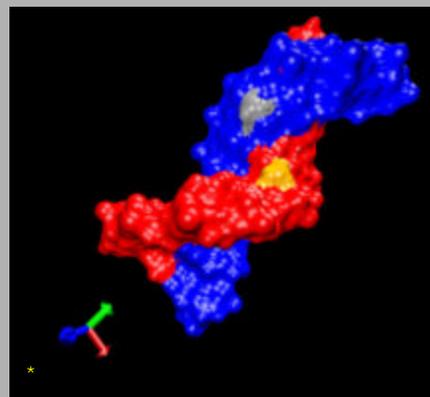
- Characteristic of the heterochromatic state
- Predominantly in pericentric DNA and repetitive DNA sites
- Absent in areas flanking silent genes
- Also associated with silencing of euchromatic genes

Covalent modifications of DNA:

3. Methylation of DNA

5'-Cytosine methylation (5mC)

- Most common form of DNA modification in eukaryotes
- Contributes to the stability of pericentromeric heterochromatin
- Maintains epigenetic expression states
- Silencing of imprinted genes

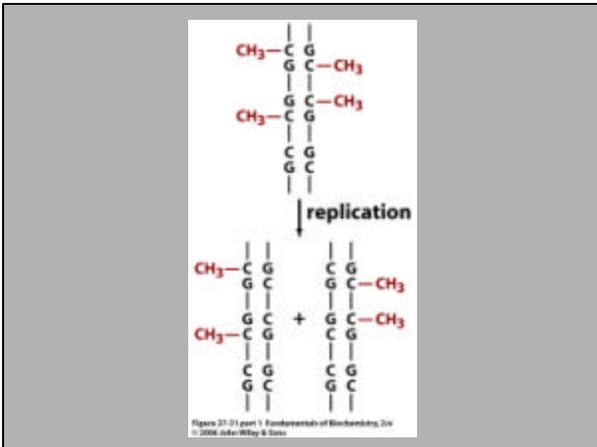
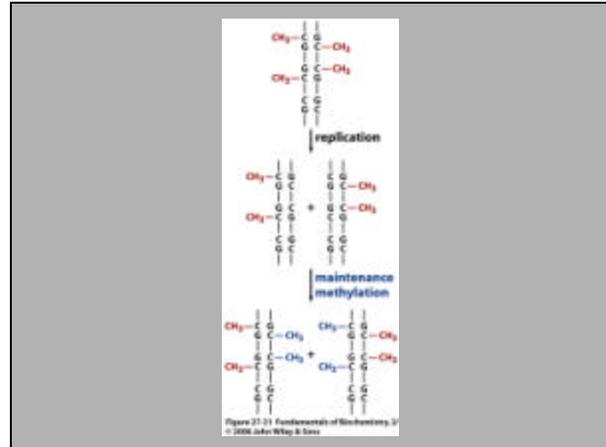
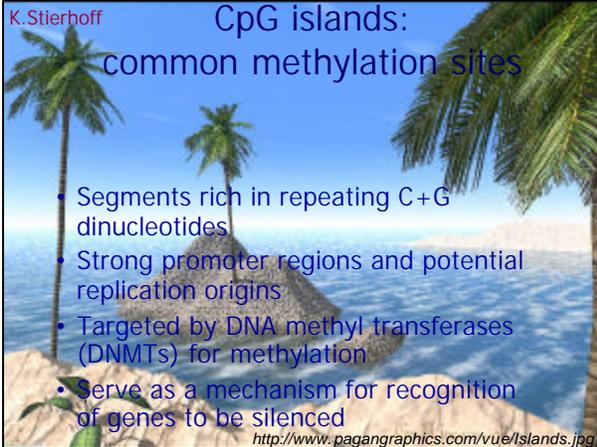


K. Stierhoff

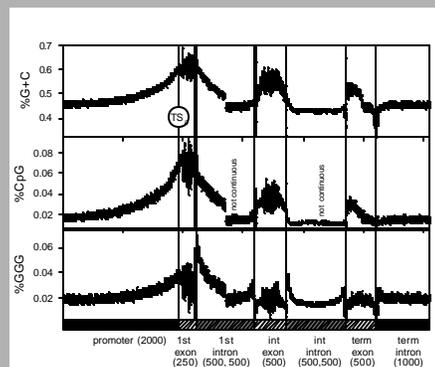
CpG islands: common methylation sites

- Segments rich in repeating C+G dinucleotides
- Strong promoter regions and potential replication origins
- Targeted by DNA methyl transferases (DNMTs) for methylation
- Serve as a mechanism for recognition of genes to be silenced

<http://www.pagangraphics.com/vue/islands.jpg>



Gene Fine-Structure: motifs



Majewski & Ott, 2002, Genome Research, 12:1827-1836

Epigenetics

- At the heart of this new field is a simple but contentious idea – that genes have a 'memory'. That the lives of your grandparents – the air they breathed, the food they ate, even the things they saw – can directly affect you, decades later, despite your never experiencing these things yourself. And that what you do in your lifetime could in turn affect your grandchildren.

<http://www.bbc.co.uk/sn/tvradio/programmes/horizon/ghostgenes.shtml>

Jean-Baptiste Lamarck (1744-1829)



- "Lamarck was the first man whose conclusions on the subject excited much attention. This justly celebrated naturalist first published his views in 1801. . . he first did the eminent service of arousing attention to the probability of all changes in the organic, as well as in the inorganic world, being the result of law, and not of miraculous interposition." (Darwin, 1861)

Vitalism



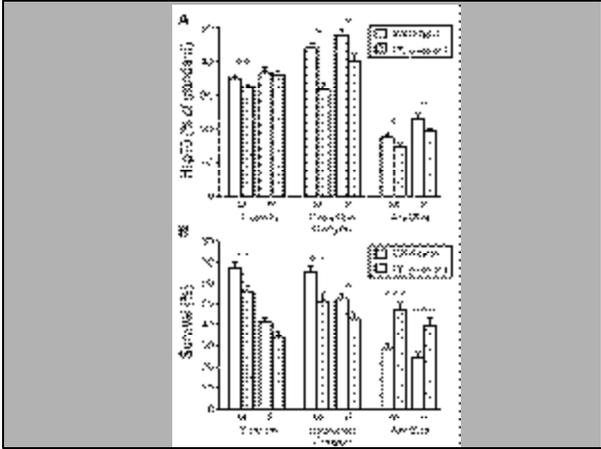
- Lamarck is credited with making the first large advance toward modern evolutionary theory by being the first to propose a mechanism by which the gradual change of species might take place.

Modification of Heat Shock Gene Expression in *Drosophila melanogaster* Populations via Transposable Elements

David A. Levine,¹ Peter Mikolaj,^{1*} Amanda B. Hahn,¹ Brian R. Beckmann,² and Martin A. Lynch^{1*}

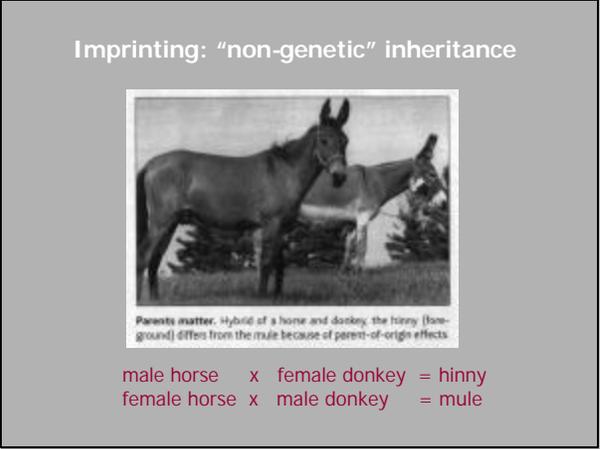
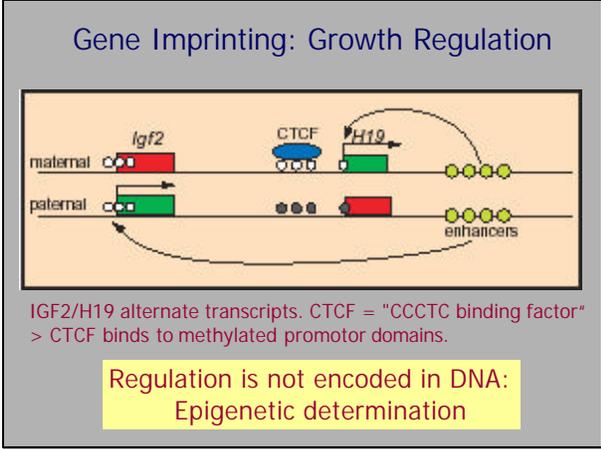
Mol. Biol. Evol. 20(1):135–144, 2003

ABSTRACT Transposable element insertion alters *Hsp70* expression and substrate thermal tolerance (T_{50}). *Hsp70* levels (measured by ELISA). Hierarchical analysis of variance (ANOVA) of replicate lines raised within group (i.e., US present vs. US absent) shows a significant reduction of *Hsp70* in lines with TE insertions for F1 female males and for Evolution Canyon and Arizona males and females ($P < 0.01$, $P < 0.01$, $P < 0.01$, $P < 0.01$, respectively). Similar T_{50} results and Evolution Canyon lines with TE insertions have reduced substrate thermal tolerance, and Arizona lines with the *T* element insertion have increased thermal tolerance (nested ANOVA, $P < 0.05$, $P < 0.01$, $P < 0.001$, $P < 0.001$).



Gene Imprinting

What is "imprinting?"
 "Imprinted genes" don't rely on traditional laws of Mendelian genetics, which describe the inheritance of traits as either dominant or recessive. In Mendelian genetics, both parental copies are equally likely to contribute to the outcome. The impact of an imprinted gene copy, however, depends only on which parent it was inherited from. For some imprinted genes, the cell only uses the copy from the mother to make proteins, and for others only that from the father.



Cloning alters imprinting

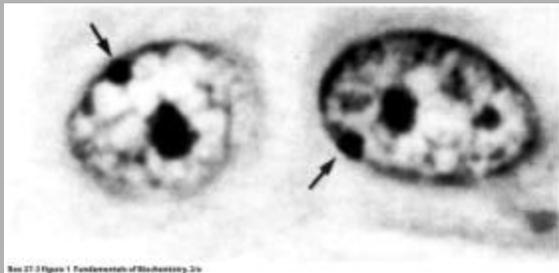


Gene Silencing



Box 27.3 Figure 3 Fundamentals of Biochemistry, 2/e

Barr Bodies



Box 27.3 Figure 1 Fundamentals of Biochemistry, 2/e

Wild find: Half grizzly, half polar bear



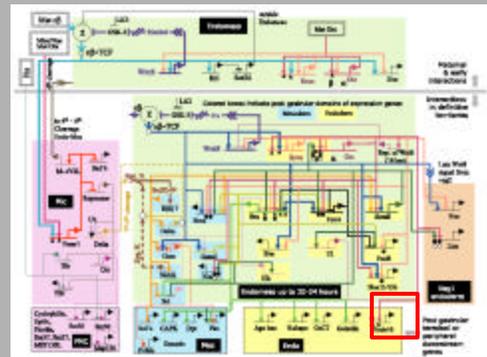
What defines a species? A Genome? A pattern of Gene Regulation?

11MAY06; <http://msnbc.msn.com/id/12738644/>

King and Wilson, 1975

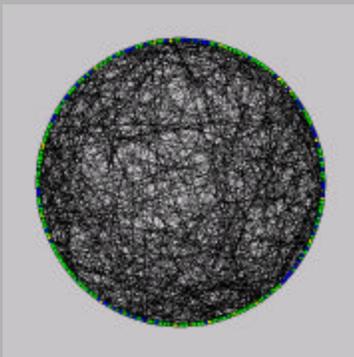
- “. . . all the biochemical methods agree that the genetic distance between humans and the chimpanzee is probably too small to account for their substantial organismal differences . . .”
- “We suggest that evolutionary changes in anatomy and way of life are more often based on changes in the mechanisms controlling the expression of genes than on the sequence changes in proteins.”

Science is Beautiful

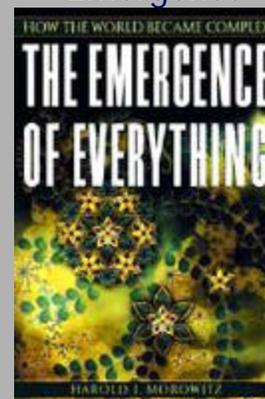


Davidson et al., 2002, Science

But LIFE isn't pretty . . .



Emergence



Life isn't pretty

