



# A map of terminal regulators of neuronal identity in *Caenorhabditis elegans*

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Our present day understanding of nervous system development is an amalgam of insights gained from studying different aspects and stages of nervous system development in a variety of invertebrate and vertebrate model systems, with each model system making its own distinctive set of contributions. One aspect of nervous system development that has been among the most extensively studied in the nematode *Caenorhabditis elegans* is the nature of the gene regulatory programs that specify hardwired, terminal cellular identities. I first summarize a number of maps (anatomical, functional, and molecular) that describe the terminal identity of individual neurons in the *C. elegans* nervous system. I then provide a comprehensive summary of regulatory factors that specify terminal identities in the nervous system, synthesizing these past studies into a regulatory map of cellular identities in the *C. elegans* nervous system. This map shows that for three quarters of all neurons in the *C. elegans* nervous system, regulatory factors that control terminal identity features are known. In-depth studies of specific neuron types have revealed that regulatory factors rarely act alone, but rather act cooperatively in neuron-type specific combinations. In most cases examined so far, distinct, biochemically unlinked terminal identity features are coregulated via cooperatively acting transcription factors, termed terminal selectors, but there are also cases in which distinct identity features are controlled in a piecemeal fashion by independent regulatory inputs. The regulatory map also illustrates that identity-defining transcription factors are reemployed in distinct combinations in different neuron types. However, the same transcription factor can drive terminal differentiation in neurons that are unrelated by lineage, unrelated by function, connectivity and neurotransmitter deployment. Lastly, the regulatory map illustrates the preponderance of homeodomain transcription factors in the control of terminal identities, suggesting that these factors have ancient, phylogenetically conserved roles in controlling terminal neuronal differentiation in the nervous system. © 2016 The Authors. *WIREs Developmental Biology* published by Wiley Periodicals, Inc.

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## INTRODUCTION

When Sydney Brenner established *Caenorhabditis elegans* as a model system his vision was to first draw a series of maps—anatomical, lineage and functional maps—that describe this simple metazoan organism and to then use these maps as a starting





TABLE 1 | Functional Map of the Extrapharyngeal Nervous System

Sensory Neuron	Function	Reference	Interneuron	Function	Reference	Motor neuron	Function	Reference
ADE	Mechanosensory	17,18	ADA			AS		
ADF	Dauer formation	19	AIA	Processing sensory information	20	AVL	Defecation	21
ADL	Olfaction (repulsive)	22	AIB	Reversal, pausing, integrating sensory information	20,23,24	DA	Locomotion	25
AFD	Thermosensation	26	AIM	Sexual attraction		DB	Locomotion	25
ALA	Sleep, mechanosensory	27,28	AIN			DD	Locomotion	21
ALM	Mechanosensory	29	AIY	Locomotion, integrating sensory information	26,30	DVB	Defecation	21
ALN			AIZ	Locomotion, processing sensory information	26,30	HSN	Egg-laying	
AQR	Aggregation, O <sub>2</sub> sensation	31,32	AUA	Aggregation	31	PDA		
ASE	Gustation	33	AVA	Command interneurons	25,34	PDB		
ASG	Gustation	19,33	AVB	Command interneurons	25,34	RIM	Reversal behavior, feeding circuit	23,35
ASH	Mechanosensory, gustation	36	AVD	Command interneurons	25,34	RMD	Head movement, foraging	23,37
ASI	Dauer formation, feeding state, chemosensory, thermosensory	19,33,38	AVE	Command interneurons	25,34	RME	Head movement	21
ASJ	Dauer formation and recovery	19	AVF	Egg-laying/locomotion	39	RMF		
ASK	Gustation	33	AVG	Pioneer/guidepost	40	RMG	Aggregation	41
AVM	Mechanosensory	29	AVH			RMH		
AWA	Olfaction	33	AVJ			SAB	Head movement	42
AWB	Olfaction	33	AVK			SIA	Guidepost	43
AWC	Olfaction, thermosensation	33,44	BDU	Mechanosensory	45	SIB	Guidepost	43
BAG	CO <sub>2</sub> sensation	46	CAN	Fluid homeostasis		SMB	Sinusoidal locomotion	23
CEP	Mechanosensory	17,18	DVA	Stretch reception	47	SMD	Omega turns	23
FLP	Mechanosensory	36	DVC			VA	Locomotion	25
IL1	Head bends, foraging	37	LUA	Pausing		VB	Locomotion	25
IL2	Nictation behavior	48	PVC	Command interneurons	25	VC	Egg-laying	49
OLL	Pathogen avoidance behavior	50	PVN			VD	Locomotion	21
OLQ	Mechanosensory, head bends, foraging	36,37	PVP					
PDE	Mechanosensory	17,18	PVQ					

TABLE 1 | Continued

Sensory Neuron	Function	Reference	Interneuron	Function	Reference	Motor neuron	Function	Reference
PHA	Gustation, mechanosensory	45,51	PVR					
PHB	Gustation, mechanosensory	45,51	PVT	Pioneer/guidepost	52			
PHC	Heat avoidance	45,53	PWW					
PLM	Mechanosensory	29	RIA	Thermosensory processing, quiescence	26,54			
PLN			RIB	Reversal behavior	23,30			
PQR	Aggregation, O <sub>2</sub> sensation	31,32	RIC	Feeding circuit	35			
PVD	Mechanosensory, thermosensory	55	RID					
PVM	Mechanosensory	29	RIF	Dwelling	56			
URA			RIG					
URB			RIH	Processes nose touch	57			
URX	O <sub>2</sub> sensation	31,32	RIP	Coupling touch and pharyngeal pumping	25			
URY			RIR					
			RIS	Quiescence	58			
			RIV	Omega turns	23			
			SAA					
			SDQ					
38			42					24

Not every behavior associated with a given cell is shown. Usually the first identified behavior is shown. For more in-depth coverage, see Ref 59,60.

this review, I shall describe molecular maps of the *C. elegans* nervous system and summarize how important they have been to understand the acquisition of terminal neuronal identity features, allowing us to now establish a conglomerate *regulatory map* of the nervous system.

## MOLECULAR MAPS OF THE *C. ELEGANS* NERVOUS SYSTEM

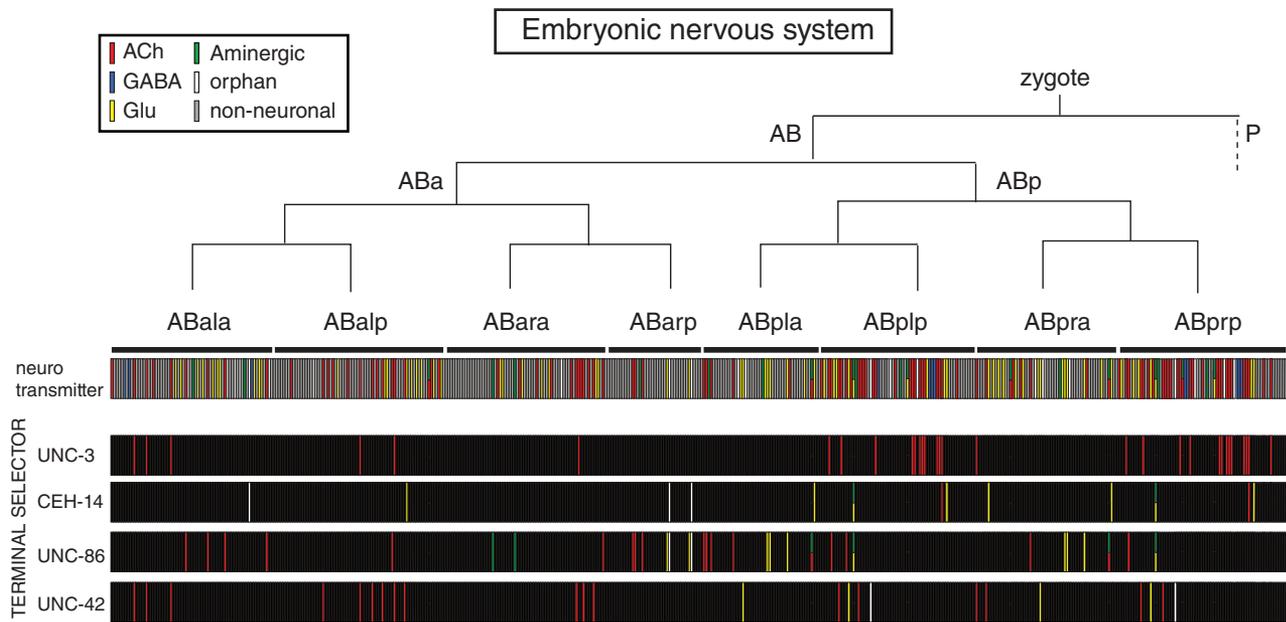
Ever since reporter gene technology was introduced into *C. elegans*, several thousand reporter lines have been generated to monitor the expression of specific genes (examples are shown in Figure 2(a)). In many cases, reporter genes were generated for genes with suspected functions in the nervous system, such as sensory receptors,<sup>22,67</sup> neuropeptides,<sup>68,69</sup> ion channels,<sup>70</sup> neurotransmitter receptors,<sup>71</sup> or putative neuronal adhesion/recognition molecules.<sup>52</sup> As expected, most of these reporter constructs showed neuron-type specific expression profiles. In addition, the reporter-based expression analysis of the many genes characterized for various phenotypes within or outside the nervous system yielded a tremendous number of additional reagents to monitor neuron-type specific gene expression. Since expression patterns are commonly analyzed in the context of a mature nervous system (larval or early adult stages), in which the identity of neurons can be most readily defined, there has been an inadvertent bias toward the characterization of expression patterns in postmitotic, mature neurons. Even though the precise sites of cellular expression of many reporter constructs (particularly those resulting from large scale expression screens conducted in Vancouver<sup>72</sup>) have not been determined, the site of expression of 868 reporter genes within the nervous system have been analyzed with single neuron resolution by the *C. elegans* community, creating more than 260,000 data points (868 × 302). These data points can be extracted from Wormbase and are displayed in Figure 2(b). On average, each of these 868 reporters is expressed in 10 neurons (with a range of 1–110 neurons; very few reporter genes are expressed exclusively in single neuron classes and those that are encode mostly sensory receptor proteins). And, on average, any given neuron type is associated with the expression of 28 distinct reporter genes (ranging from at least 3 to as many as 133). The extent to which each neuron type can be associated with molecular markers is unprecedented in other models, including flies and mice. While gene expression atlases have been generated in these models,<sup>73,74</sup> they

usually suffer from a lack of cellular resolution owing to the much more complex cellular anatomy of the fly and mouse nervous systems.

It is important to point out that these molecular maps describe *regulatory endpoints*, i.e., terminal effector genes that are continuously expressed throughout the life of the neuron and that most often code for proteins that define the mature, functional and anatomical properties of a postmitotic neuron type (e.g., ion channels, sensory receptors, neurotransmitter receptors, and neuropeptides). Equally important, owing to their unsystematic generation by many different labs for many different purposes, these transgenic markers provide a relatively unbiased snapshot of functionally unrelated identity features of a mature neuron.

## AN (ALMOST COMPREHENSIVE) NEUROTRANSMITTER MAP

One specific subtype of molecular brain maps is a neurotransmitter map. Neurotransmitter maps are invaluable complements to any anatomical map (specifically, a connectome) as they inform us about the nature of information flow in the nervous system. Like any other organism, the *C. elegans* nervous system utilizes a plethora of distinct neurotransmitter systems, from fast-acting neurotransmitters (GABA, glutamate, and acetylcholine) to aminergic neurotransmitters (dopamine, serotonin, octopamine, and tyramine) to more than 200 modulatory neuropeptides.<sup>75</sup> Given the diversity of neurotransmitter systems, the neurotransmitter identity of a neuron is a key molecular identity feature of a neuron. While the identity of GABAergic and aminergic neurons has been known for a while (which amount to ~10% of all neuron classes<sup>76,77</sup>), it was only the recent analysis of glutamatergic and cholinergic neurons that brought the coverage of neurotransmitter identities to about 90% of all neurons in the nervous system. Cholinergic and glutamatergic neurotransmitter identities were inferred through the systematic expression analysis of vesicular transporters for acetylcholine (ACh) and glutamate (Glu), demonstrating that these two transmitters are the most broadly used neurotransmitters in the *C. elegans* nervous system (Figure 2(c); ACh: 52 of all 118 neuron classes; Glu 38 of all 118 neuron classes).<sup>8,78</sup> Notable features of the *C. elegans* neurotransmitter map include the broad usage of ACh and Glu in different neuron types of the nervous system (each utilized by sensory, inter, and motor neurons)<sup>8,78</sup> and its association with specific circuitry (e.g., the ventral nerve cord motor



**FIGURE 3** | Lack of correlation of lineage with neurotransmitter identity or transcription factor expression. Each bar represents an individual cell. See text for references.

neuron circuit, composed of motor neurons and innervating command interneurons is cholinergic<sup>8</sup>). Notably, from a developmental standpoint, neurons that share the same neurotransmitter show no apparent lineage relationships (Figure 3).

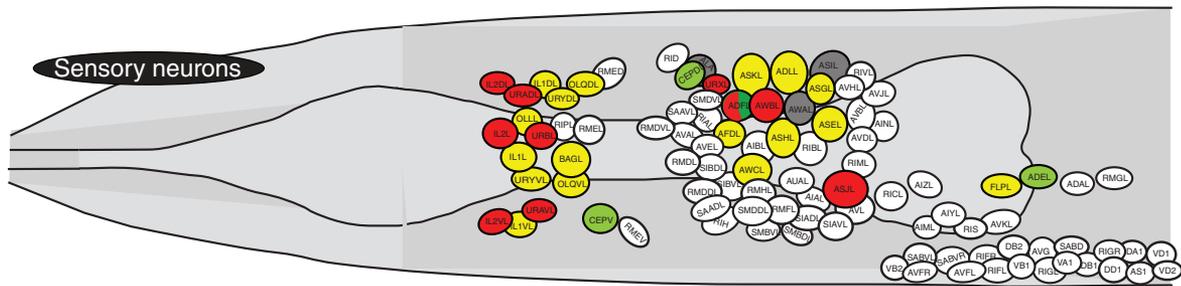
## A REGULATORY MAP OF THE NERVOUS SYSTEM

Much like the anatomical, lineage, and functional maps of the worm nervous system, available molecular maps have served as powerful starting points for incisive genetic loss of function analysis. Specifically, reporter genes that are expressed in particular neuron types have offered the opportunity to engage in a bottom-up analysis which seeks to define the regulatory factors that control these terminal neuronal identity features. This type of analysis permitted a significant expansion of the phenotypic analysis of some classical transcription factor mutants. For example, genetic elimination of the LIM homeobox gene *mec-3* phenocopies the loss of mechanosensory neuron function,<sup>63</sup> loss of the LIM homeobox gene *ttx-3* phenocopies the loss of AIY neuron function (in both cases, animals show a characteristic cryophilic thermotaxis phenotype),<sup>65</sup> and loss of the zinc (Zn) finger transcription factor *che-1* phenocopies the chemotaxis defects of ASE sensory neuron ablation.<sup>64</sup> However, it is *a priori* not clear whether such

phenocopying is the result of the respective transcription factor merely regulating one or a few function-defining genes (e.g., a chemoreceptor protein and/or mechanoreceptor channel) or whether these factors have much more profound effects on the identity of the respective neuron. The ability to phenotype the loss-of-function for a regulatory factor of course very much depends on the availability of descriptors of neuronal identity features. The existence of a relatively fine-grained molecular phenotypic space of individual neuron type (in the form of marker transgenes) has traditionally set *C. elegans* apart from other systems in which the precise impact of a regulatory pathway on the identity of a neuron often cannot be assessed with the same level of precision.

In principle, the identification of genes controlling terminal identity features for specific neurons can be expected to address the following questions: (1) are the multiple molecular features that define a specific neuron type independently regulated by distinct regulatory factors? or are they coregulated? (2) are there recurrent themes in which the identity of distinct neuron types are controlled? (3) are neurons that share specific functional features, e.g., sensory neurons, or synaptically connected neurons, controlled by the same regulatory factors?

These questions have been extensively addressed over the past decade, either by (1) directly screening for mutants in which specific molecular markers show defective expression; (2) by



Sensory	Number	Neurotransmitter	Inducers	Repressor	Reference
ADE	2	DA	<i>ast-1</i> (7/7), <i>ceh-43</i> (5/5)		82,83
ADF	2	ACh & 5HT			
ADL	2	Glu	<i>lin-11</i> (1/1)		78
AFD	2	Glu	<i>ttx-1</i> (7/7), <i>ceh-14</i> (7/7)		78,84
ALA	1	GABA	<i>ceh-14</i> (6/6), <i>ceh-17</i> (6/6)		85,86
ALM	2	Glu	<i>unc-86</i> , <i>mec-3</i> (71)*		87
ALN	2	ACh			
AQR	1	Glu	<i>unc-86</i> (1/1), <i>egl-13</i> (2/2); <i>ahr-1</i> (1/1) <i>che-1</i> (22/22 + cilium), <i>ceh-36</i> , <i>die-1</i> , <i>lim-6</i> **	<i>cog-1</i>	88–90
ASE	2	Glu			64,91
ASG	2	Glu	<i>lin-11</i> (5/5), <i>ceh-37</i> (1/1)		78,92
ASH	2	Glu	<i>unc-42</i> (5/5 + cilium)		78,93
ASI	2	unknown	<i>unc-3</i> (6/23)	<i>unc-3</i>	94,95***
ASJ	2	ACh	<i>sptf-1</i> (4/4)		96
ASK	2	Glu	<i>ttx-3</i> (4/4 + cilium)		78
AVM	1	Glu	<i>unc-86</i> , <i>mec-3</i> (71)*		87
AWA	2	unknown	<i>odr-7</i> (1/1)		62
AWB	2	ACh	<i>lim-4</i> (4/4 + cilium), <i>sox-2</i> (5/6)		97–99
AWC	2	Glu	<i>ceh-36</i> (4/4), <i>sox-2</i> (6/7), <i>die-1</i> , <i>nsy-7</i> , <i>hmbx-1</i> **		78,97,100,101
BAG	2	Glu	<i>ets-5</i> (5/5), <i>ceh-37</i> (1/1), <i>egl-13</i> (6/6), <i>egl-46</i> (3/6)		88,102,103
CEP	4	DA	<i>ast-1</i> (7/7), <i>ceh-43</i> (5/5)		82,83
FLP	2	Glu	<i>unc-86</i> , <i>mec-3</i>	<i>egl-44</i> , <i>egl-46</i>	
IL1	6	Glu	<i>sox-2</i> (2/2), <i>vab-3</i> (1/1)		104
IL2	6	ACh	<i>unc-86</i> (6/6 + cilium), <i>cfi-1</i> (6/6)		105
OLL	2	Glu	<i>sox-2</i> (3/3), <i>vab-3</i> (4/4)		104
OLQ	4	Glu			
PDE	2	DA	<i>ceh-43</i> (5/5); <i>ceh-20</i> (5/5)		82,83
PHA	2	Glu	<i>ceh-14</i> (3/3 + cilium)		78
PHB	2	Glu	<i>ceh-14</i> (3/3+ cilium)		78
PHC	2	Glu	<i>ceh-14</i> (3/3)		78
PLM	2	Glu	<i>unc-86</i> , <i>mec-3</i> (71)*	<i>egl-5</i>	87,106
PLN	2	ACh			
PQR	1	Glu	<i>unc-86</i> (2/2), <i>egl-13</i> (2/2), <i>ahr-1</i> (1/1)		88–90
PVD	2	Glu	<i>unc-86</i> , <i>mec-3</i>		
PVM	1	unknown	<i>unc-86</i> , <i>mec-3</i> (71)*		87
URA	4	ACh	<i>unc-86</i> (2/2), <i>cfi-1</i> (2/2)		107
URB	2	ACh	<i>unc-86</i> (1/1)		107
URX	2	ACh	<i>unc-86</i> , <i>ahr-1</i> (3/3), <i>egl-13</i> (4/4)		88
URY	4	Glu	<i>vab-3</i> (3/3)		78
38	87		33/38 sensory neuron classes 75/87 total sensory neurons		

**FIGURE 4 |** Terminal regulators of sensory neurons. Schematic worm with only sensory neurons colored and tabular summary of terminal regulators of neuronal identity. Color code of neurons in the schematic refer to neurotransmitter identity as show in the tabular summary. ‘Terminal regulators’ refers to the key property of these transcription factors: they are expressed in mature neurons throughout their lifetime, likely a reflection of their continuous role in maintaining the differentiated, terminal state. Early or transiently acting regulators are not shown. Only extrapharyngeal neurons are shown. Black font: most/all tested markers affected (terminal selector). Blue font: only subsets of markers affected. (x/y) indicates x markers out of y markers tested show defective expression. Homeodomain transcription factors are underlined. \* indicates that in the case of the touch neurons, expression profiling has identified at least 71 *mec-3*-dependent genes. *unc-86* is known to regulate *mec-3* expression and cooperate with *mec-3* to control touch neuron-expressed genes.<sup>79</sup> \*\* indicates that the blue labeled factors control only a small subset of left/right asymmetrically expressed chemoreceptors,<sup>80,81</sup> but not bilateral identity of these neurons. \*\*\* indicates our own unpublished data. ‘Cilium’ indicates that the respective regulators also control cilium structure, as assessed by dye-filling defects observed in the respective mutants.

examination of reporter gene expression in candidate mutants (i.e., loss-of-function mutations in transcription factors expressed in a specific neuron type); or (3) by the analysis of mutants retrieved from behavioral screens (the above-mentioned classic behavioral mutants *che-1*, *ttx-3*, *mec-3*, *unc-3*, etc.). The results of dozens of reports ordered by neuron class (sensory, inter, and motor neurons) are summarized in the regulatory maps shown in Figures 4–6. In sum, transcriptional regulators have been identified that control the differentiation of 76 of the 104 *C. elegans* extrapharyngeal neuron classes (73%) which amounts to 217 of all the 282 extrapharyngeal neurons (77%). Each of these transcription factors is a terminal regulator since their expression persists throughout the life of the neuron and in the few cases explicitly examined, they have been found to also be continuously required to maintain the differentiated state (earlier, transiently acting factors are not considered here).<sup>137</sup>

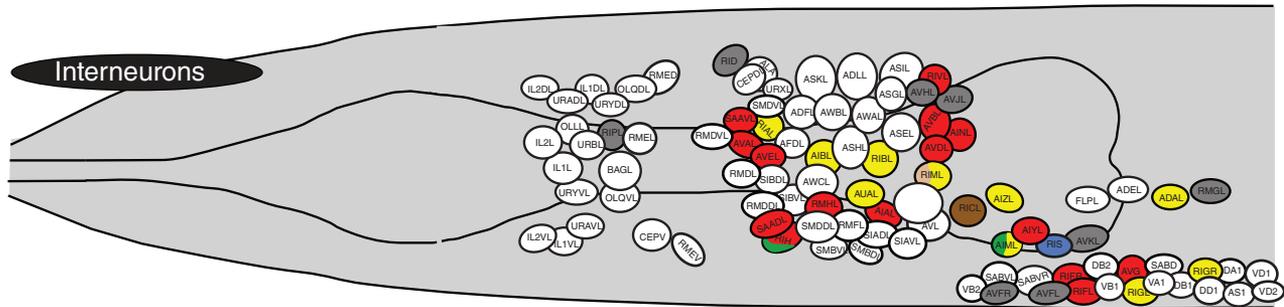
### Coregulation Versus Piecemeal Regulation

Coming back to the question posed above—what do the transcription factors that control terminal identity features of a neuron exactly do? As discussed already above, a substantial phenotypic space can be probed for most individual neuron types—from anatomy, to connectivity, to molecular markers. It is particularly informative to consider the large panel of molecular markers, i.e., the molecular maps described above (and illustrated in Figure 2), which describe a host of biochemically linked features (e.g., enzymes that act in a pathway to synthesize a neurotransmitter), but more importantly, also biochemically unlinked molecular features of a neuron (as illustrated schematically in Figure 7(a)). The unlinked nature of many of these molecular markers makes it *a priori* entirely plausible to hypothesize that distinct biochemical features are organized into distinct regulons, i.e., are controlled via distinct sets of transcription factors. Notably, however, this does not appear to be a predominant theme. On the contrary, the in-depth analysis of the differentiation programs from a number of isolated neuron types—the light touch sensory neurons, GABAergic neurons, cholinergic AIY interneurons, glutamatergic ASE sensory neurons or cholinergic ventral nerve cord motor neurons—reveal that scores of molecular markers that are coexpressed by any of these specific neuron types are *coregulated* by transcription factors expressed in these neurons (examples shown in Figure 7).<sup>7,87,91,121,126</sup> In each of these cases, the

binding sites for the respective transcription factors are known and in each of these cases, the regulation of the terminal identity markers is thought to be largely direct (Figure 7). As expected from the profound molecular defects of these neurons, the neurons are not functional and display various anatomical defects, including axonal outgrowth defects and synaptic connectivity defects. Yet in all cases examined, the neurons are still generated and even still express pan-neuronal features. In other words, the adoption of pan-neuronal identity can be genetically separated from the adoption of neuron type-specific identity. The above mentioned transcription factors have been called ‘Terminal Selectors’ due to the profound impact they have on neuronal identity. The salient features of terminal selectors are summarized in Box 1 (recently reviewed in Ref 139).

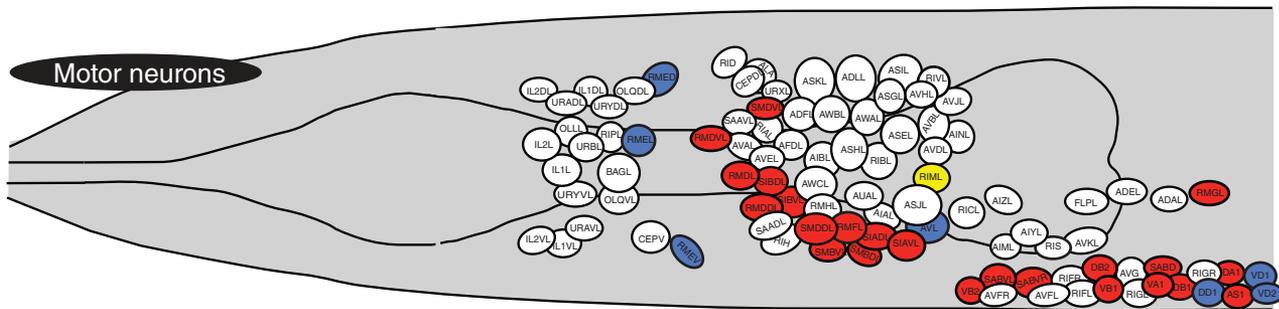
The vast majority of terminal selector targets are, by definition, terminal effector/structural genes, i.e., genes encoding for proteins involved in defining the neuron-type specific structural and functional features of a neuron (Figure 7). This sets terminal selectors apart from earlier acting transcription factors whose primary role is to trigger ensuing waves of regulatory factors (these factors are not covered here; see another review that considers these earlier acting factors<sup>145</sup>). Nevertheless, some terminal selector targets encode for regulatory factors that control specific *subroutines*, likely in conjunction with the upstream terminal selector. For example, the *ttx-3/ceb-10* terminal selector complex directly activates the expression of the homeobox gene *ceb-23* in the AIY interneurons and these factors together control expression of the G-protein-coupled receptor *sra-11*.<sup>108</sup> This regulatory architecture is a classic example of a feedforward regulatory motif and is found in other neuron types as well (Box 2).<sup>115,121,142,146</sup>

Since the in-depth analysis of a number of select cases mentioned above (Figure 7), coregulation of structural genes has been examined in many different neuron types, albeit most often in less depth (summarized in Figures 4–6). Much of this analysis was performed in the context of mapping glutamatergic and cholinergic neurotransmitter identity throughout the nervous system.<sup>8,78</sup> With this neurotransmitter map in hand, a host of regulatory factors expressed in either glutamatergic or cholinergic neurons were analyzed for how their genetic removal affects the acquisition of the respective neurotransmitter identity. In those cases where an effect was observed, it was tested whether other, unlinked biochemical identity features are also affected. In most cases, it was found that a factor that regulates neurotransmitter identity also affects the expression of other identity



Inter	Number	Neurotransmitter	Inducers	Reference
ADA	2	Glu		
AIA	2	ACh	<i>txx-3</i> (8/8)	107,108
AIB	2	Glu	<i>unc-42</i> (4/4)	*
AIM	2	Glu + 5HT	<i>unc-86</i> (3/3), <i>ceh-14</i> (3/3)	78,109,110
AIN	2	ACh		
AIY	2	ACh	<i>txx-3</i> , <i>ceh-10</i> (42/42)	7,108
AIZ	2	Glu	<i>unc-86</i> (3/3)	78
AUA	2	Glu	<i>ceh-6</i> (4/4)	78
AVA	2	ACh	<i>unc-3</i> (2/11), <i>unc-42</i> (3/8), <i>fax-1</i> (2/6)	93–111,112
AVB	2	ACh	<i>unc-3</i> (2/3)	8
AVD	2	ACh	<i>unc-3</i> (2/7), <i>unc-42</i> (2/7), <i>cfi-1</i> (2/5)	8,105,111,112
AVE	2	ACh	<i>unc-3</i> (2/8), <i>unc-42</i> (3/8), <i>fax-1</i> (3/6)	8,93,111,112
AVF	2	unknown		
AVG	1	ACh	<i>lin-11</i> (3/3), <i>ast-1</i> (2/2)	40,113
AVH	2	unknown		
AVJ	2	unknown		
AVK	2	unknown	<i>unc-42</i> (2/3), <i>fax-1</i> (2/3)	114
BDU	2	unknown	<i>pag-3</i> (10/10), <i>unc-86</i> (10/10), <i>ceh-14</i> (3/10)	115
CAN	2	unknown MA		
DVA	1	ACh	<i>unc-3</i> (2/8)	8
DVC	1	Glu	<i>ceh-14</i> (2/2)	78
LUA	2	Glu		
PVC	2	ACh	<i>ceh-14</i> (2/2), <i>cfi-1</i> (2/2), <i>unc-3</i> (2/7)	8,105
PVN	2	ACh	<i>unc-3</i> (2/2), <i>ceh-14</i> (2/2)	8
PVP	2	ACh	<i>lin-11</i> (3/3), <i>unc-30</i> (3/3)	8,40
PVQ	2	Glu	<i>pag-3</i> (1/1), <i>zag-1</i> (1/1)	116–118
PVR	1	Glu	<i>unc-86</i> + <i>ceh-14</i> (4/4)	78
PVT	1	unknown	<i>ceh-14</i> (5/10), <i>lim-6</i> (5/10) **	
PVW	2	unknown		
RIA	2	Glu		
RIB	2	GABA(+ ACh)		
RIC	2	Octopamine		
RID	1	unknown	<i>lim-4</i> (4/6)	71
RIF	2	ACh		
RIG	2	Glu		
RIH	1	ACh & 5HT	<i>unc-86</i> (5/5)	8,109
RIP	2	unknown		
RIR	1	ACh		
RIS	1	GABA	<i>nhr-67</i> (5/5), <i>lim-6</i> (8/8)	71,86,119
RIV	2	ACh	<i>unc-42</i> (2/2)	8
SAA	4	ACh	<i>sox-3</i> (3/3)	104
SDQ	2	ACh		
	42	77	26/42 interneuron classes	
			46/77 total interneurons	

**FIGURE 5 |** Terminal regulators of interneurons. Schematic worm with only interneurons colored and tabular summary of terminal regulators of neuronal identity. See legend to Figure 4 for an explanation of colors and numbers. \* indicates our own unpublished data. \*\* *lim-6* and *ceh-14* regulate, in conjunction with the *lin-14* heterochronic gene, temporally controlled but not continuously expressed genes in PVT.<sup>120</sup>



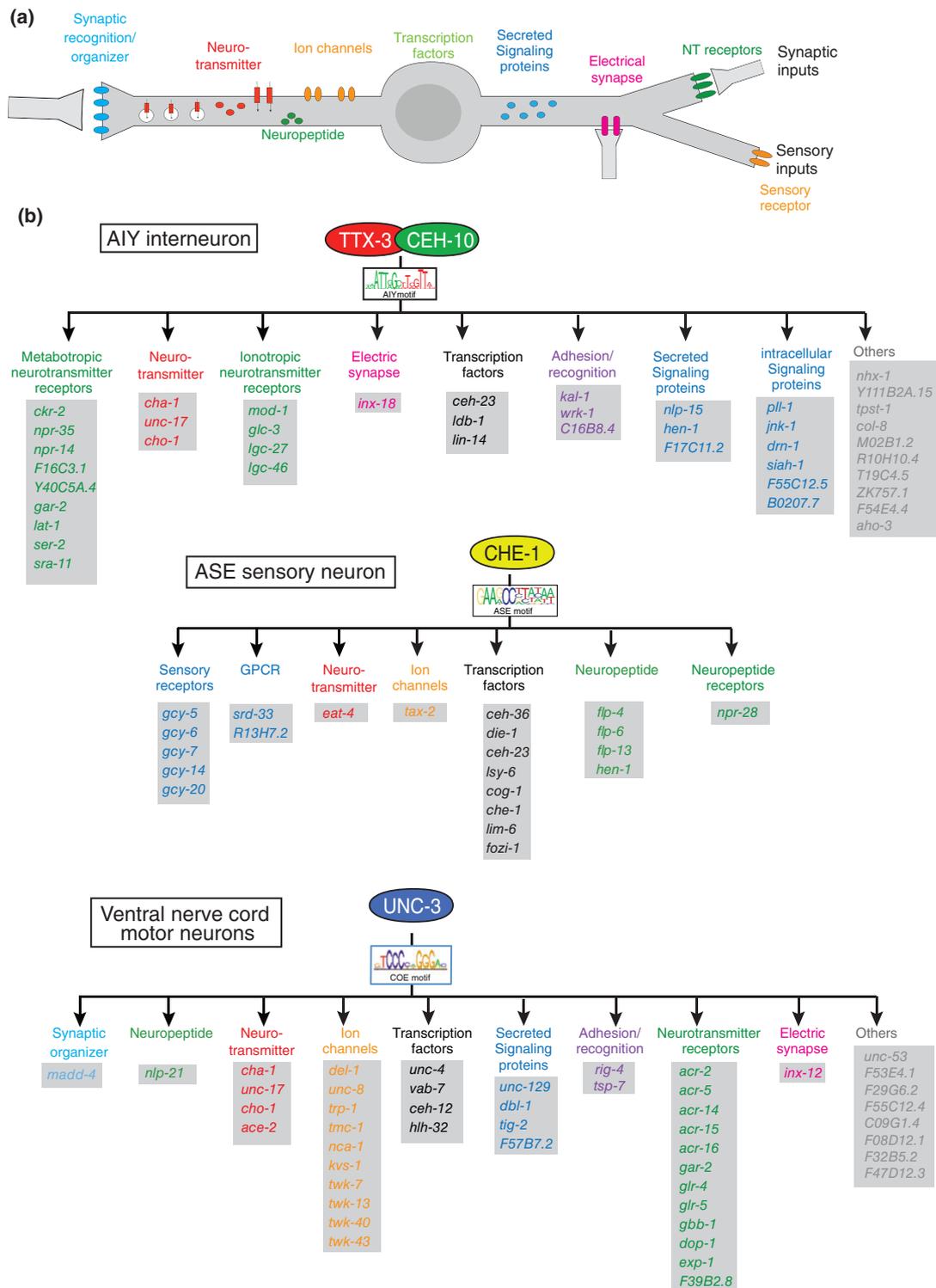
Motor	Number	Neurotransmitter	Inducers	Repressor	Reference
AS	11	ACh	<i>unc-3</i> (17/22)		121
AVL	1	GABA	<i>nhr-67</i> (4/4), <i>lim-6</i> (5/5)		86,119
DA	9	ACh	<i>unc-3</i> (26/31)	<i>unc-4</i>	42,121–124
DB	7	ACh	<i>unc-3</i> (27/32)	<i>vab-7</i>	42,121,124,125
DD	6	GABA	<i>unc-30</i> (10/10)	<i>irx-1</i>	126–129
DVB	1	GABA	<i>lim-6</i> (1/5)		86,119
HSN	2	ACh & 5HT	<i>unc-86</i> (12/12), <i>sem-4</i> (12/12)		130
PDA	1	ACh	<i>unc-3</i> (5/5)		8,131
PDB	1	ACh	<i>unc-3</i> (2/2)		8
RIM	2	Glu + Tyr			
RMD	6	ACh	<i>unc-42</i> (3/3)		8
RME	4	GABA	<i>nhr-67</i> (6/6), <i>ceh-10</i> (4/4), <i>tab-1</i> (4/4)	<i>ahr-1</i>	86,132
RMF	2	ACh			
RMG	2	unknown			
RMH	2	ACh			
SAB	3	ACh	<i>unc-3</i> (10/10)		42
SIA	4	ACh			
SIB	4	ACh			
SMB	4	ACh	<i>lim-4</i> (5/5)		133
SMD	4	ACh	<i>unc-42</i> (2/2)		8
VA	12	ACh	<i>unc-3</i> (23/26)	<i>unc-4</i>	42,121–124
VB	11	ACh	<i>unc-3</i> (26/29)	<i>ceh-12</i>	42,121,124,134
VC	6	ACh			
VD	13	GABA	<i>unc-30</i> (10/10)	<i>unc-55</i> , <i>alr-1</i>	126–129,135,136
	24	118	17/24 motor neuron classes		
			96/118 total motor neurons		

**FIGURE 6** | Terminal regulators of motor neurons. Schematic worm with only motor neurons colored and tabular summary of terminal regulators of neuronal identity. See legend to Figure 4 for an explanation of colors and numbers.

features.<sup>8,78</sup> In a number of cases, the substantial number of markers tested (>20; Figures 4–6) make a compelling case that factors that regulate neurotransmitter identity regulate large sets of genes expressed in the terminally differentiated neuron, i.e., that many distinct identity features of a terminally differentiated neuron are coregulated. Even in cases where the sample size of examined marker is relatively small, it appears reasonable to extrapolate the effect to the many other genes expressed in the terminally differentiated neuron.

Even though the concept of coregulation appears to apply broadly, the cholinergic command interneurons, a group of interconnected neurons that innervate ventral nerve cord motor neurons, present a notable exception. In these neurons, the *unc-3*

transcription factor, which coregulates many, independent terminal identity features (including neurotransmitter identity) in ventral nerve cord motor neurons, appears to only control the acquisition of cholinergic neurotransmitter identity for all command interneurons.<sup>8</sup> More than a dozen additional markers expressed in select subsets of command interneurons are not affected in *unc-3* mutants. The additional identity markers (a good number of them encoding for ionotropic Glu receptors) are in turn controlled in a cell-type specific, piecemeal manner by the *unc-42* homeobox gene, the *fax-1* nuclear hormone receptor, or the *cfi-1* ARID-type transcription factor.<sup>93,105,111,112</sup> Hence, it appears that in some cases, neuronal identity is controlled in a piecemeal manner through parallel acting identity regulators.



**FIGURE 7 |** Terminal selector regulons. (a) Schematic illustration of terminal identity features that are controlled by terminal selector-type transcription factors. These identity features are continuously expressed throughout the life of a neuron. (b) Three examples of terminal selector regulons. All genes shown here were shown to be direct targets of the indicated terminal selectors.<sup>7,121,138</sup> In addition to the genes shown here, scores of additional genes have been identified as being expressed in the respective neuron types and containing binding sites for the respective regulators, but these additional genes have not been validated for terminal selector-dependence.

## BOX 1

## TERMINAL SELECTORS OF NEURONAL IDENTITY

Terminal selectors are transcription factors that induce expression of the terminally differentiated properties of mature neuron types.<sup>139</sup> These factors work mostly in combinations, e.g. as heterodimers that cooperatively bind DNA<sup>7,140</sup> to directly control the expression of effector genes that define the functional properties of a neuron type. Terminal selectors are continuously expressed throughout the life of a neuron and are required to not only induce but also maintain the differentiated state of a neuron, a feat achieved mostly through autoregulation (Box 2).<sup>137</sup> Terminal selectors are not only required to induce specific differentiation programs, but are also sufficient to do so, albeit only in some cellular contexts.<sup>7,115,141</sup> This context dependency is likely dictated by the need of proper cofactors,<sup>115</sup> but also by a chromatin environment that may be refractory to terminal selector activity.<sup>141</sup>

However, at this point we cannot exclude that the above mentioned factors (*unc-3*, *unc-42*, and *fax-1*) are mere subroutine regulators that operate in the context of aforementioned feedforward motifs, downstream of as yet unknown terminal selectors for command interneuron identity.

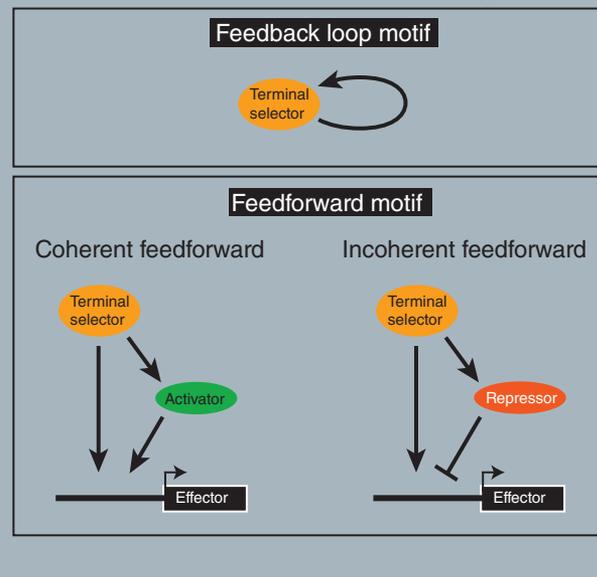
## Other Features of the Regulatory Map

Two other themes of the regulatory map are striking. First, transcription factors are used over and over again in distinct neuron types. Remarkably, four transcription factors are required to specify the identity of 50 distinct neuron classes, almost half of all neuron types in the *C. elegans* nervous system (*unc-3*: 16 neuron classes; *unc-86*: 14 neuron classes; *ceb-14*: 10 neuron classes; *unc-42*: 10 neuron classes). Note that these four transcription factors are deeply conserved (*unc-3* = EBF/Collier; *unc-86* = Brn3; *ceb-14* = Lhx3/4, *unc-42* = Prop1). In each neuron class, these factors appear to act in combination with other factors and this combinatorial code appears to provide specificity. This combinatorial coding scheme is displayed in Figure 8. For example, the POU homeobox gene *unc-86* acts as a regulator of terminal identity in 14 distinct neuron classes and it appears to

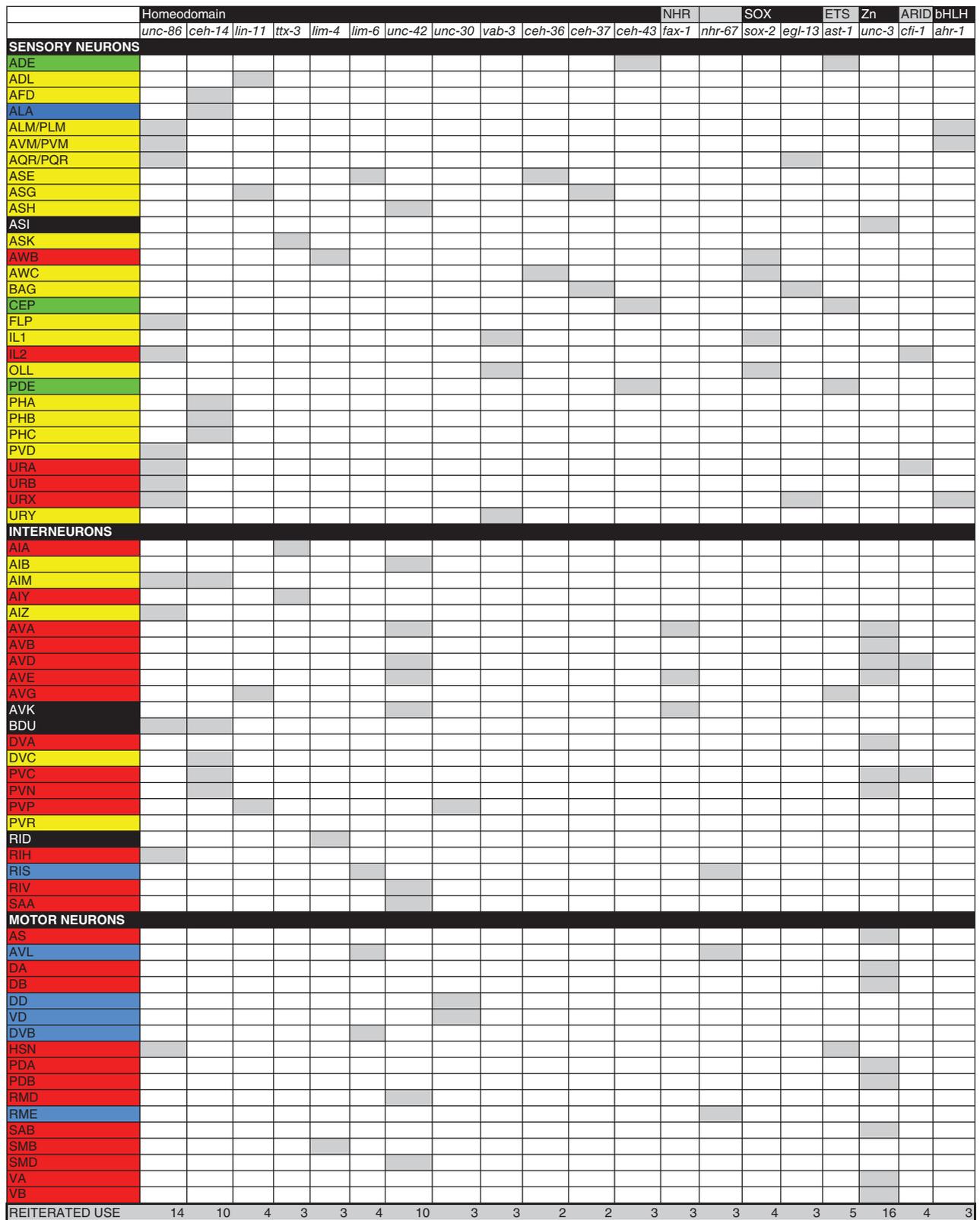
## BOX 2

## REGULATORY NETWORK MOTIFS

Three types of network motifs<sup>142</sup> employed in the context of neuronal specification and terminal selector function in *C. elegans*. The autoregulatory feedback loop is employed to ensure maintained terminal selector expression and, hence, maintained terminal effector gene expression.<sup>137,143</sup> Feedforward loops involve intervening transcription factors. Coherent feedforward loops have been found in other systems to filter transient input signals,<sup>142</sup> but even though frequently observed,<sup>108,115</sup> their function in terminal selector-mediated gene expression control remains to be shown. Incoherent feedforward loops occur in the context of *C. elegans* motor neuron class specification or lateralization of gustatory neuron function,<sup>121,144</sup> as discussed in the text.



operate in conjunction with specific cofactors in distinct neuron classes, such as the LIM homeobox gene *mec-3* in touch sensory neurons,<sup>140</sup> the *ceb-14* LIM homeobox gene in a number of distinct interneurons,<sup>78</sup> the *pag-3* Zn finger transcription factors in one specific interneuron type,<sup>115</sup> or the *ttx-3* LIM homeobox gene in a neurosecretory sensory neuron.<sup>107</sup> When reused, the same transcription factor may not necessarily perform as a terminal selector: it can work as a terminal selector in one neuron type or as a subroutine regulator in another. For example, *ceb-14* operates as a terminal selector in 10 different neuron types,<sup>78,84,85</sup> but operates only as



**FIGURE 8 |** Redeployment of regulators of terminal neuronal identity in distinct neuron types. Data are extracted from Figure 4–6. Coloring scheme indicates neurotransmitter identity: yellow = Glu, red = ACh, green = aminergic, black = unknown. Only transcription factors that operate in >1 class are shown

a subroutine regulator (controlling neuropeptide expression) in the BDU neurons.<sup>115</sup>

Another theme is the striking preponderance of employment of homeodomain transcription factors. While these transcription factors make up only ~10% of all transcription factors in the *C. elegans* genome, a vast number of identified terminal regulators are homeodomain transcription factors and those that are not most frequently collaborate with a homeodomain transcription factor (homeodomain transcription factors are underlined in Figures 4–6). Reusage of the same transcription factors, as well as the preponderance of homeodomain transcription factors may indicate the evolutionary history of cell types in the nervous system. Homeodomain proteins may have had very early roles in specifying ancestral neuron types.

Are there other obvious, underlying themes or logical patterns by which transcription factors are used and reused? If one considers the lineage history of each individual neuron type, no obvious patterns emerge. First, if one just considers terminal identity features, it is already evident that the, e.g., neurotransmitter identity does not obviously correlate with lineage (Figure 3). Second, transcription factor expression profiles also show a lack of correlation with lineage. This is illustrated by mapping the expression pattern of four transcription factors that control the terminal identity of at least 50 distinct neuron types on the lineage diagram (Figure 3). The color-coding in this illustration also shows that neurotransmitter identity generally does not correlate with transcription factor usage; i.e., the same transcription factor can operate in neurons of different neurotransmitter identities. The only exception is the *unc-3* transcription factor, which represents a remarkable case of a transcription factors not only being committed to defining only cholinergic neuron identity, but doing so in the context of a specific circuit, the VNC motor circuit.<sup>8</sup>

## DIVERSIFICATION BY REPRESSORS

As summarized in Figures 4–6 not every factor that controls terminal neuron differentiation is an inducer, i.e., a likely activator of some, many, or all terminal features of a neuron. In fact, one of the earliest identified regulatory factors in *C. elegans* is the *unc-4* homeobox gene.<sup>16</sup> *unc-4* mutants were initially characterized as synaptic specificity mutants, in which the synaptic input to a specific motor neuron subtype (VA) is altered in a manner that resembles that of another motor neuron subtype (VB).<sup>16</sup> *unc-4*

has since been shown to repress not just VB-specific synaptic wiring patterns in the VA neurons but other identity features of the VB neurons as well.<sup>122</sup> Additional repressor proteins (e.g., *cog-1* or *vab-7*) have since been identified whose loss results in de-repression or entire switches of neuronal identity programs.<sup>125,148</sup> The repressor nature of proteins like UNC-4 or COG-1 is indicated by their proven or probable direct association with the corepressor protein UNC-37 (orthologous to *Drosophila* Groucho), which recruits histone deacetylases to repress gene expression.<sup>148,149</sup>

Intriguingly, the repressor proteins mentioned above exert their negative effect (either directly or indirectly) on terminal effector genes that are themselves direct targets of terminal selectors. For example, the acetylcholine receptor subunit *acr-5* is expressed in B-type motor neurons and is a direct target of *unc-3* in these neurons.<sup>121</sup> In A-type motor neurons, however, *acr-5* is repressed by *unc-4*, and *unc-4* is itself a target of *unc-3*.<sup>121,122</sup> *unc-3* therefore ensures that one of its direct targets is only expressed in a subtype of motor neurons, by inducing the expression of a subtype-specific repressor, *unc-4*. This regulatory configuration constitutes an *incoherent feedforward motif* (Box 2).<sup>142</sup>

The principle of modifying a terminal selector-induced differentiation program through selective repression in neuronal subtypes has been observed in another intriguing neurobiological context, namely the development of left/right asymmetric neuronal subtype specification. The left and right ASE neurons are the two main gustatory neurons in the worm and their terminal differentiation program is directly controlled by the *che-1* terminal selector.<sup>80</sup> While the majority of terminal features of ASE are expressed in both ASE neurons, a subset of putative chemoreceptor proteins, encoded by the *gcy* genes, are expressed exclusively in the left or the right ASE neuron. *gcy* genes are also direct targets of *che-1* but the ability of *che-1* to activate *gcy* genes is restricted by ASEL- or ASER-subtype specific regulatory factors.<sup>144</sup> Two of these repressors are the miRNA *lisy-6* (ASEL-specific) and its target, the homeobox gene *cog-1* (ASER-specific). Both *lisy-6* and *cog-1* are also direct targets of *che-1*.<sup>150,151</sup>

The overall logic of incoherent feedforward regulation is to diversify a *ground state* into various sub-states. In an evolutionary context, one could envision an ancestral state in which multiple neurons were induced by the same transcription factor; the recruitment of a repressor in subsets of these neurons may have then diversified the spectrum of targets of the original inducer.

## REGULATION OF PANNEURONAL FEATURES

One aspect of neuronal differentiation that has been remarkably unexplored in most model organisms is the acquisition of panneuronal features. A recent study addressed this problem in some depth, using a panel of genes that are expressed in all neurons throughout the nervous system (mostly, but not exclusively, genes involved in the synaptic vesicle cycle).<sup>152</sup> Some surprising themes emerged from the analysis of the regulation of more than a dozen panneuronal genes. To appreciate these themes it is important to first consider the *cis*-regulatory architecture of genes that are expressed in a neuron-type specific manner. As schematically indicated in Figure 9, *cis*-regulatory control regions of neuron-type specific genes are organized in a modular manner, composed of response elements to neuron-type specific terminal selectors. For example, the choline reuptake transporter *cho-1* (involved in clearance of the breakdown product of ACh at cholinergic synapses) contains separable modules with validated binding sites for TTX-3/CEH-10, required and sufficient for expression in the cholinergic AIY interneurons and a module with a binding site for UNC-3, which is required and sufficient for expression of *cho-1* in ventral nerve cord motor neurons.<sup>121</sup> Mutation of these sites in the context of fosmid-based reporters indicates the requirement of these single sites for expression in specific neuron types. This theme reiterates over many of the other neuron-type specific terminal effector genes tested. The *cis*-regulatory control regions of pan-neuronal genes are organized in a strikingly distinct manner, characterized by redundant, independently acting regulatory inputs (Figure 9).<sup>152</sup> Viewed from an evolutionary perspective, this regulatory architecture indicates that pan-neuronal genes have accumulated responsiveness to many different regulatory factors expressed in a terminally differentiated neuron, perhaps with the purpose of ensuring robustness of gene expression.

## HOW IS THE REGULATORY MAP ESTABLISHED?

While terminal differentiation programs have been described in many neuron types throughout the *C. elegans* nervous system, much less is known about earlier neuronal patterning events in *C. elegans*. One obvious question is how the expression of terminal selector-type transcription factors is restricted to specific cell types and therefore, how the regulatory map

described above is established. An earlier review has covered a few aspects of neuronal lineage control in *C. elegans*.<sup>145</sup> I will focus here instead on three aspects of early neuronal patterning, some of which directly relating to the control of terminal selectors.

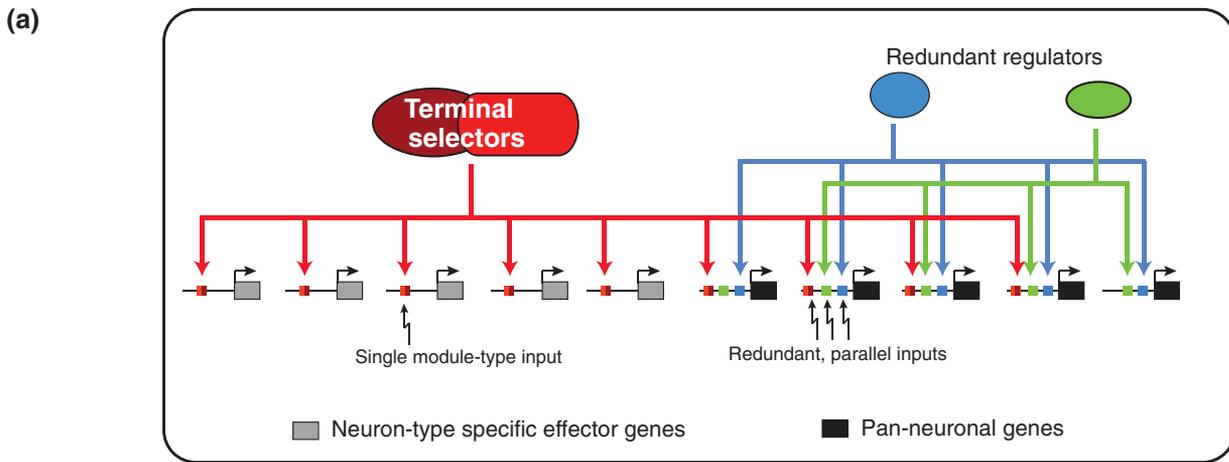
### The Binary Wnt System

In the 1990s, Ralf Schnabel, Jim Priess and others discovered an intriguing binary patterning system that operates during *C. elegans* embryogenesis.<sup>153,154</sup> A noncanonical Wnt signaling system results in an anterior/posterior difference in the activity of transcriptional outputs of the Wnt system.<sup>155</sup> This system has subsequently been explicitly shown to also be involved late in embryonic nervous system patterning, directly regulating the expression of terminal selectors of neuronal identity.<sup>156</sup> This work, previously reviewed in Ref 157 provided the first link of terminal patterning of neuronal identity to earlier patterning events, demonstrating a transition from *transient regulatory states* to *terminal, maintained regulatory states*. Recent work describes how this system operates in distinct neuroblasts.<sup>158</sup>

Because of its binary nature, the anterior/posterior patterning system can obviously not act alone to specify the complex expression patterns of terminal selectors. The Wnt output regulators must interact with other transcription factors. The above-mentioned studies identified several such factors as being involved in defining terminal selector expression.<sup>156,158</sup> The multiplicity of regulatory inputs into terminal selector loci has led to the suggestion of an *hourglass regulatory architecture*, in which terminal selectors are nodes that integrate various transient regulatory inputs into a stable, maintained regulatory state.<sup>159</sup>

### Differences and Similarities in Early Patterning—The bHLH and SoxB/C Cases

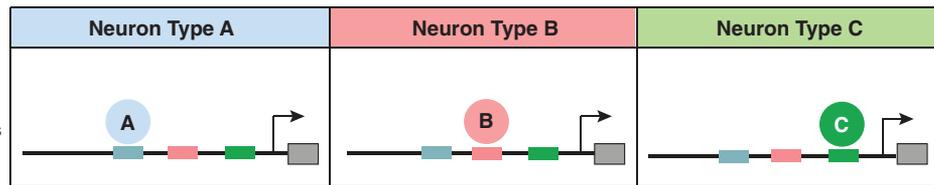
Specific types of basic helix–loop–helix transcription factors operate as proneural genes throughout the animal kingdom and they have also been identified in *C. elegans*. For example, in one case, a proneural gene *hbl-14* controls the neuronal (vs hypodermal) identity of a lineage that produces the gustatory ASE neurons.<sup>160</sup> As expected, *hbl-14* is expressed earlier in the lineage than the terminal selector of ASE identity (the *che-1* transcription factor), but its expression persists long enough to make it conceivable that *hbl-14* may be involved in directly controlling *che-1* expression, perhaps in conjunction with the nuclear



**(b) Types of modular regulatory architecture**

**Non-redundant modular architecture**

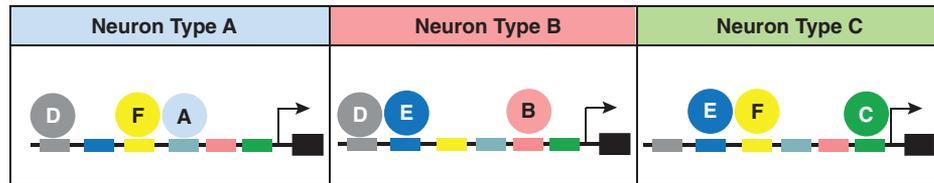
EXAMPLE: Expression of neuron-type specific neurotransmitter pathway genes in multiple distinct neuron types  
A, B, C: terminal selectors



Individual *cis*-regulatory modules are: - REQUIRED for cell type specific expression  
- SUFFICIENT for cell type specific expression

**Redundant modular architecture**

EXAMPLE: Panneuronal genes  
A, B, C: terminal selectors  
D, E, F: Parallel factors, operating in many different neuron types



Individual *cis*-regulatory modules are: - NOT REQUIRED for expression in any neuron type  
- Sufficient to drive OVERLAPPING expression in distinct neuron types

**FIGURE 9** | Regulation of pan-neuronal identity. (Reprinted with permission from 152. Copyright 2015)

hormone receptor *nhr-67*, another upstream regulator of *che-1* expression.<sup>132</sup> Similarly, the postembryonically generated touch receptor neurons AVM and PVM fail to be generated in animals lacking the proneural gene *lin-32/Atonal*,<sup>161</sup> which may be involved in directly or indirectly activating expression of the terminal selector of AVM/PVM identity, *unc-86*.<sup>162</sup> Whether proneural bHLH genes are required for neuronal fate induction in all neurons of the nervous system (a notion that is surprisingly unexplored in other systems) is currently being investigated.

A recent study shows that one aspect of early neuronal patterning in *C. elegans* displays a remarkable difference to early neuronal patterning in other

organisms.<sup>104</sup> The HMG box transcription factor SOX-2, a member of the SoxB subfamily, is deeply conserved sequence-wise throughout the animal kingdom. Its function has been addressed in a wide range of animals from deuterostomes (chordates, echinoderms, and hemichordates) and protostomes (Ecdysozoa and Lophotrochozoa) to even earlier diverging animal lineages such as cnidarians. In all these cases, *sox-2* was shown to be expressed in neuronal precursors (upstream of the above-mentioned proneural bHLH genes) and whenever functional evidence was available, a role for *sox-2* in nervous system development was elucidated.<sup>163</sup> Curiously, *sox-2* function in *C. elegans* is different. *sox-2* is not

broadly expressed in neuronal precursors and *sox-2* has no function in embryonic neurogenesis.<sup>104</sup> Again in contrast to other organisms, the SoxC-type *sox-3* gene also has no role in embryonic neurogenesis.<sup>104</sup> *C. elegans sox-2* appears to rather be involved in driving terminal differentiation of select neuron types, as well as in the specification of a subset of postembryonic neuroblast.<sup>97,104</sup> The absence of a neurogenic *sox-2* function in *C. elegans* may relate to what *sox-2* does in other organisms—maintaining the pro-neuronal developmental potential of neuroepithelial cells during phases of cell proliferation in the developing nervous system.<sup>163</sup> Such expansion may not occur in *C. elegans* embryogenesis.

### Redundancy of Early Regulators

It is remarkable how few regulators of early neuronal patterning have been retrieved through genetic mutant screens in *C. elegans*. At first sight, a relatively trivial explanation could be that essential pleiotropic functions of regulatory factors may hinder retrieval from genetic screens. However, hypomorphic alleles of essential early patterning genes or even regulatory null alleles (i.e., loss of a gene only in specific cells due to mutations in *cis*-regulatory elements) have been retrieved in screens for terminal differentiation mutants. For example, a mutant allele of the essential Distalless-like homeobox gene *ceb-43*, retrieved from a genetic screen, disrupts dopaminergic neuron differentiation and is defined by a deletion of a distal enhancer required for *ceb-43* expression in dopaminergic neurons.<sup>82</sup> Also, RNAi-based screens have been conducted for early regulators of ASE lineage specification and differentiation, recovering little more than the above-mentioned, and somewhat expected proneural bHLH factor for this lineage, *hlh-14*.<sup>160</sup> One very intriguing possibility for the poor retrieval rate of early patterning genes is suggested by an older study<sup>164</sup> and a more recent study.<sup>165</sup> Priess and colleagues found that early patterning in the ABa lineage, which generates about half of the *C. elegans* nervous system, is controlled by two redundantly acting T-box genes, *tbx-37* and *tbx-38*.<sup>164</sup> Both genes are close paralogs and both need to be genetically eliminated to observe patterning defects. Notably, T-box genes expanded significantly in *C. elegans*, and many come in closely paralogous pairs.<sup>166</sup> It will be most interesting to determine whether it is a common theme that T-box factors act redundantly during early patterning decisions.

An intriguing, more recent example of redundancy shows that two unrelated homeobox genes, the Pitx-type homeobox gene *unc-30* and the Otx-

type homeobox gene *ceb-36* act redundantly in early neuronal lineage decisions.<sup>165</sup> Both genes act as terminal selectors in defined neuronal cell types,<sup>100,126</sup> but apparently also moonlight as patterning factors at earlier time points in lineages where their expression overlaps. It is tantalizing to think that early patterning in *C. elegans* is highly buffered through redundantly acting factors.

### CONCLUDING REMARKS

More than half a century after Sydney Brenner first formulated his *C. elegans* research program,<sup>1,2</sup> it is deeply satisfying to see how the *C. elegans* field has moved toward fulfilling Sydney Brenner's vision of using the tools of the microbial genetic trade, in combination with his visionary map making efforts, to understand how a nervous system develops. One reason this research program has been particularly successful in the nervous system is the lack of pleiotropies associated with regulators of terminal neuronal identity. In fact, such lack of pleiotropies was recognized by Brenner very early in his analysis of behavioral mutants by electron micrographical analysis.<sup>167</sup> Molecular, functional and expression studies subsequently revealed that most transcription factors that are components of the regulatory map are exclusively expressed in the nervous system, i.e., they do not have what could be essential functions elsewhere which could have prevented their retrieval from forward genetic screens. Within the nervous system many of these factors also appear to be committed to controlling terminal differentiation, without being involved in earlier patterning events. One exception to this notion are the *unc-30* and *ceb-36* terminal selectors, which, apart from their terminal selector function in distinct neuron types, have redundant function in controlling earlier lineage decisions.<sup>165</sup> These findings illustrate the importance of not solely relying on forward genetic screens, but also taking into account expression patterns and hence possibly redundant gene functions.

One major future challenge lies in connecting terminal regulators of neuronal identity to early lineage patterning events. Using automated lineage tracing in combination with RNAi-mediated gene knockdown, Du et al. have recently identified a large number of genes with roles in early lineage specification.<sup>168</sup> How these genes are coupled to the induction of expression of terminal selectors requires future exploration.

In addition to studying early neuronal patterning events, a great number of questions remain at

the level of terminal differentiation programs. For example, the nature of the combinatorial codes of transcription factors that control the differentiated state should be more extensively characterized, perhaps with a specific focus on the ~100 homeobox genes encoded by the *C. elegans* genome. Importantly, we need a much more comprehensive understanding of the extent to which terminal differentiation programs are controlled in a coregulatory manner by terminal selector-type transcription factors versus being regulated in a piecemeal manner by distinct cohorts of transcription factors. One important step in this direction needs to be a systematic transcriptome analysis of each and every neuron in the worm. This is now technically feasible and it is easy to predict that the worm, after having been the first organism with a lineage, connectome, and genome, will also be the first with a complete expression atlas with single-cell resolution. The

regulatory programs that control panneuronal genes (e.g. synaptic vesicle machinery) also need to be better understood. The plasticity of the terminally differentiated state will also need to be examined on a much more detailed level. For example, how do postmitotic, embryonically generated neurons alter their differentiated state at defined postembryonic time points? How does circuit activity impinge on the differentiated state of specific neuronal circuit components? How does the sexual identity of the organism impinge on neuronal differentiation? Many of these questions can be addressed by continuing to pursue Sydney Brenner's vision, building higher resolution and now multidimensional maps (gene expression maps at distinct time points, under distinct external conditions), and by then exploiting the unique strengths of the *C. elegans* model system to genetically dissect these molecular maps through classic mutant analysis.

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