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25 Abstract

26

27The two essential insect hormones, ecdysteroids and juvenile hormones, are 28possessed not only by insects, but also widely by arthropods, and regulate 29various developmental and physiological processes. In contrast to the 30 abundant information about molecular endocrine mechanisms in insects, the 31 knowledge of non-insect arthropod endocrinology is still limited. In this 32review, we summarize recent reports about the molecular basis of these two 33 major insect hormones in the freshwater microcrustacean Daphnia, a keystone taxon in limnetic ecology and a bioindicator in environmental 3435 studies. Comprehensive comparisons of endocrine signaling pathways 36 between insects and daphnids may shed light on the regulatory mechanisms 37 of various biological phenomena and, moreover, evolutionary processes of 38 arthropod species.

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40

41 **Highlights:**

42 - Ecdysteroids and juvenile hormones synergistically regulate various
43 phenomena in Arthropoda.

44 - Endocrine systems in non-insect arthropods are poorly understood.

45 - Endocrine systems differ in complexity among taxa, although general
46 outline is conserved.

47

48 **Keywords:**

- 49 ecdysteroid, juvenile hormone, Daphnia pulex, Daphnia magna, hormonal
- 50 crosstalk

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68 1. Introduction

69

70The freshwater microcrustacean or water flea, Daphnia (Branchiopoda: 71 Cladocera), is a keystone taxon in limnetic ecology and is widespread around 72the world [1-3]. Generally, daphnids reproduce by a process referred to as 73cyclical parthenogenesis [4]. By employing clonal reproduction during spring 74and summer when conditions are warm and food is abundant, female 75daphnids lay eggs in the brood chamber situated in their dorsal region. The 76offspring are reared in the brood chamber until hatching and released into 77the water column immediately before molting. Under favorable conditions, 78adult daphnids have a reciprocally synchronized cycle of molting and 79reproduction throughout their lives. On the other hand, when environmental 80 conditions become less favorable (e.g., a decrease in day length, temperature 81 and food), they produce male offspring in a process referred to as 82environmental sex determination and employ sexual reproduction which 83 increases genetic variation through recombination and the likelihood of 84 survival under harsh environmental conditions [5]. Thus, these small 85 crustaceans have very complicated life cycles and can alter their survival 86 strategies drastically in response to the surrounding environment [6]. It has 87 recently been demonstrated that these survival mechanisms are regulated by 88 a variety of physiological and endocrine systems. For example, endocrine 89 factors such as ecdysteroids and juvenile hormones (JHs), which are among

90 the most widely studied and well known insect hormones, are also considered 91 to play important roles in daphnids [7, 8]. For instance, topical application 92of ecdysteroids or their agonists on Daphnia magna causes a delay and/or 93 defect in molting, and consequently death [9-12]. Similarly, exposure to JHs 94or their analogs decreases the number of offspring in many daphnia species, 95and the sex ratio of offspring becomes male-biased, which is a typical 96 example of the disruption of sex determination by chemicals [13-18]. In 97 addition to the occurrence of clonal reproduction in daphnids, which is useful 98 for producing large numbers of genetically identical organisms, their high 99 sensitivity to insect hormones prompted the Organization for Economic 100 Cooperation and Development (OECD) to establish a biological assay system 101 for screening the hormonal activities of chemicals using daphnids as a model 102organism **[19-20]**. However, in contrast to insects, a lack of basic information 103 about daphnid (and other non-insect arthropods) endocrine systems is an 104 important limitation. Indeed, this has resulted in the OECD test guidelines 105 being applied in the absence of developmental, physiological, and/or 106 molecular information of the mode of action (MoA) and adverse effects of 107 chemicals.

Under these circumstances, as the draft genome sequence of *D*. *pulex* was determined [21] and gene-function analytical methods, such as
RNAi, TALEN and CRISPR/Cas9, were established in succession [22-27],
striking findings and advances in the technical and genetic aspects of daphnid

112genetics have emerged. In this review, we summarize recent reports on the 113molecular basis of biosynthesis; reception and signaling cascades of two 114major arthropod hormones, ecdysteroids and JHs, in Daphnia; and how these 115findings have increased the potential suitability of Daphnia as a model for 116 environmental studies. Knowledge is not only important for removing the 117"black boxes" in biological assay systems, but it also helps to shed light on 118 the regulatory mechanisms of various biological phenomena and to clarify the 119 complicated life cycle observed in daphnids.

121 2. Insect hormones – biosynthesis and signaling

122

123 Before discussing the endocrinology of daphnids, it is important to understand 124 the ecdysteroid- and JH-signaling pathways in insects. Ecdysteroids and JHs 125work in a synergistic manner to regulate the development and 126metamorphosis of most (perhaps all) insects studied to date [28, 29]. 127Numerous studies on insect endocrinology have been undertaken using 128traditional model insects, such as the fruit fly (Drosophila melanogaster), red 129flour beetle (Tribolium castaneum) and moths (Bombyx mori and Manduca sexta) [7, 8, 29-33]. Although the endocrine systems and their underlying 130 131 molecular mechanisms can differ markedly between divergent species, the 132endocrinology of more evolutionary related species such as insects are 133 considered to be conserved.

134 Schematic pathways for both ecdysteroid and JH biosynthesis and 135 their receptors can be seen in Fig. 1A. In insects, ecdysteroids are 136 synthesized in a specific organ called the prothoracic gland (PG). Cholesterol 137 contained in food is converted into the end product, ecdysone, by the action 138of a series of particular enzymes, and then ecdysone is released into 139 hemolymph [33-43]. At the target peripheral cells, ecdysone is converted 140 into 20-hydroxyecdysone (20E), an active form of an ecdysteroid, by shade (shd) [44]. Among these ecdysteroidogenic genes, spook (spo), phantom 141 142(phm), disembodied (dib), shadow (sad) and shd are referred to as

143 "Halloween genes", as knockout of these genes showed the naked cuticle 144 phenotype in flies as a result of ecdysteroid synthesis deficiency [45-46]. 145Another major insect hormone, JH, is synthesized in the corpora allata (CA). 146 JH biosynthesis starts with the mevalonate pathway, which is common in 147eukaryotes (and some prokaryotes) [47]. Farnesyl pyrophosphate (FPP), an 148end product of the mevalonate pathway, is then converted by a series of 149 enzymes into active forms of JH, such as juvenile hormone III (JH III), which 150is most commonly found in insects. These active JHs are released into the 151hemolymph before exerting a variety of functions in the target peripheral cells 152[48-55]. This synthetic pathway differs slightly between Lepidoptera and 153other insect taxa. In the former, JHs are produced using juvenile hormone 154acid (JH acid) as an intermediate whereas the latter JHs are produced using 155methyl farnesoate (MF) as an intermediate. Although the cholesterol 156 biosynthetic (mevalonate-squalene) pathway is considered highly conserved 157in many species, insects are found to be lacking the squalene synthase and 158genes involved in the squalene pathway, which means that insects are unable 159to synthesize cholesterol and therefore dependent on direct dietary sources 160 **[56]**.

161

162



Γ

Metamorphosis

to adult

Metamorphosis to pupa

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165

166 Fig. 1. A schematic view of the ecdysteroid and juvenile hormone (JH) 167 signaling pathways in insects. (A) The pathways from biosynthesis in the 168 specific organs to reception at peripheral target cells. (B) Hormonal crosstalk between ecdysteroid and JHs during regulation of metamorphosis. 169 Abbreviations: PG, prothoracic grand; CA, corpora allata; Farnesyl-PP, 170 171 farnesyl pyrophosphate; MF, methyl farnesoate; JH III, juvenile hormone III; 17220E, 20-hydroxyecdysone; EcR, ecdysone receptor; USP, ultraspiracle; Met, 173Methoprene-tolerant; SRC, steroid receptor coactivator; nobo, noppera-bo; 174nvd, neverland; sro, shroud; spo, spook; spok, spookier; phm, phantom; dib, 175disembodied; sad, shadow; shd, shade; FP, farnesyl phosphatase; FDH, 176farnesol dehydrogenase; FaDH, farnesal dehydrogenase; FAMeT, farnesoic 177acid O-methyltransferase; MFE, methyl farnesoate epoxidase; FAE, farnesoic 178acid epoxidase; JHAMT, juvenile hormone acid O-methyltransferase; BR-C, 179 Broad-Complex; Kr-h1, Krüppel homolog 1.

180

181

In target peripheral cells, ecdysteroids and JHs bind to specific receptors (Fig. 1). The active ecdysteroid, 20E, transformed from ecdysone by *shd*, binds to a member of the nuclear receptor superfamily, ecdysone receptor (EcR) **[57]**. When EcR binds 20E, it forms a heterodimer with

186 another nuclear receptor superfamily protein, ultraspiracle (USP) [58, 59]. 187 Following association with cofactors, such as steroid receptor coactivator 188 (SRC), the EcR complex then binds to a specific sequence on the genome 189 (ecdysone response element: EcRE) and acts as a transcription factor [58-190 **60]**. Unlike the ecdysteroids, the JH receptor was only discovered relatively 191 recently. Juvenile hormone III and other JHs are bound by the basic helix-192 loop-helix-Per-Arnt-Sim (bHLH-PAS) family protein, Methoprene-tolerant 193 (Met) [61-63]. After heterodimerization with SRC, which is another bHLH-194 PAS protein and a component of the EcR complex, in response to binding to 195 JHs, the Met complex binds to the JH response element (JHRE) and acts as a 196 transcription factor, similar to EcR [64-66].

197 Ecdysone receptor complex transduces signaling to downstream 198 factors by regulating the transcription of quite various genes [67, 68]. The 199 transcription factors, Broad-Complex (BR-C) and E93, which are pupal- and 200 adult-specifier genes, respectively, are representative targets that are 201 directly regulated by EcR [69-81]. In contrast to EcR, the downstream 202 signaling of the JH receptor is less understood, primarily because the Met/SRC 203complex has only recently been discovered. However, the transcription of the 204zinc finger transcription factor, *Krüppel homolog 1 (Kr-h1)*, which is directly 205regulated by the Met/SRC complex in response to binding to JHs, has been 206 extensively studied [82-85]. Recent studies using *B. mori* demonstrated that 207*Kr-h1* prevents both larval-pupal and pupal-adult metamorphosis by binding

- 208 directly to the promoter region of *BR-C* and *E93*, repressing their expression,
- $209\,$ $\,$ and in so doing, forming the molecular basis of a mutual inhibitory action $\,$
- 210 ("status quo") of JHs [86, 87] (Fig. 1B).
- 211

212 3. Ecdysteroids in *Daphnia*

213

Like all members of the Ecdysozoa and Arthropoda, daphnids grow through molting. However, as mentioned previously, there are two major differences between daphnids and insects: 1) in contrast to insects which do not molt at the adult stage, daphnids continue to molt and increase in size over the course of their lives; 2) molting and reproduction are reciprocally synchronized in adult daphnids. Consequently, ecdysteroids are considered to be necessary for survival throughout their lifetime **[88, 89]**.

221

222

223Ecdysteroid biosynthesis 3.1.

224

225Although the Y-organ in decapods is known to be responsible for ecdysteroid synthesis [90, 91], little is known about where ecdysteroids are synthesized 226227and released in other crustaceans, such as daphnids. Recent effort to identify 228key genes in ecdysteroidogenesis of *D. magna* by cloning led to the discovery 229of the genes neverland (nvd), which converts cholesterol into 7-dehydro 230cholesterol at the first step of the synthesis, and *shd*, which converts 231ecdysone to an active form of the ecdysteroid 20E in target cells [12]. In 232addition, D. magna has two nvd homologs (nvd1 and nvd2), and these were 233expected to be paralogs acquired specifically in daphnids. At both embryonic

234and adult stages, *nvd1* was strongly expressed in gut epithelial cells **[12, 92]**. 235Embryonic knockdown of *nvd1* by RNAi showed a striking reduction in the 236internal ecdysteroid titer and a delay of development by inhibition of 237embryonic molt [92]. A similar developmental delay was also observed in 238shd RNAi embryos [92]. These results strongly suggest that both nvd1 and 239shd are involved in the ecdysteroidogenesis in D. magna, and that nvd1-240expressing gut epithelial cells may be responsible for ecdysteroid synthesis. 241On the other hand, nvd2 was expressed in germ cells of the ovary where nvd1 242was absent [92]. Further studies are necessary to determine whether nvd2 243is also involved in the ecdysteroidogenesis. In addition, several other genes 244involved in ecdysteroid synthesis can be found in the daphnid genome (e.g., 245phm and dib), and expression and functional analyses of these genes could 246be instrumental for elucidating where ecdysteroids are synthesized [93] 247(**Table 1**).

- 249
- 250
- 251

Table	1.	Accession	numbers	of	Daphnia	homologs	of	ecdysteroid	and
juvenil	e h	ormone sig	gnaling-rel	ate	d genes				

Gene name	Daphnia magna	Daphnia pulex	Reference		
Ecdysteroid biosynthesis					
nobo	?	?			

	nvd	BAQ02388, BAQ02389	EFX86361, EFX88304, EFX60729	[12, 92]
	sro	?	?	
	spo/spok	KZS09664	EFX88041	
	Cyp6t3	?	?	
	phm	KZS17835	EFX85499	
	dib	KZS10280	EFX63066	
	sad	KZS16986	EFX70970	
	shd	BAF35770	EFX77008	
Ecdy	steroid receptor			
	EcR	BAF49030	EFX79409	[94]
	USP	BAF49028	EFX88423	[94]
Ecdy	vsteroid-responsiv	e gene		
	E74	KZS09932	EFX89297	
	E75	ABP48738	ADB79814	[98, 99]
	HR3	ACY56690	ACY56691	[98, 99]
	HR4	KZS12701	EFX67867	
	betaFTZ-F1	BAU20372	EFX77612	
	DDC	KZS20105	EFX90074	
	BR-C	KZS07124	EFX90040	
	E93	?	?	
_				
Juve	nile hormone bios	synthesis	2	
	FP	?	?	
	FDH	KZS13936	EFX8/469	
	FaDH	KZS05270	EFX/1031	
	FAMeI/JHAMI	?	BAH86593	[104]
	FAE/MFE	lost?	lost?	[109]
Juve	enile hormone rece	eptor		
	Met	BAM83855	BAM83853	[110]
	SRC	BAM83854	BAM83856	[110]

Juvenile hormone-responsive gene

Kr-h1	KZS09055	LC270151	Miyakawa et al. unpublished
hairy	?	?	

Accession numbers in italic indicate computational gene models based on the genome sequences.

252

- 253
- 254 3.2. Ecdysteroid receptors

255

256Homologs of both EcR and USP have been isolated from *D. magna*, and both 257have the characteristic structure of the nuclear receptor superfamily [94]. 258The two-hybrid luciferase assay using mammalian cultured cells transfected 259with *D. magna EcR*, *USP* and *Drosophila Taiman* (the same as SRC) 260demonstrated that Daphnia EcR and USP form a heterodimer specifically in 261response to ecdysteroids such as ecdysone and 20E [94, 95]. Homologs of 262 these ecdysteroid receptors are also found in the *D. pulex* genome [96] 263(**Table 1**), suggesting that daphnids bind to ecdysteroids by employing a similar (or the same) receptor system to that of insects. 264

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267 3.3. Downstream signaling of ecdysteroids

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The heterodimer of EcR and USP acts as a transcription factor and activates downstream genes **[58-60]**. When *D. magna* embryos were injected with a

271 reporter plasmid containing insect EcRE fused to GFP and exposed to 20E,
272 the fluorescent intensity increased dose-dependently with 20E exposure [97].
273 These results suggest that ecdysteroid receptors have the same molecular
274 function in insects and daphnids, although the direct targets of the receptors
275 are not yet known in daphnids.

276Among various ecdysteroid-responsive genes in insects [67, 68], 277hormone receptor 3 (HR3) and E75 have already been isolated in both D. 278pulex and D. magna [98, 99]. In D. magna, HR3 expression was upregulated 279 in response to 20E, whereas E75 expression remained unchanged [98]. 280Although ecdysteroid-responsive genes such as E74, HR4 and β FTZ-F1 have 281been identified in the daphnid genome (Table 1), their involvement in the 282ecdysteroid signaling pathway in daphnids remains unknown. In order to 283clarify how daphnids regulate and synchronize their elaborate molting and 284reproduction cycles, and to perform a detailed functional analysis of each 285candidate gene, a comprehensive analysis of all of the molecular pathways 286(i.e., from hormone biosynthesis to the expression of biological phenomena) 287 is considered necessary [100].

288

289

4. Juvenile hormones in Daphnia

290

In addition to ecdysteroids, JHs play very important roles in the reproduction and development of daphnids. In particular, their roles in sex determination is both unique and essential for their life history **[13-18, 101]**.

294

295

296 4.1. Juvenile hormone biosynthesis

297

298The current progress status regarding studies on the JH-synthesizing organ 299 in daphnids is similar to that for studies on ecdysteroids. Although the 300 mandibular organ (MO) is known to be the site of synthesis in decapods [102, 301 **103]**, homologous organs have not been found in daphnids and related taxa. 302 However, a considerable number of homologous genes involved in JH 303 biosynthesis in the insect CA, have been identified in the genomes of daphnids, 304 implying the existence of the same molecular synthesis pathway (**Table 1**). 305 Among these genes, especially juvenile hormone acid O-methyltransferase 306 (JHAMT)/farnesoic acid O-methyltransferase (FAMeT) has the ability to 307 convert farnesoic acid (FA) into MF, indicating that daphnids also appear to 308 produce MF [104]. Decapods use MF as an active form of JH, without 309 converting it to JH III [105-107]. Although unconfirmed, daphnids are 310 considered to use MF as an active JH ligand, mainly because the male-

induction activity of MF is higher than it is for JH III [14, 108] and also
because of the loss of *methyl farnesoate epoxidase* (*MFE*), a member of *cyp15*,
that converts MF to JH III in insects [109]. However, given that several
similar sequences could be found in a genome-wide survey for *MFE* genes
(Table 1), further studies are awaited.

316

317

318 4.2. Juvenile hormone receptors

319

320 We recently cloned and functionally analyzed the JH receptor in daphnids for 321 the first time in crustaceans. Similarly to insects, the JH receptor was a JH-322dependent heterodimer complex comprising Met and SRC, which responded to various JH analogs in addition to MF and JH III [110]. Ligand sensitivity 323 324 profiles against these various JHs corresponded well with the male-induction 325 activity of each chemical, suggesting that the JH receptor, Met, is a molecular 326 target when sex determination is disrupted by exposure to exogenous JHs. 327 Moreover, we found that two of the eight amino acids comprising the JH-328 binding pocket in Met differed between insects and daphnids, and that a single 329 amino acid mutation of an insect-type residue into Daphnia Met caused a 330 marked increase in response to JH III, just as in insect JH receptors [108, 110]. It is possible that a change in the ligand selectivity of the JH receptor, 331 332 Met, is related to the difference observed in the innate JH ligands between

insects and crustaceans. If so, then understanding the molecular evolution of
JH receptors is one of the important topics in the evolution of the JH signaling
pathway in Arthropoda.

336

337

338 4.3. Downstream signaling of juvenile hormones

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340 Activation of the JH signaling pathway causes a lot of physiological changes 341 in daphnids. One of the well-studied examples is environment-dependent 342 male production [13, 14]. We recently used RNA-seq analysis to screen 343 genes downstream of the JH signaling pathway that are activated when males 344 are produced. The results showed that *hemoglobin*, serine protease, and 345numerous other genes (many of which are functionally unknown because of 346 a lack of homology to known genes) were upregulated in male-producing 347mothers [111]. Both *hemoglobin* and *serine protease* genes have also been 348 reported to be upregulated after topical application of JHs to D. magna at the 349 juvenile stage (before starting reproduction), suggesting that these genes are 350 typical downstream factors of the JH signaling pathway in daphnids [112]. 351 It is considered likely that these factors are involved in male determination 352 in the ovary of parental daphnid, and after that, which fate-determined eggs 353 spontaneously express the male specific gene, *doublesex*, in daphnids **[113**, 354114].

355On the other hand, some Daphnia species are known to produce 356 defensive morphs or structures in response to the presence of predators (i.e., 357 so called "inducible defense" mechanisms) [115-117], and JHs are also 358involved in regulation of the morphogenesis in these defensive morphs [118, 359**119**]. We previously proposed a signaling cascade model describing how, in 360 individuals that have received chemical stimuli released by predators, the JH 361 signaling pathway is activated and morphogenesis occurs in response to the 362 involvement of several morphogenetic and cell-proliferating factors [96].

363 In this way, the molecular underpinnings of a variety of biological 364 phenomena exhibited by daphnids, as well as the role of the components of 365 the JH signaling pathway in these processes, are becoming increasingly clear. 366 However, aspects related to the proximate signaling of JH, such as the direct 367 target genes of the JH receptor, Met, are still unknown. In insects, one such 368 direct target is *Kr-h1*, which is a well-studied and very important downstream 369 component of JHs [82-87]. Although daphnids possess a Kr-h1 ortholog, the 370 findings of our recent study using a reporter assay to clarify the function of 371 Daphnia Kr-h1 strongly suggested that this ortholog is not involved in JH 372signaling (Miyakawa et al. unpublished). Consequently, identifying primary JH 373 responsive genes is considered crucial for obtaining a comprehensive 374 understanding of the various molecular characteristics of the JH signaling 375pathway in daphnids.

376

377 5. Summary and future directions

378

379 Ecdysteroids, JHs and their signaling pathways, are extremely important 380 endocrine systems that elaborately regulate a vast array of physiological 381 phenomena, not only in insects, but also in daphnids. While daphnid 382endocrinology is still less understood than that for the model insect species 383 (e.g., *D. melanogaster* and *B. mori*), the overall nature of the hormonal 384 pathways in daphnids has been gradually elucidated using a variety of 385molecular approaches since the draft genome of *D. pulex* was published. 386 Findings published to date have shown that the endocrine systems of insects 387 and daphnids, while generally conserved and similar in terms of their overall 388 outline, differ in certain respects. It is possible that these slight differences in 389 the molecular signaling pathways could serve as a basis for the novel traits 390 or life histories acquired by specific taxa; for example, environmental sex 391 determination and inducible defense in daphnids.

In many cases, ecdysteroids and JHs do not act independently of each other, with final developmental processes often being a sequel to complicated crosstalk between the two signaling pathways **[7, 8, 29]**. Recent studies have demonstrated that a cofactor of the EcR complex, SRC, is the heterodimeric partner of the JH receptor, Met **[64-66]**, and that Kr-h1, a direct target of the JH/Met/SRC complex, acts as a repressor of *BR-C* and *E93* expression by ecdysteroid signaling **[86, 87]**; the molecular basis of the

399 hormonal crosstalk has thus been partly elucidated. We have already 400 successfully established several variations of reporter assay systems that can 401 be used to analyze gene regulatory relationships within both ecdysteroid and 402 JH signaling pathways in daphnids [94, 108, 110]. By comparing not only 403 expression patterns and functions of individual genes, but also connections 404 of each component of signaling pathway between insects and daphnids using 405 these systems, we expect to understand how the alterations of endocrine 406 systems have occurred in an ancestor of insects after diverging from 407 branchiopod crustaceans.

To date, study of arthropod endocrinology has mainly relied on the specific taxa, holometabolous insects and decapod crustaceans. To understand the evolutionary processes of arthropod diversity from the aspect of physiological regulation, further studies should be performed using various arthropods broadly (i.e., hemimetabolous insects, non-decapod crustaceans, myriapods, arachnids, etc.).

414

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