TRANSGENICS WITH GONADAL MICROINJECTION IN DIOECIOUS CAENORHABDITIS NEMATODES

Le Tho Son[™], Nguyen Thi Thu

College of Forestry Biotechnology and F-School, Vietnam National University of Forestry, Hanoi, Vietnam

^{III}To whom correspondence should be addressed. E-mail: sonlt@vnuf.edu.vn

Received: 09.12.2023 Accepted: 18.03.2024

ABSTRACT

Biological research with nematode models is increasing to understand the phenomenon of molecular genomes, genetics, and biological comparison. Different methods have been developed to produce genetically modified organisms that have the desired characteristics. Found in 1985, the gonadal microinjection in *Caenorhabditis elegans* has been obtained greatly effective for transformations. To other nematodes, this transformation methodology could play an important role in studying genetics and genomics within and among the species. Research methods with several other non-*C. elegans* round nematodes were adopted the microinjections to do transformation. In this research of transformation, we report the results of transgenics for different plasmids in eight dioecious species (*C. portoensis, Caenorhabditis* sp. 33, *C. brenneri, C. nigoni, C. sinica, C. imperialis, C. nouraguensis*, and *C. remanei*). We gained the stable transgenes of the first four species and failed the last four.

Keywords: and rodioecious, *Caenorhabditis*, fluorescent protein, microinjection, *myo-2*, *sur-5*, transformation.

INTRODUCTION

New species of *Caenorhabditis* nematodes are being discovered every year (Kiontke *et al.*, 2011; Felix *et al.*, 2014; Dieter Slot, 2017; Kanzaki *et al.*, 2018). A detailed study of their biology can be fruitful, especially for comparative questions in evolutionary biology with the *Caenorhabditis* nematodes. In this respect, *C. briggsae* has been the main model (Gupta *et al.*, 2007), partly because it is also a hermaphroditic species and was the second nematode to be sequenced (Stein *et al.*, 2003). Inclusion of other species has increased over time, and their study has covered topics such as evolutionary developmental biology (Kiontke *et al.*, 2007; Braendle, Felix, 2008; Huang *et al.*, 2014), sperm competition and sperm size evolution (LaMunyon, Ward, 1999; Vielle *et al.*, 2016), speciation and hybrid incompatibility (Woodruff *et al.*, 2010; Ross *et al.*, 2011; Ting *et al.*, 2014; Bi *et al.*, 2015), and genome evolution (Le *et al.*, 2017; Yin *et al.*, 2018).

Many of the comparative studies would benefit from suitable tools to conduct genetic manipulations. As satellite species to the well-known model C. elegans, other Caenorhabditis species can adapt many preexisting tools to engineer the genome, for example, transgenesis (Rieckher et al., 2009), CRISPR/Cas9 (Clustered regularly interspaced palindromic short repeats/CRISPR-associated protein 9) (Lo et al., 2013), TALENS (transcription activatorlike effector nucleases) (Lo et al., 2013; Wei et al., 2014a; Wei et al., 2014b), ZFNs (zincfinger nucleases) (Wood et al., 2011), MosTIC (Mos1 excision-induced transgeneinstructed gene conversion) (Robert, Bessereau, 2007), and MosSci (Mos1mediated Single Copy Insertion) (Frokjaer-Jensen et al., 2008).

Transgenesis in C. elegans is typically achieved through gonadal microinjection (Stinchcomb et al., 1985; Evans, 2006) or microparticle bombardment (Praitis et al., 2001). Although both techniques are used in nematode species (Hashmi et al., 1995; Higazi et al., 2002; Grant et al., 2006; Li et al., 2006; Semple al., 2010; et Cinkornpumin, Hong, 2011; Shao et al., 2012), microinjection is more regularly used because microparticle bombardment needs a good selectable marker, requires large numbers of nematodes (Praitis et al., 2001), and thus is more costly (Praitis, 2006).

In microinjection of the Caenorhabditis nematodes species, one or several plasmids (or DNA molecules) are co-injected into the syncytial gonads of hermaphrodites in androdioecious species (C. elegans, C. briggsae, and C. tropicalis) or females in dioecious species (C. brenneri, C. angaria, and Caenorhabditis sp. 2) (Fire, 1986; Fire et al., 1990; Fire et al., 1991; Kennedy et al., 1993; Fire et al., 1998; Evans, 2006; Nuez, Felix, 2012). The plasmids in the cell assemble into presumably linear extrachromosomal arrays. The formation of arrays seems to be enhanced by overlapping sequences although such homologous homology is not necessary (Stinchcomb et al., 1985; Fire, 1986; Mello et al., 1991). The gonadal microinjection is often aided by the co-injection of a gene rescue or dominant-phenotype markers such as unc-119 (Maduro, Pilgrim, 1995), rol-6 (su1006) (Kramer et al., 1990; Mello et al., 1991), unc-22 (Fire et al., 1991), green fluorescent proteins (GFP), red fluorescent protein (RFP), or yellow fluorescent protein (YFP) (Chalfie et al., 1994; Gu et al., 1998; Miller et al., 1999; Hutter, 2003; Wenick, Hobert, 2004).

The transformation rate varies in F1 generations from low to high, often less than 2% of progeny (Fire, 1986), although rarely as high as 90% (Kadandale et al., 2009). This was found to simultaneously depend on multiple factors, including the sequences, concentration, and size of the injected constructs as well as the practical skill (Fire, 1986; Fire et al., 1990; Mello et al., 1991). The gonadal microinjection method is likely a hallmark of research because it allows any exogenous DNA constructs to be introduced into the organisms. However, the method is technically and biologically challenging and requires excessive effort. This research reports the transgenesis to generate the transgenes for studying transformation ability, the evolution of genome sizes (Le et al., 2017), and the pharynx in eight dioecious Caenorhabditis nematodes.

MATERIALS AND METHODS

Nematode strains: C. brenneri (CB5161), C. nigoni (BRC10093), C. imperialis (EG5716), C. nouraguenis (JU2079), C. portoensis (EG4788), C. sp. 33 (BRC10016), C. remanei (PB4641), and C. remanei (BRC310). Each species was genetically identified by ourselves or kindly provided by collaborators (Le *et al.*, 2017). The worms were regularly cultured repeatedly on nematode growth media seeded with *Escherichia coli* OP50 strains.

Plasmids: pDD04Neo [*C. elegans myo-*2::*GFP*]; pPD158.87 [*C. elegans sur-*5::*GFP*]; pCFj104 [*Pmyo-3::mCherry::unc-*54], and pPD135.83 [pLET::GFP].

General microinjection: Transformation by gonadal microinjection was adapted from androdioecious Caenorhabditis nematodes (Evans, 2006; Kanzaki et al., 2018) for dioecious species. Briefly, female worms at the young adult stage were mounted on the microscopic pad. They were injected bilaterally with one or two drops of the injection mixture into the gonads. In detail, 20 ng/ μ L pDD04Neo with and without 100 $ng/\mu L$ pPD158.87 was injected in C. portoensis; 5, 10, and 20 ng/ μ L of pDD04Neo in Caenorhabditis sp. 33; 20 ng/µL pDD04Neo with 100 ng/µL pPD158.87 in C. brenneri; 20 ng/µL pDD04Neo with and without 100 ng/µL pPD158.87; and 150 ng/µL of *hsp16/4* and hsp16/2 in C. nigoni.

After, the injected worms were recovered with a sugar solution on *E. coli* OP50-seeded plates before three to five L4-stage or young males were added. We looked for the transgenic F1 offspring expressing the fluorescence marker, i.e. GFP, under microscopes in the next days until the injected worm stopped laying eggs. Each transgenic F1 individual was picked onto a single new *E. coli* OP50-seeded plate, on which three to five L4 of the other sex were added to reproduce the F2 progeny. Beyond F2s, each transgene was transferred in chunks to a new *E. coli* OP50-seeded plate every two weeks.

RESULTS

We tested the transgenic ability for eight dioecious species, which were *C. portoensis*, *C.* sp. 33, *C. brenneri*, *C. nigoni*, *C. sinica*, *C. imperialis*, *C. nouraguensis*, and *C. remanei*, with different transgenic plasmid components (Table 1). We conducted every injection trial until getting one transgene for each nematode species.

Stable transgenes with fluorescent expression

Caenorhabditis portoensis: 50 P0 females were injected with two mixtures of constructs (either 20 ng/ μ L pDD04Neo with or without 100 ng/ μ L pPD158.87). Two transgenic F1s were produced from each dose. The unique F1 individual transferred with pDD04Neo produced many transgenic generations that had GFP expression, suggesting this is a stable transgene (Table 1).

Caenorhabditis sp. 33: 104 P0 females were injected with 5, 10, and 20 ng/ μ L of pDD04Neo. All three injected groups produced 318 transgenic F1s. One F1 transgenic individual induced by the highest construct concentration produced the next transgenic generations, indicating that it is a stable transgene (Fig. 1a and Table 1).

Caenorhabditis brenneri: 110 P0 females were injected with 20 ng/ μ L pDD04Neo and 100 ng/ μ L pPD158.87. Nighty-four F1s inherited the constructs and produced 24 stable lines (Table 1).

Caenorhabditis nigoni: 193 P0 females were injected with three mixtures of constructs (20 ng/ μ L pDD04Neo with and

without 100 ng/ μ L pPD158.87, and 150 ng/ μ L of *hsp16/4* and *hsp16/2*). The two first injected groups produced 25 transgenic F1s. Among the F1s, 24 of the first group were reproductive for transgenes in many generations, suggesting they were stable transgenic lines (Table 1).

In our research, we successfully conducted stable transgenes for four dioecious species (C. portoensis, C. sp. 33, C. brenneri, and C. nigoni). They expressed GFP in the pharynx, suggesting that *myo-2::GFP* in pDD04Neo was expressed. Previously, the same transformation was reported for the five dieocious species (C. brenneri, C. angaria, C. sinica, C. nigoni, C. remanei, C. sp. 2, and C. inopinata (Nuez, Felix, 2012), and C. inopinata (Kanzaki et al., 2018)). In our knowledge, proved the first we transformation for C. portoensis and Caenorhabditis sp. 33, indicating that they are accessible to exogenous vectors by the gonadal microinjection (Table 1). We assumed that the pDD04Neo is sensitive to the pharyngeal expression in different Caenorhabditis species.

Non-stable transgenes without fluorescent expression

Caenorhabditis sinica: 115 P0 females were injected with the same construct mixtures to *C. nigoni*. Four F1s were transformed for the injected vectors but none of them were producible for the next transgenic generations (Table 1).

Caenorhabditis imperialis: 28 P0 females were injected with 20 ng/ μ L pDD04Neo and 100 ng/ μ L pPD158.87 for 28 P0 females. None of the F1s and F2s express the transformation (Table 1).

Caenorhabditis nouraguensis: Fourteen P0 females were injected with 20 ng/ μ L pDD04Neo plus 100 ng/ μ L pPD158.87 for 14 P0 females. A single F1 was transgenic but did not continue the transgenes in any progeny generations (Table 1).

Caenorhabditis remanei: 378 P0 females of two strains were injected with nine mixtures of constructs (pDD04Neo with and without pCFj104) that had little changes in vector concentrations. 135 F1 offspring were transgenic but none of them were reproductive for the transgenic F2s (Table 1).



Figure 1. Larvae of *C*. sp. 33 (*myo-2::GFP*) expressing GFP in the pharynx of the F2 offspring generation (white arrow).

Species (strain)	Injection	Plasmid	Trial	P0	F1	F2	Expression
C. portoensis	1 st	20 ng/µL pDD04Neo + 100 ng/µL pPD158.87	1	25	1	0	None
(EG4788)	2 nd	20 ng/µL pDD04Neo	1	25	1	many	Pharynx [†]
	1 st	5 ng/µL pDD04Neo	1	40	5	0	None
C. sp. 33 (BBC10016)	2 nd	10 ng/µL pDD04Neo	1	28	13	0	None
(BRO10010)	3 rd	20 ng/µL pDD04Neo	1	36	300	1	Pharynx [†]
C. brenneri (CB5161)	1 st	20 ng/μL pDD04Neo + 100 ng/μL pPD158.87 4 1		110	94	24	Pharynx, Intestine [†]
C. nigoni (BRC10094)	1 st	150 ng/µL (hsp16/4 + hsp16/2)	1	25	0	0	None
	2 nd	20 ng/µL pDD04Neo	2	87	1	0	None
	3 rd	20 ng/µL pDD04Neo + 100 ng/µL pPD158.87	4	81	24	many	Pharynx, Intestine [†]
<i>C. sinica</i> (BRC10093)	1 st	150 ng/µL (hsp16/4 + hsp16/2)	1	25	0	0	None
	2 nd	20 ng/µL pDD04Neo	1	50	1	0	None
	3 rd	20 ng/µL pDD04Neo + 100 ng/µL pPD158.87	1	40	3	0	None
C. imperialis (EG5716)	1 st	20 ng/µL pDD04Neo + 100 ng/µL pPD158.87	1	28	0	0	None
C. nouraguensis (JU2079)	1 st	20 ng/µL pDD04Neo + 100 ng/µL pPD158.87	1	14	1	0	None
C. remanei (PB4641)	1 st	200 ng/µL pDD04Neo	1	30	6	0	None
	2st	10 ng/µL pDD04Neo	1	65	36	0	None
	3 rd	7.5 ng/µL pDD04Neo	1	25	0	0	None
	4 th	100 ng/µL pDD04Neo + 100 ng/µL pCFj104	1	20	2	0	None
	5 th	2.5 ng/µL pDD04Neo + 125 ng/µL pCFj104	1	44	1	0	None
	1 st	20 ng/µL pDD04Neo	1	42	42	0	None
C romanai	2 nd	10 ng/µL pDD04Neo	1	35	8	0	None
(BRC310)	3 rd	5 ng/µL pDD04Neo	1	55	5	0	None
	4 th	20 ng/µL pDD04Neo + 50 ng/µL pPD135	2	62	35	0	None

Table 1. Transgenesis in diocelous ouenomabulits nematoues	Table	1.	Transgenesis	in	dioecious	Caenorhabditis	nematodes
--	-------	----	--------------	----	-----------	----------------	-----------

[†]The expression was already published (Le et al., 2017).

In our research, we failed to make transgenic lines that were stable for four species. *C. imperialis* did not produce any transgenic F1. In contrast, three other species (*C. sinica*, *C. nouraguensis*, and *C. remanei*) produced many transgenic F1s and no transgene in the next generations, suggesting that the *myo-*2::*GFP* constructs were expressed in the *Caenorhabditis* nematodes but the extrachromosomal arrays might not be inherited in germlines (Mello *et al.*, 1991; Rieckher *et al.*, 2009). However, for a better chance of getting a stable transgene, the number of P0 injections should be increased, resulting in numerous transgenic F1s by which a few stable transgenic F2 offspring are reproduced. For example, in this research, *C. brenneri* and *C. nigoni*, each after four subsequent trials, were effective. Other timeconsuming methods would be initiated with new construct designs with the precise understanding of genome sequences.

CONCLUSION

Eight species (C. portoensis, Caenorhabditis sp. 33, C. brenneri, C. nigoni, C. sinica, C. *imperialis*, C. nouraguensis, and *C*. remanei) were injected with different plasmid mixtures. The first four of them were successfully transformed and well expressed the myo-2::GFP in pDD04Neo and sur-5::GFP in pPD158.87 in the pharynx through multiple generations. Among these. С. portoensis and Caenorhabditis sp. 33 were the first successful for microinjection. The last four of the tested species were failed for transformation.

ACKNOWLEDGEMENT

We thank Dr. John Wang at the Biodiversity Research Center, Academia Sinica, Taiwan for allowing us to do microinjections in the laboratory.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

REFERENCES

Bi Y, Ren X, Yan C, Shao J, Xie D, Zhao Z (2015) A Genome-wide hybrid incompatibility landscape between Caenorhabditis briggsae and C. nigoni. *PLoS Genet* 11(2): e1004993. https://doi.org/10.1371/journal.pgen.1004993.

Braendle C, Felix MA (2008) Plasticity and errors of a robust developmental system in different environments. *Dev Cell 15*(5): 714-724. https://doi.org/10.1016/j.devcel.2008.09.011.

Chalfie M, Tu Y, Euskirchen G, Ward WW, Prasher DC (1994) Green fluorescent protein as a marker for gene expression. *Science* 263(5148): 802-805. https://doi.org/10.1126 /science.8303295.

Cinkornpumin JK, Hong RL (2011) RNAi mediated gene knockdown and transgenesis by microinjection in the necromenic Nematode Pristionchus pacificus. *J Vis Exp* (56): e3270. https://doi.org/10.3791/3270.

Dieter Slot WS, Lewis Stevens, Wim Bert and Mark Blaxter (2017) Caenorhabditis monodelphis sp. n.: defining the stem morphology and genomics of the genus Caenorhabditis. *BMC Zoology* 2(4): 15. https://doi.org/10.1186/s40850-017-0013-2.

Evans TC (2006) Transformation and microinjection. *WormBook.* T. C. e. R. Community. https://doi.org/10.1895/wormbook .1.108.1.

Felix MA, Braendle C, Cutter AD (2014) A streamlined system for species diagnosis in Caenorhabditis (Nematoda: Rhabditidae) with name designations for 15 distinct biological species. *PLoS One* 9(4): e94723. https://doi.org/10.1371/journal.pone.0094723.

Fire A (1986) Integrative transformation of Caenorhabditis elegans. *EMBO J* 5(10): 2673-2680. https://doi.org/10.1002/j.1460-2075.1986.tb04550.x.

Fire A, Albertson D, Harrison SW, Moerman DG (1991) Production of antisense RNA leads to effective and specific inhibition of gene expression in C. elegans muscle. *Development* 113(2): 503-514. https://doi.org/10.1242/ dev.113.2.503.

Fire A, Harrison SW, Dixon D (1990) A modular set of lacZ fusion vectors for studying gene expression in Caenorhabditis elegans. *Gene* 93(2): 189-198. https://doi.org/10.1016/0378-1119(90)90224-F.

Fire A, Xu S, Montgomery MK, Kostas SA, Driver SE, Mello CC (1998) Potent and specific genetic interference by double-stranded RNA in Caenorhabditis elegans. *Nature* 391(6669): 806-811. https://doi.org/10.1038/35888.

Vietnam Journal of Biotechnology 22(1): 99-107, 2024. DOI: 10.15625/vjbt-19892

Frokjaer-Jensen C, Davis MW, Hopkins CE, Newman BJ, Thummel JM, Olesen SP, Grunnet M, Jorgensen EM (2008) Single-copy insertion of transgenes in Caenorhabditis elegans. *Nat Genet* 40(11): 1375-1383. https://doi.org/10.1038/ng.248.

Grant WN, Skinner SJ, Newton-Howes J, Grant K, Shuttleworth G, Heath DD, Shoemaker CB (2006) Heritable transgenesis of Parastrongyloides trichosuri: a nematode parasite of mammals. *Int J Parasitol* 36(4): 475-483. https://doi.org/10.1016/j.ijpara.2005.12.002.

Gu T, Orita S, Han M (1998) Caenorhabditis elegans SUR-5, a novel but conserved protein, negatively regulates LET-60 Ras activity during vulval induction. *Mol Cell Biol* 18(8): 4556-4564. https://doi.org/10.1128/MCB.18.8.4556.

Gupta BP, Johnsen R, Chen N (2007) Genomics and biology of the nematode Caenorhabditis briggsae. *WormBook*: 1-16. https://doi.org/10. 1895/wormbook.1.136.1.

Hashmi S, Hashmi G, Gaugler R (1995) Genetic transformation of an entomopathogenic nematode by microinjection. *J Invertebr Pathol* 66(3): 293-296. https://doi.org/10.1006/jipa. 1995.1103.

Higazi TB, Merriweather A, Shu L, Davis R, Unnasch TR (2002) Brugia malayi: transient transfection by microinjection and particle bombardment. *Exp Parasitol* 100(2): 95-102. https://doi.org/10.1016/S0014-4894(02)-8.

Huang RE, Ren X, Qiu Y, Zhao Z (2014) Description of Caenorhabditis sinica sp. n. (Nematoda: Rhabditidae), a nematode species used in comparative biology for C. elegans. *PLoS One* 9(11): e110957. https://doi.org/10. 1371/journal.pone.0110957.

Hutter H (2003) Extracellular cues and pioneers act together to guide axons in the ventral cord of C. elegans. *Development* 130(22): 5307-5318. https://doi.org/10.1242/dev.00727.

Kadandale P, Chatterjee I, Singson A (2009) Germline transformation of Caenorhabditis elegans by injection. *Methods Mol Biol* 518:

123-133. https://doi.org/10.1007/978-1-59745-202-1_10.

Kanzaki N, Tsai IJ, Tanaka R, Hunt VL, Liu D, Tsuyama K, Maeda Y, Namai S, Kumagai R, Tracey A, Holroyd N, Doyle SR, Woodruff GC, Murase K, Kitazume H, Chai C, Akagi A, Panda O, Ke HM, Schroeder FC, Wang J, Berriman M, Sternberg PW, Sugimoto A, Kikuchi T (2018) Biology and genome of a newly discovered sibling species of Caenorhabditis elegans. *Nat Commun* 9(1): 3216. https://doi.org/10.1038/ s41467-018-05712-5.

Kennedy BP, Aamodt EJ, Allen FL, Chung MA, Heschl MF, McGhee JD (1993) The gut esterase gene (ges-1) from the nematodes Caenorhabditis elegans and Caenorhabditis briggsae. *J Mol Biol* 229(4): 890-908. https://doi.org/10.1006/jmbi. 1993.1094.

Kiontke K, Barriere A, Kolotuev I, Podbilewicz B, Sommer R, Fitch DH, Felix MA (2007) Trends, stasis, and drift in the evolution of nematode vulva development. *Curr Biol* 17(22): 1925-1937. https://doi.org/10.1016/j.cub.2007. 10.061.

Kiontke KC, Felix MA, Ailion M, Rockman MV, Braendle C, Penigault JB, Fitch DH (2011) A phylogeny and molecular barcodes for Caenorhabditis, with numerous new species from rotting fruits. *BMC Evol Biol* 11: 339. https://doi.org/10.1186/1471-2148-11-339.

Kramer JM, French RP, Park EC, Johnson JJ (1990) The Caenorhabditis elegans rol-6 gene, which interacts with the sqt-1 collagen gene to determine organismal morphology, encodes a collagen. *Mol Cell Biol* 10(5): 2081-2089. https://doi.org/10.1128/MCB.10.5.2081.

LaMunyon CW, Ward S (1999) Evolution of sperm size in nematodes: sperm competition favours larger sperm. *Proc Biol Sci* 266(1416): 263-267. https://doi.org/10.1098/rspb.1999. 0631.

Le TS, Yang FJ, Lo YH, Chang TC, Hsu JC, Kao CY, Wang J (2017) Non-Mendelian assortment of homologous autosomes of different sizes in

males is the ancestral state in the Caenorhabditis lineage. $Sci \quad Rep \quad 7(1): 12819.$ https://doi.org/10.1038/s41598-017-13215-4.

Li X, Massey HC, Jr., Nolan TJ, Schad GA, Kraus K, Sundaram M, Lok JB (2006) Successful transgenesis of the parasitic nematode Strongyloides stercoralis requires endogenous non-coding control elements. *Int J Parasitol* 36(6): 671-679. https://doi.org/ 10.1016/j.ijpara.2005.12.007.

Lo TW, Pickle CS, Lin S, Ralston EJ, Gurling M, Schartner CM, Bian Q, Doudna JA, Meyer BJ (2013) Precise and heritable genome editing in evolutionarily diverse nematodes using TALENs and CRISPR/Cas9 to engineer insertions and deletions. *Genetics* 195(2): 331-348. https://doi.org/10.1534/genetics.113. 155382.

Maduro M, Pilgrim D (1995) Identification and cloning of unc-119, a gene expressed in the Caenorhabditis elegans nervous system. *Genetics* 141(3): 977-988. https://doi.org/10.1093/genetics/141.3.977.

Mello CC, Kramer JM, Stinchcomb D, Ambros V (1991) Efficient gene transfer in C.elegans: extrachromosomal maintenance and integration of transforming sequences. *EMBO J* 10(12): 3959-3970. https://doi.org/10.1002/j.1460-2075.1991.tb04966.x.

Miller DM, Desai NS, Hardin DC, Piston DW, Patterson GH, Fleenor J, Xu S, Fire A (1999) Two-color GFP expression system for C. elegans. *Biotechniques* 26(5): 914-918, 920-911. https://doi.org/10.2144/99265rr01.

Nuez I, Felix MA (2012) Evolution of susceptibility to ingested double-stranded RNAs in Caenorhabditis nematodes. *PLoS One* 7(1): e29811. https://doi.org/10.1371/journal.pone. 0029811.

Praitis V (2006) Creation of transgenic lines using microparticle bombardment methods. *Methods Mol Biol* 351: 93-107. https://doi.org/10.1385/1-59745-151-7:93. Praitis V, Casey E, Collar D, Austin J (2001) Creation of low-copy integrated transgenic lines in Caenorhabditis elegans. *Genetics* 157(3): 1217-1226. https://doi.org/10.1093/genetics/ 157.3.1217.

Rieckher M, Kourtis N, Pasparaki A, Tavernarakis N (2009) Transgenesis in Caenorhabditis elegans. *Methods Mol Biol* 561: 21-39. https://doi.org/10.1007/978-1-60327-019-9_2.

Robert V, Bessereau JL (2007) Targeted engineering of the Caenorhabditis elegans genome following Mos1-triggered chromosomal breaks. *EMBO J* 26(1): 170-183. https://doi.org/10.1038/sj.emboj.7601463.

Ross JA, Koboldt DC, Staisch JE, Chamberlin HM, Gupta BP, Miller RD, Baird SE, Haag ES (2011) Caenorhabditis briggsae recombinant inbred line genotypes reveal inter-strain incompatibility and the evolution of recombination. *PLoS Genet* 7(7): e1002174. https://doi.org/10.1371/journal.pgen.1002174.

Semple JI, Garcia-Verdugo R, Lehner B (2010) Rapid selection of transgenic C. elegans using antibiotic resistance. *Nat Methods* 7(9): 725-727. https://doi.org/10.1038/nmeth.1495.

Shao H, Li X, Nolan TJ, Massey HC, Jr., Pearce EJ, Lok JB (2012) Transposon-mediated chromosomal integration of transgenes in the parasitic nematode Strongyloides ratti and establishment of stable transgenic lines. *PLoS Pathog* 8(8): e1002871. https://doi.org/10.1371 /journal.ppat.1002871.

Stein LD, Bao Z, Blasiar D, Blumenthal T, Brent MR, Chen N, Chinwalla A, Clarke L, Clee C, Coghlan A, Coulson A, D'Eustachio P, Fitch DH, Fulton LA, Fulton RE, Griffiths-Jones S, Harris TW, Hillier LW, Kamath R, Kuwabara PE, Mardis ER, Marra MA, Miner TL, Minx P, Mullikin JC, Plumb RW, Rogers J, Schein JE, Sohrmann M, Spieth J, Stajich JE, Wei C, Willey D, Wilson RK, Durbin R, Waterston RH (2003) The genome sequence of Caenorhabditis briggsae: a platform for comparative genomics. Vietnam Journal of Biotechnology 22(1): 99-107, 2024. DOI: 10.15625/vjbt-19892

PLoS Biol 1(2): E45. https://doi.org/10.1371/journal.pbio.0000045.

Stinchcomb DT, Shaw JE, Carr SH, Hirsh D (1985) Extrachromosomal DNA transformation of Caenorhabditis elegans. *Mol Cell Biol* 5(12): 3484-3496. https://doi.org/10.1128/MCB.5.12. 3484.

Ting JJ, Woodruff GC, Leung G, Shin NR, Cutter AD, Haag ES (2014) Intense spermmediated sexual conflict promotes reproductive isolation in Caenorhabditis nematodes. *PLoS Biol* 12(7): e1001915. https://doi.org/10.1371/ journal.pbio.1001915.

Vielle A, Callemeyn-Torre N, Gimond C, Poullet N, Gray JC, Cutter AD, Braendle C (2016) Convergent evolution of sperm gigantism and the developmental origins of sperm size variability in Caenorhabditis nematodes. *Evolution* 70(11): 2485-2503. https://doi.org/10.1111/evo.13043.

Wei Q, Shen Y, Chen X, Shifman Y, Ellis RE (2014) Rapid creation of forward-genetics tools for C. briggsae using TALENs: lessons for nonmodel organisms. *Mol Biol Evol* 31(2): 468-473. https://doi.org/10.1093/molbev/mst213.

Wei Q, Zhao Y, Guo Y, Stomel J, Stires R, Ellis RE (2014) Co-option of alternate sperm

activation programs in the evolution of self-fertile nematodes. *Nat Commun* 5: 5888. https://doi.org/10.1038/ncomms6888.

Wenick AS, Hobert O (2004) Genomic cisregulatory architecture and trans-acting regulators of a single interneuron-specific gene battery in C. elegans. *Dev Cell* 6(6): 757-770. https://doi.org/10.1016/j.devcel.2004.05.004.

Wood AJ, Lo TW, Zeitler B, Pickle CS, Ralston EJ, Lee AH, Amora R, Miller JC, Leung E, Meng X, Zhang L, Rebar EJ, Gregory PD, Urnov FD, Meyer BJ (2011) Targeted genome editing across species using ZFNs and TALENs. *Science* 333(6040): 307. https://doi.org/10.1126/science.1207773.

Woodruff GC, Eke O, Baird SE, Felix MA, Haag ES (2010) Insights into species divergence and the evolution of hermaphroditism from fertile interspecies hybrids of Caenorhabditis nematodes. *Genetics* 186(3): 997-1012. https://doi.org/10.1534/genetics.110.120550.

Yin D, Schwarz EM, Thomas CG, Felde RL, Korf IF, Cutter AD, Schartner CM, Ralston EJ, Meyer BJ, Haag ES (2018) Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. *Science* 359(6371): 55-61. https://doi.org/10.1126/science.aao0827.