A semi-automated high-throughput approach to the generation of transposon insertion mutants in the nematode Caenorhabditis elegans

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ABSTRACT

The generation of a large collection of defined transposon insertion mutants is of general interest to the Caenorhabditis elegans research community and has been supported by the European Union. We describe here a semi-automated high-throughput method for mutant production and screening, using the heterologous transposon Mos1. The procedure allows routine culture of several thousand independent nematode strains in parallel for multiple generations before stereotyped molecular analyses. Using this method, we have already generated >17,500 individual strains carrying Mos1 insertions. It could be easily adapted to forward and reverse genetic screens and may influence researchers faced with making a choice of model organism.

INTRODUCTION

In order to exploit the full genome sequence of Caenorhabditis elegans, a number of ambitious projects have been undertaken to address the function of all genes. Some, for example, have been based on the generation of ORFeome libraries (1,2), and include interactome (3) and structural genomics (4) projects. The C.elegans ORFeome library has also been used to carry out large-scale functional studies of gene inactivation by RNA interference (RNAi) (5), complementing previous screens based on other methodologies (6–9). Although such approaches give invaluable information about gene function, there is a clear need for the generation of stable mutant lines in as many C.elegans genes as possible. Following on from earlier work (10,11), two projects are currently underway in North America (12) (http://celeganskoconsortium.omrf.org/) and Japan (13) (http://shigen.lab.nig.ac.jp/c.elegans/index.jsp) to achieve this aim. As of September 2006, these projects had generated 2361 (G. Moulder, personal communication) and 2036 mutant strains, respectively. To these can be added the null alleles for several hundred genes produced using other PCR-based technologies (14,15) or generated in classical genetic screens and available from the central strain repository, the Caenorhabditis Genetics Center (http://biosci.umn.edu/CGC).

An alternative approach to the generation of mutants is via the use of transposons, a method that has been applied with great success in many model systems. Indeed in C.elegans, this was the first method that was used to isolate mutants in a systematic way (16). In this ground-breaking work, a frozen library of 5000 nematode lines mutagenized by the endogenous transposable element Tc1 was generated. Through a PCR-based screen, mutants of genes of interest could be recovered from the bank. The progeny of these mutant animals were then screened by PCR, to detect individuals in which there had been imprecise excision of Tc1 and thus inactivation of the gene of interest. This method had a number of drawbacks linked to the use of an endogenous transposon. More recently, a method using the mariner-like element Mos1 from Drosophila has been established (17). In addition to being used as a mutagen in classical genetic screens, thereby accelerating greatly the speed at which mutations can be identified (18), it has also been used in a pilot-scale project to generate random insertions throughout the genome (19). Following on from the success of this pilot project that was carried out manually, as part of an ongoing collaborative effort to produce a large bank of mutants, we have developed a semi-automated high-throughput method for mutant production and screening that we describe here. With it, we have developed a capacity to handle several thousand nematode strains in parallel for multiple generations and have already generated >17,500 individual strains carrying Mos1 insertions.

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MATERIALS AND METHODS

Strains and mutagenesis

The two strains of transgenic worms used, one carrying the substrate array \((oxEx229[Mos1:Pmyo-2:GFP])\) containing multiple copies of the Mos1 transposon and associated with specific green fluorescent protein (GFP) expression in the pharynx, the other \((oxEx166[Phsp:Mos1Transposase:Punc-122:GFP;lin-15(+)])\) containing the coding sequence of the Mos1 transposon under the control of a heat-shock promoter and a coelomocyte-specific GFP reporter have been described previously (17). These are crossed to obtain individuals carrying both arrays. Then double transgenic hermaphrodites, manually picked under a dissecting epifluorescence stereomicroscope (Leica MZFLIII), were subjected to heat-shock, resulting in expression of the Mos1 transposon and consequently mobilization of Mos1 as described previously (18).

Culture medium

The Escherichia coli strain OP50.1, available from the Caenorhabditis Genetics Center, was grown overnight at 37°C with shaking in Luria–Bertani (LB) supplemented with streptomycin. The culture was centrifuged for 20 min at 3220 g, the supernatant removed and the pellet resuspended in an equal volume of M9 supplemented with cholesterol (M9+) at a final concentration of 10 µg/ml to give the M9B medium that was also supplemented with streptomycin.

Liquid culture

Worms were individually sorted into 80 µl of M9B and cultivated at 20°C with agitation (900 r.p.m. on an orbital shaker) in a box humidified with damp paper towels. After 5 days, a 5 µl aliquot of each well in the ‘A’ plates (see Figure 1) was transferred manually with a multi-channel pipette to the ‘B’ plates containing 80 µl of M9B.

Worm sorting

Sorting was carried out using a Union Biometrica COPAS Biosort (Harvard Biosciences, Boston, MA), equipped with Reflex and Profiler modules, essentially following the manufacturer’s instructions.

Well image analysis

Images of each well of a 96-well plate were acquired with a Flash Cytometer™ (Trophos, Marseille; see http://www.trophos.com/research/platform.htm). The images were subsequently processed using the ImageJ (NIH) image analysis software freely available from http://rsb.info.nih.gov/ij/. A binarized image was generated of each well and then the worms were positively discriminated from medium background, bacteria and dust (see legend to Figure 5). In the final step, particles were analyzed using the ‘analyse particle’ function. An area size filter was then applied in order to exclude particles with an area <0.015 mm² or >0.217 mm². The particles remaining in each well were assumed to be worms and their numbers in each well were automatically counted. The worm-counting results were used to automatically generate an Excel table. This table was filtered to include only those cells that contained at least three worms. This file was then read by a TECAN robot that selectively transferred the entire contents of the wells putatively containing worms to a new 96-well plate. The scripts used are available upon request.

Worm lysis, PCR and gel electrophoresis

A 2.5 µl aliquot of each well from four 96-well plates was transferred to a single 384-well plate and 7.5 µl of fresh proteinase K solution (0.1 mg/ml in water) was added to each well. Plates were incubated at 65°C for 1 h before inactivating the proteinase K at 95°C for 15 min. Then to each
well 15 μl of a PCR mixture (9 μl H2O, 0.25 μl of each of the oligonucleotides 5′-CAACCTTGACTGTCGAACCA-
CCATAG-3’, 5′-TCTGCGAGTTGTTTTGCGTGGAG-3′ at
200 ng/μl, 0.25 μl of 25 mM dNTPs, 0.25 μl of Taq at 5 U/μl,
2.5 μl of 10× buffer and 2.5 μl of 50 mM MgCl2) was added and the following PCR program performed: 3 min at 93°C, then
40 cycles of 30 s at 93°C, 33 s at 57°C, 40 s at 71°C, followed
by 5 min at 71°C. Then 7.5 μl of loading buffer was added to
each well and the entire contents loaded on to a 1.8% agarose gel.

**Gel image analysis**

After EtBr staining, an image of the 456-well gel correspon-
ding to all the 384 wells of a PCR plate was acquired with a
high-resolution CCD camera (Cohu Electronics, San Diego,
CA). A predefined grid was applied to the gel image for help-
ing the manual selection of positive lanes. Through the use of a
JAVA program a click in each predefined region of the grid
automatically loaded a ‘1’ in the corresponding cell of a 16 ×
24 Excel table. Conversely if a region of the grid was not
selected, a ‘0’ was automatically loaded in the Excel table.
An Excel Macro then split the 16 × 24 table in four 8 ×
12 tables each representing one of the four starting worm-
containing 96-well plates used to load the 384 wells PCR
plate. The resulting four Excel tables were then read by the
TECAN robot which transferred the entire contents of each
well flagged as positive to a well of a 24-well plate for sub-
sequent culture. The scripts used are available upon request.

**Transposition frequency**

After each heat-shock, at the moment of the transfer of
worms between plates A and B (Figure 1), a 5 μl aliquot
from 28 randomly selected wells was spotted onto 3.5 cm
plates containing standard NGM agar seeded with OP50.
After 3–5 days at 20°C, from each plate, 10 non-GFP L4s
(the F4 progeny from the original aliquot of F3 worms)
were transferred to a fresh plate and cultured for one further
generation. After confirming that none of the progeny was
GFP-positive, 10 L4s of the F5 generation from each plate
were transferred into PCR tubes containing 10 μl of pro-
teinase K solution and subjected to lysis and PCR analysis
as above. The 10 worms tested from each plate are all the
progeny of a single F1 parent; by pooling 10 individuals at
the F4 and F5 generations, the chance of not detecting
Mos1 in the progeny of a Mos1-positive F1 worm is reduced.
Since only F5 worms from F4 worms that gave no GFP pro-
geny were used in the analysis, it is almost certain that none
of the worms tested contains the Mos1 substrate array
(oxEx229). The transposition frequency (%) is given by 100 ×
the number of positive wells/28.

**RESULTS**

**Mos1-mediated mutagenesis**

Protocols for the mobilization of the Mos1 transposon in
*Caenorhabditis elegans* are now well established. Transgenic animals
carrying both enzyme and substrate arrays are generated by
mating individuals carrying each array and these are then
allowed to reproduce to give the parental (P0) generation
(Figure 1). The next step involves inducing transposon
mobilization by heat-shock of P0 worms carrying both
enzyme and substrate arrays (18). After recovery, worms
lay eggs that potentially contain the Mos1 transposon inte-
grated into their genome. It has been observed that animals
that retain the substrate array at this F1 generation more
frequently contain a Mos1 insertion than those F1 individu-
als that have lost the array (18). As germline transposition
is essentially limited to early meiotic nuclei of oocytes, all
mutant F1 progeny obtained from parents in which transposi-
tion has occurred will be heterozygous for each independent
Mos1 insertion. With each subsequent generation, the propor-
tion of worms heterozygous for a given locus will diminish as
the strains are driven towards the homozygous (wild-type or
mutant) genotype. After n generations following the F1, in
the absence of any selection, in the population (1/2)n of
the worms would be heterozygous and (0.5 − (1/2)n)1 homozy-
gous mutants for a given insertion. To favor the recovery of
mutants carrying homozygous insertions, we devised a
scheme to isolate mutants after at least five generations
(Figure 1).

**Distribution and culture of mutagenized worms**

To maximize the transposition frequency in a high-
throughput setting, we used the Union Biometrica COPAS
sorter to sort individual F1 worms carrying the substrate
array. To generate a synchronized population, a sorting gate
based on time-of-flight (correlated with size and hence age)
was used to identify worms at the L4 stage. Since the sub-
strate array is associated with specific GFP expression in
the pharynx, the Profiler was used to identify those worms
carrying it and discriminate them from those carrying the
transposase array (associated with specific GFP expression
in the coelomocytes) and from double transgenic worms
carrying both (Figure 2). The sorting speed is dependent upon
the density of the worms in the sample, and the proportion
of individuals fitting the selection criteria, but under typical
conditions, the machine filled a 96-well plate with worms
in <3 min. This distribution was very accurate (Figure 3A).

In small-scale mutagenesis experiments, insertion frequen-
cies as high as 75% can be obtained routinely (J. J. Ewbank
and N. Pujol, unpublished data). In the current study,
although a rate this high was occasionally achieved, it was
more often <40% and sometimes even <10% (Table 1).

Following distribution, worms were cultured for 5 days at
20°C with shaking. In this time, worms that were properly
fertile produced a large number of F3 progeny. In a typical
experiment 81% (n = 1824) of wells contained a large popu-
lation of worms. An aliquot of each well was then transferred
to a well of a new 96-well plate with fresh medium and the
worms cultured for a further 3 days. Again at this stage,
good growth was generally seen and in a typical experiment
93% (n = 1824) of wells that contained a large population of
worms at the F3 generation gave a large population of F4 and
then F5 worms. Overall, therefore, on average 75% of wells
at this stage contained worms, among which there were in
theory 47% of individuals carrying two alleles of a given
Mos1 insertion, giving a combined 35% chance of recovering
a single worm that was homozygous for a given insertion
present in the F1 population.
Recovery of mutants

The COPAS sorter can be equipped with an accessory, the Reflex module, that allows recovery of worms from 96-well plates. Briefly, 200 \( \mu l \) of sheath fluid is pumped into a well and then all the contents are aspirated and passed through the analyzer. The standard program takes 55 min per 96-well plate. To improve this performance, a shorter custom Reflex cycle was instituted wherein only 100 \( \mu l \) of sheath fluid was added and a 60 \( \mu l \) sample aspirated from the well. This resulted in significant reduction in the time for each well to be treated and a whole plate could be analyzed in 36 min, increasing by >50% the number of plates that could be handled during an 8 h period (13 versus 8).

A stringent combination of standard and Profiler parameters was applied to select a single non-fluorescent worm from each well. These were automatically transferred to individual wells of a fresh 96-well plate. The COPAS machine was capable of performing this analysis and sorting in an accurate manner (Figure 3B).

Table 1. Production figures for each week over a 10-week period

| F1 worms | Transposition frequency\(^a\) (%) | Number of \(Mosl\)-positive F5 strains (%) | Cumulative total\(^b\) |
|----------|----------------------------------|------------------------------------------|----------------------|
| 3648     | 36.5                             | 330 (9.0)                                | 7676                 |
| 3648     | 33.3                             | 353 (9.7)                                | 8029                 |
| 3648     | 26.0                             | 401 (11.0)                               | 8430                 |
| 3648     | 34.3                             | 205 (5.6)                                | 8635                 |
| 3552     | 9.4                              | 130 (3.7)                                | 8765                 |
| 3648     | 8.3                              | 160 (4.4)                                | 8925                 |
| 3648     | 34.3                             | 341 (9.3)                                | 9266                 |
| 3552     | 46.9                             | 378 (10.6)                               | 9644                 |
| 3556     | 30.2                             | 224 (6.3)                                | 9868                 |
| 4128     | 32.3                             | 255 (6.2)                                | 10 123               |

\(^a\)The frequency was measured for a sample of 28 \( \times \) 10 worms as described in Materials and Methods.

\(^b\)Since the start of the project.

The overall workflow for this second part of the procedure is shown in Figure 4. During the initial stages of the project, before final protocol optimization, when the proportion of empty wells at the F6 generation was relatively elevated, the first step was to capture an image of each 96-well plate using a Flash Cytometer\(^{TM}\). This system allows snapshot acquisition of entire wells (0.2 s/well) followed by digital image analysis. For the current project, publicly available image analysis software was used to allow automated recognition of nematodes (Figure 5). In this way, the wells that contained at least three worms were identified. The information regarding full and empty wells was then transformed into

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**Figure 2.** The COPAS Profiler can discriminate between worms carrying different transgenic arrays and can be used to sort worms of a desired genotype. Fluorescent micrographs (upper panels) and profiles (lower panels) for individual worms carrying the substrate array (A), the transposase array (B), associated with specific GFP expression in the pharynx and in the coelomocytes, respectively, or both (C). Fluorescence is measured in arbitrary but constant units. Time-of-flight is a measure of length (24).

**Figure 3.** Sorting efficiency with the COPAS machine. (A) Sorting at the F1 stage. Bars represent the average for two independent trials of 96 wells, with error bars showing the standard deviation. The percentage of worms expressing GFP was calculated counting only those wells that contained a single worm; 100% of the singled worms had GFP expression in the pharynx. (B) Sorting at the F4 stage. Data are shown for a typical 96-well plate.

**Figure 4.** The overall workflow for this second part of the procedure is shown. During the initial stages of the project, before final protocol optimization, the proportion of empty wells at the F6 generation was relatively elevated, the first step was to capture an image of each 96-well plate using a Flash Cytometer\(^{TM}\). This system allows snapshot acquisition of entire wells (0.2 s/well) followed by digital image analysis. For the current project, publicly available image analysis software was used to allow automated recognition of nematodes (Figure 5). In this way, the wells that contained at least three worms were identified. The information regarding full and empty wells was then transformed into
to amplify specifically the Mos1 sequence was carried out directly in these plates (see Materials and Methods for details). The resulting mixture from each well was then loaded robotically onto a single 456-lane agarose gel. After electrophoretic migration and ethidium bromide staining, an image of the gel was captured. At the early part of the project, band-calling, to flag positive lanes contain the Mos1-associated PCR product, was done entirely manually. Subsequently, a point-and-click interface was developed to accelerate this process and make it less error-prone (Figure 6). In both cases, either manually or semi-automatically, the information regarding Mos1-positive wells was used to construct a new macro to allow cherry-picking of worms from the 96-well plates onto 24-well agarose, suitable for shipping. The subsequent characterization of the individual Mos1 insertion sites was carried out by remote laboratories and will be the subject of a future publication.

The production figures for a 10-week period during which the cumulative total of Mos1-positive strains passed the 10 000 mark are presented in Table 1. Surprisingly, there was no apparent correlation between the rate of transposition measured in the F3 generation and the final yield of Mos1-positive strains (Figure 7; $y = 0.25x$, $R^2 = 0.3$ for a linear curve fit). Overall, the procedure was relatively inefficient, with an average of 7 Mos1-positive strains obtained for each 96-well plate of individual F1 worms. This low yield was counterbalanced by the capacity to process very large numbers of individual clones in parallel; on average more than 3650 strains (incoming or outgoing, 7300 total) were handled per week during this period (Table 1). So, despite the low yield, more than 17 500 strains have thereby been generated to date.

**DISCUSSION**

At present, combining the results from systematic program- 
mes and traditional genetic screens, there are mutants for roughly a quarter of *C. elegans* genes. The project we describe here is intended as a complement to these, as the Mos1 insertion mutants can serve as the starting point for the engineering of specific genomic loci, allowing, for example, the production of specific mutant alleles, reporter strains or TAP-tagged proteins. The possibility of using transposon insertion mutants to introduce predetermined point mutations into the *C. elegans* genome was first demonstrated nearly 15 years ago (20). More recently, methods for homologous gene targeting (21) and a general strategy for gene conversion (22) have been described.

The feasibility of generating a large bank of Mos1 insertion mutants has been established previously (19). That study showed that, apart from the rDNA locus on chromosome 1 that constitutes a hotspot, there was no particular insertion bias for Mos1 in the *C. elegans* genome. But unfortunately, although 914 independent random Mos1 insertion mutants were generated, roughly one-fourth of the identified inser- 
tions could not be found when frozen strains were thawed. This was suggested to be linked to the precarious freezing of heterozygous strains (19). Given this disappointingly low rate of recovery, we adopted a more laborious strategy that

**Figure 4.** Downstream processing workflow for F6 generation worms. The numbered solid arrows indicate the successive steps. In this idealized schema, in the first step (1) individual 96-well plates containing worms in liquid culture were analysed with the Flash cytometer™ to identify wells full of worms (red and pink) and those that were empty or that contained only a few worms (light blue). The contents of each well determined to contain worms was transferred to a fresh 96-well plate (2). A small aliquot of each well from four such master plates was then transferred to a 384-well plate (3). A proteinase K (PK) solution was added to each well (4) and the plates incubated at 65°C for 1 h to lyse the worms before heat-inactivating the proteinase. A PCR mixture containing Mos1-specific primers was added (5) and a standard PCR performed. Electrophoresis loading buffer (LB) was then added to each well (6) and the contents of each well were then transferred robotically to a 456-lane agarose gel. After migration, an image of the gel was taken and the lanes containing Mos1-specific PCR amplicons identified (7). This information was then used to cherry-pick the remaining contents of the master 96-well plates onto 24-well agar plates spotted with bacterial food (8). After 3–5 days, to allow the recovery and reproduction of the worms, these plates were then shipped to remote laboratories for analysis. Wells marked with a cross represent Mos1-positive samples. Only parts of 384-, 96- and 24-well plates are shown for clarity. Steps (1) and (2) were eliminated when the proportion of worm-containing wells exceeded 70%.

A small aliquot of each well was taken from the 96-well plates and transferred to a 384-well plate. The worms in each well of the 384-well plate were then lysed and a PCR

**a programming macro to command a Tecan™ robot. The robot cherry-picked an aliquot of liquid from wells determined to contain worms, transferring it to a master 96-well plate. As the efficiency of the early steps improved, this part of the process became unnecessary and the plates containing worms of the F6 generation were processed without well redistribution.**
Figure 5. Successive steps in image analysis to determine whether a well contains worms. An image of each entire well of a 96-well plate was acquired automatically (A) and processed in successive steps using the ImageJ (NIH) software: overall light and contrast enhancement (B), loading of a circular region and inversion of gray level at each pixel inside the region (C), binarization on the basis of gray level at each pixel in the entire image (D), removal of all the selected particles outside the loaded region (E) and removal of all the particles shorter than a minimum size (F).

Figure 6. Identification of Mos1-positive samples. Samples were loaded on an agarose gel and subject to electrophoretic separation. After EtBr staining, an image of the gel was captured. Results for two representative gels are shown (A and B). A predefined grid was overlaid on the image, in this case the gel shown in B (C) and lanes containing a Mos1-specific PCR amplicon identified, as shown by the red boxes (D).
drives the strains to homozygosity before they are cryopreserved, thereby circumventing the problem. A corollary of this is that the number of strains handled had to be increased 3-fold to counterbalance the fact that only 35% of single worms selected at the F4 stage would be homozygous for a given insertion present in the F1 population. Indeed, almost half (46.9%) of the single F4 worms will have completely lost a given insertion. Additionally, there is the possibility of certain insertions being counter-selected. For example, if an insertion provokes a lethal recessive mutation, such that homozygous mutants do not reproduce, then at the F4 stage, 71.4% of individuals would be wild-type and only 28.6% heterozygous for the lethal mutation. Taken together with the relatively low transposition frequencies obtained, this meant that large numbers of samples had to be manipulated (Table 1). By combining the use of the COPAS Biosort for the distribution of individual worms with a liquid handling robot for sampling from populations, we were able to implement an efficient production workflow. To increase further the throughput of the procedure, a number of improvements could be envisioned. Currently, one of the limiting steps is the band-calling step. Since the Mos1-specific amplicon has a fixed size, it is likely that band detection could be completely automated. As it stands, on an average ~14 strains have to be screened to find one that is Mos1-positive. Clearly, any stable improvement in the overall yield would be helpful, but this has so far been elusive. Indeed, given the lack of strict correlation between observed transposition frequency and the proportion of Mos1-positive strains obtained at the end (Figure 7), it is not clear what parameters should be changed to boost the overall efficiency. A more radical amelioration would be the use of a transposable element containing a marker, such as a gene encoding a fluorescent protein, which would allow direct screening for individuals carrying transposon insertions. As the Mos1 transposon can only carry short exogeneous DNA sequences (17), such an approach must await the development of other transposons able to carry larger inserts and compatible with germline transposition in C. elegans. Nevertheless, the results presented here clearly show that high-throughput methods can be developed using existing transposon technologies and successfully applied to a project that aims to benefit the increasing number of researchers who use C. elegans as a model.

The generation of a large collection of Mos1 mutants is especially relevant now that techniques have been developed to exploit such a resource through engineering of the C. elegans genome by homologous recombination by another partner of the NEMAGENETAG consortium [V. Robert and J. L. Bessereau, personal communication (23), http://www.wormbase.org/db/misc/paper?name=WBPaper0027447]. The technique, termed MosTIC (Mos1-induced transgene-instructed gene conversion) allows (i) the introduction of point mutations, (ii) the engineering of deletions and (iii) the knock-in to a specific genomic locus of gfp at sites at least 500 bp on each side of a Mos1 insertion site (Robert et al., manuscript submitted). Consequently, Mos1 insertions in intronic and intergenic regions are potentially as useful as those that are within exons as the starting point for gene-specific recombinering.

Finally, this work clearly demonstrates that methods can be developed that allow the handling of very large numbers of nematode strains in parallel. Currently, we are treating up to 120 96-well plates per week (11 520 individual strains). These techniques could be readily adapted to numerous different experimental problems. For example, genetic screens for maternal or grand-maternal effect mutants are notoriously difficult because of their clonal nature. The procedure described here would be well suited to such screens. For reverse genetic genome-wide RNAi screens close to 20 000 clones need to be handled. Plate pouring and handling is often a limiting factor. Using the Biosort, such a screen could in theory be performed in <2 weeks.

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