

Index

- A/B chorion genes
 chromosomal organization, 233–4
 5' flanking region, 233, 235
 gene conversion, 235, 239, 242
 GGXGGX repeats, 241–2
 nucleotide sequence relationships, 232f, 233–5
 subgroup classification, 233–4
 temporal regulation, 184, 185f
see also chorion gene families; chorion genes; chorion promoter
- Abraxas glossulariata*, 26
- actin gene, 408
- Agrotis segetum*, 343–4
- alanine tRNA, 275–8; *see also* alanine tRNA gene; silk gland
- alanine tRNA genes
 chimeric promoter function, 289, 290f
 chromosomal arrangement, 278
 differential template efficiency, 289–91
 downstream promoter sequences, 281
 number, 277–8
 organization, 278
 promoter, 279–80, 288f
 RNA transcription factor, 285–8, 291
 structure, 288f
 tissue-specific expression, 277–8
 transcription factor binding, 283–5
 transcriptional regulation, 289–91
 types, 277
see also polymerase III; polymerase III promoter
- aldehyde oxidase, 353, 364
- Anagasta kuehniella*, *see* *Ephestia kuehniella*
- anagenesis, 112, 113
- ANT-C, *see* *Antennapedia* complex
- antenna
 anatomy, 344–9
 development, 361–2
 model system, 365–7
 morphogenesis, 348–9
 neuron composition, 344
 olfactory dendrite protein (RP11), 356–7, 360–1
see also odorant binding proteins; odorant degrading enzymes; olfactory system
- Antennapedia* complex
Bm Antennapedia, 160, 177, 178f, 179, 180, 268, 270
Bm Sex combs reduced, 160, 179, 180f, 268, 270
Bombyx mori homologues, 45, 160, 268
 homeobox genes, 171, 268
 homeodomain, 176–7
Manduca sexta homologues, 160
 mutant transformations, 159–60, 169–71
 segment specification, 176
see also mutation, No crescent; segmentation gene hierarchy
- Antheraea pernyi*
 antibacterial proteins, 374, 376t, 378
 chorion 5' flanking region, 192
 chorion transgenic expression, 193–4

- general odorant binding protein, 355
- genome organization, 15
- pheromone binding protein, 355
- primordial germ cells, 161
- retroposons, 105
- Antheraea polyphemus*
 - antenna development, 348–9
 - choriogenesis, 122–3, 124f, 135–6, 219–20; *see also* Chapter 7
 - odor degrading enzymes, 351–3
 - odorant binding proteins, 354–6
 - olfactory proteins, 349, 350t
 - sex pheromone, 352
 - wing epidermal mRNA expression, 307, 308
 - see also* odorant binding proteins, RP11
- Antheraea yamamai*, 259
- antibacterial proteins
 - correlation with hemocyte responses, 383–4
 - covalent modification, 386–7, 390–2
 - defensins, 382, 387, 390–1
 - developmental regulation, 386–7
 - diptericins, 382
 - hemolin, 381–2, 386–7
 - induction, 382–5
 - intracellular sorting, 389–90
 - P4 protein, *see* hemolin,
 - P5 proteins, *see* attacins,
 - P9 proteins, *see* cecropins,
 - regulatory sequences, 388–9
 - sapecins, 382, 391
 - tissue specificity, 385–6
 - transcript abundance, 387–8
 - see also* attacins; cecropins; hemolin; lysozyme
- antibacterial response, *see* insect immunity
- Apis mellifera*, 105, 370, 374, 377t
- apoptosis, 8
- artificial diet, 64
- arylphorin, 10, 309–11
- Atrachya menetriesi*, 145
- attacins
 - posttranslational modification, 390–1, 392
 - regulatory sequences, 388–9
 - RNA synthesis elicitors, 385

- role in antibacterial response, 11, 380–1, 390–1, 393, 394f
- structure, 380
- transcript abundance, 387
- autoapomorphy, 112
- Autographa californica*, 96, 401
- baculovirus
 - characterized genes, 416–17
 - families, 400
 - host range, 400–1
 - late functions, 408–10
 - long-term cultivation, 19
 - structure, 400
 - tissue culture, 18, 19
 - tissues infected, 415–16
 - transducing vectors, 401, 402t, 403, 405–8
 - transforming vectors, 401, 402t, 408–10
 - transplacement vectors, 402, 417
 - see also* baculovirus expression vectors; baculovirus vectors, design
- baculovirus expression vectors
 - advantages, 403–4, 405
 - applications, 399, 401–3
 - chorion protein production, 192–3, 405t, 405, 412t
 - diuretic hormone production, 404, 405t, 411, 412t
 - eclosion hormone production, 404, 405t, 412t
 - generation of, 401–3
 - insecticidal protein production, 410–15
 - juvenile hormone esterase production, 404, 405t, 411, 412t
 - limitations, 399
 - recombinant protein yield, 403–4
- baculovirus vectors, design
 - cellular expression cassettes, 418–19
 - control of late functions, 408–10
 - early viral promoters, 417–18
 - ecosystem impact, 420
 - homologous recombination, 410
 - host incapacitation, 415–16, 419
 - immediate early viral promoters, 416–17
 - insect neuropeptides, 420–4
 - late viral promoters, 415–16
 - promoter duplications, 417–18
 - repetitive elements, 409–10

Index

531

- toxin molecules, 420
- Beadle, G., 12
- bithorax complex
- Bombyx mori* homologues, 45, 160–1, 171–5, 179, 180f, 268
 - cis*-regulatory regions, 178–9
 - Drosophila melanogaster*, 165, 176, 177, 178, 180f
 - functional similarity of E complex, 171–2, 173–5
 - gain of function mutations, 170
 - homeobox genes, 171, 173f, 174
 - homeodomains, 177–8
 - insect homologues, 165
 - loss of function mutations, 169–70
 - Manduca sexta* homologues, 160–1
 - structure, 168f, 180f
 - see also E complex
- Bkm, see *Ephestia kuehniella*
- Bm abdominal-A*, see bithorax complex, *Bombyx mori* homologues
- Bm Abdominal-B*, see bithorax complex, *Bombyx mori* homologues
- Bm Antennapedia*, see *Antennapedia* complex
- Bm engrailed*, 268
- Bm invected*, 268
- Bm Sex combs reduced*, see *Antennapedia* complex
- Bm Ultrabithorax*, see bithorax complex, *Bombyx mori* homologues
- Bm1* element
- chromosomal distribution, 81–3
 - copy number, 81
 - evolutionary origin, 83–5
 - model for reverse transcription, 85
 - promoter, 85, 279–80
 - structure, 84f
 - use in baculovirus vectors, 409–11
 - see also retroposon
- BMCI*, see retrotransposable element
- BmX*, see retroposon
- Boman, H., 11
- bombykol, see sex pheromone
- Bombyx mandarina*
- cytogenetics, 34
 - haploid chromosome number, 35
 - Hc proteins, 44
 - hybrids with *Bombyx mori*, 34, 36
 - outer chorion layers, 188, 219
- Bombyx mori*
- aldehyde oxidase, 353
 - anteroposterior axis determination, 153
 - antibacterial protein synthesis elicitors, 384
 - antibacterial proteins, 374, 376t
 - cecropins, 378
 - choriogenesis, 136
 - chorion genes, 16
 - cuticle genes, 307
 - eclosion hormone, 9
 - embryonic development, 166–8
 - genome, repetitive sequences, 246; see also Chapter 3
 - genome organization, 80
 - genome size, 23, 77, 81, 225
 - genomic abundance of mobile elements, 104
 - geographic races, 35, 36, 43, 74
 - hormone titers, 299
 - JH action in imaginal disc differentiation, 296
 - pheromone binding protein, 355
 - primordial germ cells, 162
 - segment-specific fate map, 151–2, 155
 - sex pheromone, 353
 - syncytial blastoderm, 155
 - see also Chapters 2 and 6–10
- Bounhiol, J. J., 4, 5
- Butenandt, A., 6–7
- BX-C*, see bithorax complex
- Byasa alcinous*, 161
- Caenorhabditis elegans*, 34, 242–3, 277, 281
- Calpodes ethlius*, 17, 299, 310f
- carotenoid binding protein, 64
- Caspari, E., 12
- cecropins
- biological activity, 11, 379–80
 - intracellular sorting, 389–90
 - posttranslational modification, 390, 391–2
 - regulatory sequences, 388
 - role in antibacterial response, 391–2, 393, 394f
 - structure, 378–9
 - transcript abundance, 387
- Ceratitis capitata*, 195
- Chippendale, G. M., 9

Chironomus tentans, 14, 297

chorion

aerople crowns, 123, 124f, 135–6, 183, 188

cholesteric liquid crystal, 121, 188

diapause, 43, 188

distortions and defects, 188–9

Drosophila melanogaster, 186, 187f

evolution, selective forces, 121–2

filler, 131, 188, 190

framework, 122, 186, 219

gene structure and organization, 190–2

helicoidal lamellae, 121–2

lamellogenesis, modes, 122–3, 132f, 186–7

lamellogenesis, phylogenetics, 123–5, 126–30t, 132f

micropyle, 183

model system, 16, 181

morphogenesis, 135–6, 186–8

morphology, 120–2, 186, 187f

mutants, 21, 39t, 42–3, 185–6, 187, 406

outermost layer, 43, 187–8

physiological functions, 121–2, 188–9

regional differentiation, 183

sieve layer, 121

trabecular layer, 121, 131, 187f

see also chorion gene families; chorion genes

chorion gene families

arms, 131, 190

central domain, 131, 133, 134f, 190

concerted evolution, 239–43

diapause, 219

evolutionary adaptation, 219–20

gene conversion initiation sites, 240, 242, 244

gene conversion patterns, 239

gene conversion rates, 243–4

recombination hotspot (GGXGGX repeat), 225, 240, 241–3, 246–7

sequence comparisons, interspecific, 133, 134f, 190–1

sequence comparisons, nonchorion, 133–5

superfamily, 131, 190

temporal class, 184–5

see also A/B chorion genes; chorion genes; ErA/ErB chorion genes; Hc chorion genes

chorion genes

antisense transcripts, 192

Bm1 and *Bm2* elements near, 81–2, 237

chromosome clusters, 42, 220–1

chromosome domains, 228

chromosome translocation, 185, 222f, 224–5

cis-regulatory elements, 195–200

cloning strategy, 221–4

correlation of genetic and physical maps, 224–5, 227

expression in baculoviruses, 192–3, 405, 406–7, 412t

expression in transgenic *Drosophila*, 193–200

expression, spatial, 183–4

expression, temporal, 184–6, 219–20

5' flanking region, 192

genetic analysis, 220–1, 222f

organization, 191–2

pseudogenes, 227–8, 233

sequence comparison, moth vs. fruit fly, 190–2

see also A/B chorion genes; chorion gene families; ErA/ErB chorion genes; Hc chorion genes; mutation

chorion promoter

bidirectionality, 193, 194, 196f, 198, 199f, 204

enhancer properties, 198

GATA-1 recognition sequence, 206

HMG-I binding motifs, 211

multiple *cis*-regulatory elements, 200

mutagenesis, 197–200

spatial regulation, 194

TCAGCT hexamer, 195–8, 208, 209–10

temporal specificity, 194, 198–200

vertebrate hormone receptor recognition element, 207

chorion transcription factors

Bombyx mori, 202f, 208–13

cloned, 202f

developmental regulation, 211

differential splicing, 208

DNase footprinting, 205–6, 207

Drosophila melanogaster, 202f, 206–8

GATA-1 homologue, 210

GATA-1 recognition site, 206

Index

533

- gel shift assays, 201–6
 HMG DNA-binding domain, 206, 211
 HMG homologues, 210–11, 212f
 nuclear hormone receptor superfamily, 206–8
 TCACGT hexamer binding, 201, 208, 209–10
 temporal regulation, 210
trithorax binding domain, 211, 212f
 yeast SNF2 homologue, 211
 zinc finger superfamily, 206, 207–8, 210, 211, 212f
- chromosome
 banding, 34
 centromeric DNA, 31
 crossing over, 26, 31–3
 diffuse kinetochore, 29–31, 34
 elimination chromatin, 32
 heterochromatic region, 78
 in situ hybridization, 30f, 34, 68, 75
 lepidopteran, 23
 loop domains, 31
 meiotic behavior, 26, 29, 31–3
 recombination nodule, 32–3
 Robertsonian fusion, 35
 sex chromatin body, 27
 supernumerary, 29, 34
 synaptonemal complex, 27, 31–2, 34
 telomeric sequence, 29, 30f, 31
 unstable fragments, 69
- cladogenesis, 111–12
 Clever, U., 14
 cocoonase, 10, 14
 complex locus, 42, 45; *see also* E complex
corpora allata, 4–5, 6, 294f, 295
corpora cardiaca, 294f
 Crampton, H. E., 4
 cuticle
 genes, 301–4, 307–8
 mechanical properties, 17, 299
 melanization mutant, 58
 proteins, 15, 17, 19, 299–301
 sclerotization, 305
see also epidermis
- Cydia pomonella*, 28
- Dahm, K. H., 5
 δ -endotoxin, 413–14
Diacrisia virginica, 161
 diapause, 8–9, 43, 188, 219
- Diatraea grandiosella*, 9
- Ditrysia
 early embryogenesis, 146–7
 lamellar chorion, 123–5, 132f,
 molecular systematics, 116–20
 phylogenetic relationships, 115, 116f,
 117f, 124–5
- diuretic hormone, *see* neuropeptide
- DNA
 injection, 398
 nonrepetitive sequences, 78
 polymorphism, 74
 reassociation kinetics, 77, 83, 105
 telomeric, 31
 transformation, 398
- Dong*, *see* R element
- Dopa decarboxylase, 305–6, 307f
- dosage compensation, 27
- Drosophila melanogaster*
 antibacterial proteins, 374, 377t
 antibacterial response, 370
 cecropins, 379
 choriogenesis, 16; *see also* Chapter 7
 common sequence motifs with silk
 gland promoters, 259, 261
 cuticle protein, 404
 Dopa decarboxylase, 305
 ecdysteroid receptors, 333–4
 embryogenesis, 108–9; *see also* Chapters 5 and 6
 FMR/Famide-related peptides, 421–2
 genome organization, 80
 JH action, 298
 mobile elements, 79, 80, 100f, 102, 104
 neuronal death, 334
 rDNA insertion elements, 86–90, 94
 retrotransposable elements, 97
 salivary gland chromosome puffing,
 297, 298
 sepia mutant, 59
 tRNA^{Arg} promoter, 281
- Drosophila virilis*, 259, 261f
- Duclaux, 9
- E complex
 deletions, 173–4
 homeodomains, 172–3, 173f
 mutations, 44–5, 159–60, 168–9
 pseudo-allelic gene complex, 170–1
 schematic structure, 174f, 180f

- see also* bithorax complex
- ecdysone
 dendritic loss, 326–7
 isolation, 6–7
 receptor, 306, 314, 317
 role in metamorphosis, 294f, 295
see also ecdysteroid; ecdysteroid receptor
- ecdysteroid
 action in antennal development, 364
 commitment peak, 8, 296, 301
 control of molting, 295
 effects on neuronal remodeling, 326–8, 361–4
 induction of salivary gland chromosome puffing, 297
 induction of transcription factors, 297, 317–19
 interaction with juvenoids, 15, 298–9
 mode of action, 296–7
 neural developmental events, 363f
 olfactory development, 361–4
 putative response elements, 317
 regulation of eclosion hormone, 337f, 338
 regulation of neuronal death, 330–1, 332f, 333, 361, 363, 364
 regulation of odorant binding proteins, 361–3, 364
 regulation of wing metamorphosis, 19
 responsive cell lines, 19
 titers, 299, 300f
 trigger of premetamorphic behavior, 334–5
 trigger of spinning behavior, 296
see also ecdysone; ecdysteroid receptor
- ecdysteroid receptor
Drosophila melanogaster, 314–15, 364
 JH effects, 320
Manduca sexta, 315–17, 364
 role in neuronal death, 333–4
- eclosion hormone
 actions, 9–10, 336
 baculovirus-mediated synthesis, 404, 405t
 hormonal triggers, 8, 9
 response pathway, 336–8
 role in metamorphosis, 294f, 295
 structure, 9, 336
 target tissue sensitivity, 336
- egg-specific protein, 40, 310, 313–14, 317
- eggshell, *see* chorion
- Eleodes*, 370, 374
- embryogenesis
 blastokinesis, 167
 cortical determinants, 152–3
 dorsal closure, 159, 168
 literature, early lepidopteran, 140–3t
 evolutionary patterns, 108
 fate mapping, 144, 145, 151–2, 155
 hormone regulation, 293
 of derived Lepidoptera, 145–7
 primordial germ cells, 161–2
 stages in *Bombyx mori*, 166–8
see also germ anlage; germ band; segmentation gene hierarchy
- Ephestia kuehniella*
 Bkm element, 72
 cytogenetics, 34
 egg cauterization, 151
 hemolin homologue, 381
 one-gene–one-enzyme hypothesis, 12
 sex heterochromatin, 27
 sex-limited translocation, 27, 34
 synaptonemal complex, 32
 WZ bivalent, 26
- Ephrussi, B., 12
- epidermal gene regulation
 Dopa decarboxylase, 305–6, 307f
 insecticyanin, 304–5
 larval cuticle genes, 301–4
 pupal and adult cuticle genes, 307–8
see also epidermis
- epidermis
 hormone effects on, 301; *see also* JH
 JH binding constants, 319
 membrane-bound vesicles, 51–8
 mutations affecting, 50–60
 proteins, 19
 structure and development, 299–301
see also epidermal gene regulation
- ErA/ErB chorion genes
 chromosome organization, 235–7
 gene conversion, 239, 242, 243, 244, 245–6
 GGXGGX repeats, 241–2
 nucleotide sequence similarities, 236f, 237–9, 243–4
 recombination, 238, 240
 selection pressure, 238

Index

535

- see also* chorion gene families, chorion genes
- even-skipped, 157, 264, 265F
- Exoporia, 112, 113f, 115
- fat body
- antibacterial protein synthesis, 378, 385–6
 - follicle-specific protein, 314
 - function, 308
 - hormonal regulation of specific proteins, 308–14
 - sepiapterin reductase mutant, 56t, 59
 - role in metamorphosis, 294f, 295
 - urate storage granules, 51
 - vitellogenesis mutant, 40
 - xanthine dehydrogenase, 52f, 58
- fate-mapping, *see* embryogenesis
- female-specific protein, *see* egg-specific protein
- fibroin genes
- Antheraea yamamai*, 259
 - cis*-acting elements, 266–7
 - core promoter, 257
 - direct isolation, 14
 - flanking sequence motif conservation, 259, 261–3
 - H chain, 61, 252
 - homeodomain binding sites, 264–6
 - L chain, 61, 252
 - protein-binding regions, 259, 260f, 261f, 261–2
 - spatial regulation, 253
 - temporal expression, 253–4
 - transcription factors, 259, 262–4
 - tRNA stimulation of *in vitro* transcription, 276
 - upstream promoter element, 257, 258–9, 260f
 - see also* silk genes
- Finlayson, L. H., 8
- flavonoid, 63
- flavoprotein, 10
- fluorescence *in situ* hybridization, *see* chromosome
- follicle, 40, 181–2
- follicle cell, *see* follicular epithelium
- follicular epithelium, 10, 40, 181–2, 406–7
- Fukuda, S., 5, 6, 9
- Galleria mellonella*
- allatectomy, 296
 - antibacterial proteins, 374, 376t
 - antibacterial response, 370, 385
 - arylphorin, 309–11
 - cuticle genes, 307, 308
 - E75 homologue, 318
 - effects of larval allatectomy, 8
 - epidermal RNA expression patterns, 307
 - hormonal effects on spinning behavior, 335
 - hormone titers, 299
 - insecticidal protein expression, 412t, 413
 - JH II bioassay, 5
 - JH-suppressible proteins, 312–13
 - wing imaginal disc culture, 19
 - WZ bivalent, 27
- gap genes, *see* segmentation gene hierarchy
- Garel, J.-P., 13
- Gaw, Z.-Y., 19
- germ anlage
- morphological changes, 146–7, 148f, 153, 154f
 - primitive lepidopteran, 147f
 - relation to germ band, 108, 144
 - representative types, 145f
- germ band
- long vs. short, 108–9, 144–5
 - lepidopteran features, 145–7
 - evolution, 109, 147
 - segment-specific fate map, 151–2
 - extension, 146–7, 148f
 - see also* germ anlage
- germ cells, *see* embryogenesis
- Gilbert, L. I., 7
- gin-trap reflex, 328, 329f, 363
- Glossata, 112, 113f, 115
- glycine tRNA genes, 275, 279
- Goldschmidt, R., 18
- Grace, T. D. C., 19
- Graphium sarpedon*, 34
- gynandromorph, 26
- gypsy moth, *see* *Lymantria dispar*
- Hasegawa, K., 9
- Hc chorion genes
- chromosomal organization, 226f, 227–8

- copy number, 43, 230
- 3' flanking region, 230, 231
- 5' flanking region, 228, 229, 231
- gene conversion barriers, 244–5
- gene conversion evidence, 230–2
- gene conversion frequency, 243
- gene conversion gradients, 240–1
- gene conversion patterns, 239
- GGXGGX repeats, 240–1
- introns, 244, 245
- nucleotide divergence, 244
- nucleotide sequence relationships, 226f, 228–30
- see also* chorion gene families, chorion genes
- Heliconis* spp., 27
- Heliiothis subflexa*, 74
- Heliiothis virescens*
 - arylphorin, 309, 311
 - insecticidal protein expression, 412t, 414–15
 - molecular linkage map, 74
 - recombinant juvenile hormone esterase, 404, 405t
 - recombinant scorpion toxin expression, 414–15
- hemocytes
 - encapsulation, 372–3, 374
 - lysozyme, 378
 - morphotypes, 372
 - nodule formation, 383, 392, 394f
 - regulation of response, 383–4
 - response time, 373
 - role in hemostasis, 371, 372
- hemolin
 - biological significance, 11
 - posttranslational processing, 386–7, 391f
 - role in antibacterial response, 381–2, 393, 394f
 - structure, 381
- hemolymph proteins, 10–12, 28, 64, 308–14; *see also* antibacterial proteins
- hemostasis, *see* insect immunity
- Hennig, W., 112
- heterochrony, 111
- heterogametic sex chromosome, 23, 33–4, 35
- Heteroneura, 113f, 115, 123
- Holm, P. B., 31
- homeobox, 156–7, 171, 174, 178, 179, 266, 267–9, 270f
- homeodomain, 173–4, 176–7, 180, 264–6, 267F
- homeotic genes, *see* bithorax complex; E complex; mutation, Extra leg; mutation, homeotic; mutation, No crescent
- Hyalophora cecropia*
 - chorion, 122f, 136
 - cuticle, 17, 19, 307
 - diuretic hormone, 404
 - early tissue culture, 18, 19
 - egg cortex, 152–3
 - egg maturation, 296
 - humoral immunity, 11, 12; *see also* Chapter 14
 - isolated abdomen bioassay, 6, 7
 - JH purification, 5
 - oocyte-specific sequence, 134–5
 - recombinant diuretic hormone, 404–6
 - source of JH II, 5
 - vitellogenesis, 10, 313
 - wing development, 3
- hydroxyecdysone, *see* ecdysone, ecdysteroid
- Hymenoptera, 109
- imaginal disc
 - antenna, 348
 - eye transplantation, 12
 - JH action, 296
 - ovarian transplantation, 40
 - potential developmental mutants, 66–8
 - tissue culture, 19
- imaginal nest cells, 363
- immunoglobulin superfamily, 381
- insect immunity
 - adaptive humoral immune responses, 370, 373
 - allograft rejection, 373
 - antibacterial response, working model, 392–3, 394f
 - development of bactericidal activity, 373–4
 - hemofibrin, 371–2, 392, 394f
 - hemostasis, 371–2
 - humoral immunity, 11

Index

537

- nonlepidopteran antibacterial response, 370
- pioneering studies, 370
- wound healing, 371–2, 378
- see also* attacins, cecropins, hemocytes, hemolin, lysozyme
- insecticyanin, 304–5
- insectotoxin-1, 413, 414–15
- insectotoxin,***, 414
- intersegmental muscles, 330, 331, 332f, 361, 363t
- iron-binding proteins, 10
- isoxanthopterin, 51, 59
- JH
 - I, 5, 6
 - II, 5
 - III, 6, 298
 - acid, 6
 - control of metamorphosis, 4, 19, 15, 294f, 295–6
 - corporata allata, 4–5, 6
 - ecdysteroid modulator, 298–9
 - effect on dendritic sprouting, 327, 328
 - effect on gin-trap cuticle, 328, 329f
 - effect on premetamorphic behavior, 335
 - esterase, 404, 405t, 411, 423t
 - larval diapause, 9
 - mode of action, 298–9
 - potential role in neuronal death, 331, 333, 334
 - purification, 5–6
 - receptor, 319–20
 - role in egg maturation, 313
 - titers in metamorphosis, 299, 300f
 - see also* JH, gene action
- JH, gene action
 - arylphorin, 311
 - Dopa decarboxylase, 305–6
 - ecdysteroid receptors, 320
 - insecticyanin, 304
 - larval cuticle genes, 302–4
 - methionine-rich storage protein, 310f, 311–12, 317
 - microvitellogenin, 314, 317
 - pupal and adult cuticle genes, 307–8
 - suppressible serum proteins, 312–13
 - vitellogenin, 314
 - see also* JH
- JH mimics, *see* JH
- juvenile hormone, *see* JH
- juvenoids, *see* JH
- Kafatos, F. C., 16
- Kalf, G. F., 18
- Karlson, P., 6–7, 14
- Kopec, S., 4
- larval-specific protein, 310f, 311, 313–14
- Lepidoptera
 - germ band, 108
 - molecular systematics, 110
 - phylogeny, 110, 113–16, 117f
 - primitive, 119–20
 - primitive ancestors, 114–15
 - species number, 110, 114
 - Leucophaea maderae*, 298
 - lipopolysaccharide, 378, 384–5
 - lipoprotein I, 10
 - Lockshin, R. A., 8
 - Locusta migratoria*, 108, 298
 - Luehdorfia japonica*, 161
 - Luzula*, 34
 - Lymantria dispar*
 - chorion sequences, 133, 134f
 - discovery of first neurohormones, 4
 - pheromone binding protein, 354
 - phylogeny, 116f
 - R1 elements, 93
 - lysozyme
 - intracellular trafficking, 390
 - posttranslational processing, 391f
 - regulatory sequences, 388
 - role in antibacterial response, 11, 375–8, 383–5
 - structure, 375
 - synthesis elicitors, 383, 385
 - transcript abundance, 387
 - Mag*, *see* retrotransposable element
 - male accessory gland, 298
 - Malpighian tubules, 27
 - Mamestra brassicae*, 296
 - mandibular glands, 27
 - Manduca sexta*
 - black larvae, 7–8
 - choriogenesis, 136
 - developmental synchrony, 8
 - eclosion hormone, 9, 404, 405t

- embryonic segmentation, 156
- gap gene homologues, 155
- homeotic genes, 160–1
- juvenoids, bioassay, 7, 8
- pair-rule genes, 156
- primordial germ cells, 161
- segment-polarity gene homologues, 157
- TN-1* antigens, 156
- see also* Chapters 11–14
- maternal inheritance, 21
- Mayer, A. G., 4
- meiosis, *see* chromosome, meiotic behavior
- melanization, 305, 371, 372, 392; *see also* mutation
- mellitin, 379
- metamorphosis
 - gene set paradigm, 15
 - see also* Chapters 11 and 12
- methionine-rich storage protein, 10, 310f, 311–12, 317
- microsatellite, 72, 73
- mite toxin, 413t, 414
- mobile elements
 - DNA transposition, 80
 - genome distribution, 104–5
 - retroelements, 98–9, 100f, 103
 - see also* retroposon, retrotransposable element
- Musca domestica*, 26, 105, 413t
- mutation
 - appendage development, 66–8, blister, 66, 68
 - body plan, 44–50
 - chemical induction, 36
 - chorion, 21, 39t, 42–4, 185–6, 187, 220, 222f, 224, 406
 - cocoon color, 62t, 63–4
 - cuticle hardening, 58–9
 - dorsal closure, 44
 - egg morphology, 37–42
 - embryonic lethal, 44
 - Extra leg, 44–5, 46t, 169–75, 178, 180f; *see also* E complex
 - feeding behavior, 64–6
 - first silkworm, 12
 - gonads, 67t
 - homeotic, 13, 21, 158–61; *see also* bithorax complex; E complex; mutation, Extra leg; mutation, No crescent
 - imaginal disc, 66–8
 - irradiation induced, 36, 45
 - kidney, 44, 162–3
 - maternal effect, 44, 162–3
 - melanization, 45, 48–9t, 58–9, 60, 68, 70–1t
 - methoprene resistance, 298
 - mottled, 52–5t, 58
 - No crescent, 45, 46t, 159, 168f, 175–7, 178f, 178–80
 - Nonpreference, *see* mutation, feeding behavior
 - oily skin, 51–8
 - pigment biosynthesis, 12, 23
 - pigmentation, larval, 45, 48–9t, 50–60
 - pigmentation, pupal and adult, 68, 70t
 - pteridine metabolism, 50, 56–7t, 58–60
 - purine metabolism, *see* mutation, oily skin
 - recombination frequency, 33
 - sepia, 59
 - sex-linked, 41; *see also* sex linkage, sex-limited translocation
 - silk gland, 61–3
 - temperature-sensitive, 68
 - wing pattern, 68, 70t
- Nasonia vitripennis*, 92–3
- Nc* locus, 176–7, 179, 180f; *see also* mutation, No crescent
- Neomicropteryx nipponensis*, 147, 161
- neoteny, 108, 111
- neuronal death, 363f
 - commitment point, 331, 333
 - ecdysteroid receptors, 333–4
 - ecdysteroid regulation, 330–3, 361
 - gene regulation, 334
 - key periods, 329
 - presynaptic events, 331, 333
 - RNA synthesis, 330
 - see also* programmed cell death
- neuropeptide, 421t, 423t
 - activational effects, 335–8
 - adipokinetic hormone, 336
 - baculovirus expression products, 404–5
 - bombyxin, 336, 422t
 - bursicon, 328
 - cardioacceleratory peptides, 328

Index

539

- diapause factor, 9
- diuretic hormone, 404, 405t, 411, 412t, 422–4
- FMRFamide, 328, 336, 421t, 422, 423t
- prothoracicotropic hormone, 7, 8, 294f, 295–6, 336, 423t
- see also* eclosion hormone
- NF- κ B, 12, 388–9
- nurse cell, 40, 181–2
- odorant binding proteins
 - binding constants, 354
 - classes, 354–6
 - developmental expression, 362–3
 - ecdysteroid regulation, 361–4
 - evolution, 350, 355–6
 - general odorant binding proteins, 346, 355–6
 - isolation, 349, 354
 - neuronal specificity, 354–5
 - pheromone binding proteins, 354, 355–6
 - role in olfaction kinetics, 350, 351, 352f
 - RP11, 346, 356–7, 360–1
 - sequence comparisons, 355–6
 - sex specific expression, 350t
 - tissue specific expression, 346, 347f, 350t
- odorant degrading enzymes
 - aldehyde oxidase, 353, 364
 - antennal enzyme activities, 353
 - expression, 346, 350t, 351–2
 - isolation, 349
 - role in insect behavior, 354
 - role in olfaction kinetics, 350–3
 - sensilla esterase, 351–3
- olfaction, *see* olfactory system
- olfactory dendrite protein (RP11), *see* odorant binding proteins
- olfactory proteins
 - evolution, 350
 - isolation, 349
 - pattern specific expression, 350t
 - see also* odorant binding proteins, odorant degrading enzymes
- olfactory system
 - anatomical features, 341–4
 - development, 344, 348, 361–4
 - genetic predetermination, 342–3
 - macroglomerular complex, 342, 343–4
 - model for odor detection, 349–51, 352f
 - model for spatial and temporal control of gene expression, 365–7
 - molecular components, 349
 - neuronal targets, 343–4
 - odor perception, 341–2
 - odorant dependent morphological change, 343
 - odorant half-life, 351, 353
 - olfactory specificity, 342–4
 - sensillum, 344–5, 346–7, 348, 349, 352f
 - tormogen cell, 347f, 349, 363
 - transduction pathways, 357–60
 - trichogen cell, 347f, 348–9
 - vomer nasal organ, 342
 - see also* antenna, odorant binding proteins, odorant degrading enzymes
- ommochromes, 51
- oocyte
 - anteroposterior polarity, 144, 182–3
 - in egg chamber, 181–2
 - specific sequence, 134–5
 - see also* mutation, egg morphology
- oogenesis
 - meroistic, 108, 144, 146
 - panoistic, 108, 145
- ovariole, *see* ovary
- ovary, 10, 32, 182–3
- P25 gene, *see* silk genes
- pair-rule genes, *see* segmentation gene hierarchy
- Panorpida, 109–10, 113–14
- Pao*, *see* retrotransposable element
- Parnassius glacialis*, 161
- pedogenesis, 111
- peptide hormone, *see* neuropeptide
- peptidoglycan, 11, 375, 378, 384–5
- Periplaneta americana*, 370, 373
- pesticide resistance genes, 74
- phenoloxidase, 371, 372, 392
- pheromone, *see* sex pheromone
- phorbol ester, 385, 388
- Phormia terranovae*, 370, 374, 377t, 382, 391
- Piepho, H., 5, 335
- Pieris rapae*, 161
- Plodia interpunctella*, 313

- polymerase III
 in vitro transcription extracts, 278–9, 282
 isolation, 282
 origin of SINES, 79
 regulated activity, 273
 transcription factors, 282–3
see also alanine tRNA genes; polymerase III promoter
- polymerase III promoter
Alu elements, 78
cis-acting elements, 278–81
 complexity, 279
 downstream sequences, 281
 internal control region, 85, 279
 structure, 279–80
 upstream sequences, 281
see also alanine tRNA genes
- polyploidy, *see* silk gland
- Popillia japonica*, 92
- posterior silk gland, *see* silk gland
- POU domain protein, 266, 268, 269
- Precis coenia*, 158
- programmed cell death, 8; *see also* neuronal death
- prothoracic gland, 6, 294f, 295
- prothoracicotropic hormone, *see* neuropeptide
- quantitative trait loci, 72–3
- quantitative traits, 36
- R* element
Dong, 88f, 93–4, 101
 horizontal spread, 102
 integration, 90–2
 location, 79, 87, 89, 105
 open reading frames, 88f, 89–90, 93
R1Bm and *R2Bm*, 87–90, 91, 100f
R2 encoded endonuclease, 91
 species distribution, 92–3
Type I and *Type II* elements, 87, 88f
- random amplified polymorphic DNA (RAPD), 72
- Rasmussen, S. W., 31
- rDNA insertion element, *see R* element; retrotransposable element, *Pao*
- recombinant inbred line, 74–5
- recombination hotspot, 42, 240
- restriction fragment length polymorphism (RFLP), 72, 73, 74
- retroelement, 98–9, 100f, 103
- retroposon
 abundance, 104
Bm2 element, 82–3, 85
BmX element, 85, 279–80
Locusta migratoria, 105
 polymerase III transcription, 79
 short interspersed nucleotide elements (SINES), 78–9, 104t
see also Bm1 element
- retrotransposable element
BMCI, 34, 88f, 97–8
copia-like, 87, 89, 94–5, 100f, 101, 102
 group II intron, 99–101
 gypsy group, 97, 100f, 101–2, 103
 horizontal spread, 102–3
I element, 79, 94, 100f
Line 1, 79, 97–8, 104t
Line 1-like, 79–80; *see also* retrotransposable element, non-LTR group
 long interspersed nucleotide elements (LINEs), 79
Mag, 95–6, 100f, 101
 non-LTR group, 99–102, 104t
Pao, 88f, 94–5, 100f, 101
 phylogenetic relationships, 98–102
R1Dm, 93
R2Dm, 89, 90
 reverse transcriptase activity, 78, 91
 reverse transcriptase domain, 79, 94, 96, 97, 98–102
 RNA intermediate, 80
TED, 88f, 96–7, 100f, 101
- retrovirus
 evolutionary origin, 103
 genomic abundance and distribution, 104t
 origin of *Line 1*, 79
R1 and *R2* sequence comparisons, 89
 reverse transcriptase tree, 99, 100f
 structure, 89
 reverse transcriptase tree, 98–102
Rhodnius prolixus, 4, 298, 370
 ribosomal RNA, 116–19
 ribosomal RNA gene, 86, 105
 Riddiford, L. M., 7, 8
 RNA polymerase III, *see* polymerase III
 Roller, H., 5, 6

Index

541

- Samia cynthia*, 374
- Sarcophaga bullata*, 309, 412t, 413
- Sarcophaga falculata*, 413t
- Sarcophaga peregrina*
- antibacterial proteins, 374, 377t
 - antibacterial response, 370, 385
 - attacinlike protein, 392
 - attacins, 380
 - cecropins, 378–9
 - methionine-rich proteins, 312
 - sapecins, 382, 391
- satellite DNA, 77
- Sawa-j, 64
- Schistocerca americana*, 157
- Schistocerca gregaria*, 161, 168
- segmentation gene hierarchy
- compartmentation, 157–8
 - determination of anteroposterior axis, 147–9, 151–3
 - dorsoventral patterning, 149, 162–3
 - gap phenomenon, 153–5
 - homeotic genes, 158–9
 - pair-rule genes, 155–7
 - parasegments, 157–8
 - segmental specification, 151
 - sensilla esterase, 51–3
- sensillum, *see* olfactory system
- sericin, 13, 251; *see also* sericin genes, silk genes
- sericin genes
- cis*-acting elements, 266–7
 - coordinate regulation with non-silk genes, 256
 - differential RNA splicing, 254–6
 - differential transcription in vitro, 257
 - homeodomain binding sites, 264–5, 267f
 - Magnan insertion, 95
 - mapping, 61
 - transcription factors, 264
 - upstream promoter element, 257
 - see also* silk genes
- serine protease inhibitors, 10
- serine tRNA, 96, 275
- sex determination, 23, 26
- sex linkage, 21, 23, 26, 27, 64
- sex pheromone, 2, 3, 7, 352–4, 359; *see also* odorant binding proteins; olfactory system
- sex-limited translocation, 27, 34, 35, 41, 43
- short interspersed nucleotide elements (SINEs), *see* retroposon
- silk genes
- cis*-acting transcriptional elements, 266–7
 - conserved 5' flanking regions, 258–9
 - developmental regulation, 253
 - differential transcription in vitro, 257–8
 - homeodomain binding, 266, 267f
 - homeodomain-containing proteins, 264–6
 - P25, 61, 258, 261
 - protein binding regions, 259–63
 - transcription factors, 262–4
 - types, 252
 - see also* fibroin genes; sericin genes
- silk gland
- carotenoid uptake and secretion, 63–4
 - cell-free transcription extracts, 256–8, 282
 - compartments, 158, 268, 270
 - embryonic development, 250–1, 252f, 269
 - engrailed gene expression, 158
 - homeobox gene expression, 267–9, 270f
 - morphology, 250, 253f
 - mRNA enrichment, 14
 - mutations, 61, 175–6
 - polyploidy, 28, 251
 - regional specialization, 251
 - sex chromatin body, 27
 - translational specialization, 13–14, 273–6
- somatic mosaic, 58, 69
- SP1, *see* methionine-rich storage protein
- SP2, *see* arylphorin
- sperm, 28
- spider, 277
- spinning behavior, 296, 335
- Spodoptera frugiperda* cells, 404, 412t, 413
- Spodoptera littoralis*, 376t
- Spodoptera litura*, 312
- steroid receptor superfamily, 314, 317; *see also* chorion transcription factors
- 30K storage proteins, 310f, 311–12
- Sturtevant, A. H., 26
- subesophageal ganglion, 9

542

Suzuki, Y., 13
 symplesiomorphy, 112
 synapomorphy, 112–13

TED, *see* retrotransposable element

Telfer, W. H., 10

Tenebrio mollitor, 5, 308

Tineola biselliella, 152, 155

tissue culture, 18–19, 403, 404, 412–14

TN-1 antigen, 156

Toyama, K., 21

Trager, W., 18

transgenic *Drosophila*, 193–4, 198–200, 261, 398

trehalose, 18

Tribolium castaneum, 157, 159–60, 165

Trichoplusia ni, 96, 299, 312, 313, 411–15

tRNA, *see* alanine tRNA; alanine tRNA genes; glycine tRNA genes

tRNA synthetase, 274–5

Truman, J. W., 8, 9

tyrosinase, 60

Umeya, 9

vitellin, 40

Index

vitelline membrane, 121

vitellogenesis, 182

vitellogenin, 10, 310f, 313, 314

vitellogenin mRNA, 298

W chromosome

 Egg size-determining gene, 41

 female-determining role, 23, 26

 inactivation, 27

 translocation, 43; *see also* sex-limited translocation

wandering behavior, 295, 335

Wigglesworth, V. B., 4

Williams, C. M., 3, 6, 7, 9

wing patterns, 1, 68

Wyatt, G. R., 18, 19

Wyatt, S. S., 18, 19

xanthine dehydrogenase, 52f, 58

xanthommatin, 60

Yin, C.-M., 9

Z chromosome, *see* sex linkage

zairai-shu, 35, 64

zerknüllt, 264, 265f

Zophobas atratus, 370, 374, 377t