## PART B: INFORMATION ABOUT THE RELEASE APPLICATION TO BE INCLUDED ON THE PUBLIC REGISTER

### B1 The name and address of the applicant

Rothamsted Research,
West Common,
Harpenden
Hertfordshire,
AL5 2JQ
UK

### B2 A general description of the genetically modified organisms in relation to which the application is being made

The organism to be released is the oilseed *Camelina sativa* (hereafter referred to as "Camelina") and we have used genetic modification to introduce into this plant the capacity to produce the omega-3 long chain polyunsaturated fatty acids eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA). The synthesis of these health-beneficial fatty acids has been engineered so as to only occur in the seeds of the GM Camelina

The GM Camelina plants have been engineered with the novel capability to accumulate the non-native omega-3 long chain polyunsaturated fatty acids EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid) through the introduction of the biosynthetic genes for these fatty acids. Such genes are normally only found in marine microbes such as microalgae and diatoms and some oomycetes and lower plants. Synthetic genes (meaning that the native DNA sequences have been codon-optimized and chemically synthesized) from EPA- & DHA-accumulating organisms have been integrated into the genome of Camelina.

Three different constructs are described. In the first iteration (A), genes from the picoalgae *Ostreococcus tauri*, the moss *Physcomitrella patens*, the Thraustochytriaceae *Thraustochytrium* and the oomycete *Hyaloperonospora parasitica* have each been linked to seed-specific regulatory sequences and introduced into the genome of Camelina to direct the synthesis of EPA. In a second iteration (B), the first three sequences and regulatory elements are used in conjunction with single genes from both of the oomycetes, *Phytophora infestans* and *Phytophora sojae*, to direct the synthesis of EPA. In a third iteration (C), these same five genes present in B are used in conjunction with two additional genes, from *Ostreococcus tauri* and the coccolithophore *Emiliana huxleyi*. All seven of these biosynthetic genes are linked with appropriate plant-derived seed-specific regulatory elements, to direct the synthesis of both EPA and DHA.

Two iterations (A, C) also contain the visual reporter protein DsRed, which allows for the simple identification of GM Camelina seeds. The DsRed protein is derived from the marine coral species *Discosoma* sp and has been codon-optimised for expression in plants. One iteration (B) contains the selectable marker *nptII* which confers resistance to the antibiotic kanamycin, which was used to select GM Camelina plants. Kanamycin will not be used in the course

of this field trial, and the presence of the *nptII* gene is not considered a risk in the context of this trial.

**B3 The location at which the genetically modified organisms are proposed to be released**

The location of the field trial is an agricultural area forming part of an experimental farm at Rothamsted Research, Harpenden, UK and at grid reference TL 1213. The area for the proposed field trial, including controls and spacing between GM plots will cover 30mx30m in Year 1, doubling in subsequent years to reflect increased available area within our secure trial site.

**B4 The purpose for which the genetically modified organisms are proposed to be released (including any future use to which they are intended to be put).**

Current sources of omega-3 long chain polyunsaturated fatty acids such as EPA and DHA are predominantly from oily fish, and it is for this reason these two fatty acids are often called fish oils. Global provision of fish oils is currently at or beyond the level of maximum sustainability, meaning that as the world's population increases, there will be less of these health-beneficial fatty acids to go round. We have been interested in developing an alternative, sustainable source of fish oils in transgenic plants, and have produced GM Camelina plants which represent a terrestrial source of omega-3 long chain polyunsaturated fatty acids. The purpose of this experimental trial is to determine the performance of these three different GM Camelina iterations in the field, with respect to oil composition and oil quantity, and also to assess any additional phenotypic and agronomic variations. Specific questions to be examined are:

- Do the GM Camelina plants still accumulate fish oils in seed oil in the field?
- Do the GM Camelina plants still accumulate total seed oil to appropriate levels?
- Is there any further alteration to the lipidome of field-grown GM Camelina?
- Is there any difference between lines accumulating just EPA (iterations A, B) or EPA and DHA (iteration C) in terms of agronomic performance?
- Is there any advantage or disadvantage to the GM Camelina plants in terms of field-based performance?

**B5 The intended dates of the release.**

The exact timing of sowing of the trial will depend upon weather conditions at the time. The field trial start date will be in April 2014 and the plants will be harvested in Aug or Sept the same year. We intend to repeat the trial with the specified three GM lines in 2015-17.

**B6 The environmental risk assessment.**

The three GM Camelina lines are indistinguishable from the non-GM equivalent except for the modified fatty acid composition of their seeds, in particular by the presence of the health-beneficial omega-3 long chain polyunsaturated fatty acids EPA and DHA. This modified fatty acid composition is found only in the seeds of the GM Camelina and is absent from all other vegetative tissues (e.g. leaves, roots, stems). The gene donor organisms are not known to be pathogenic or allergenic to humans, and none of the genes under investigation, or the selectable or visual marker genes, are expected to result in the synthesis of products that are harmful to humans, other organisms or the environment. Any unknown hazards arising from the expression and ingestion of foreign proteins will not occur since the Camelina plants will not be consumed by humans.

The probability of Camelina seeds escaping from the trial site or the transfer of inserted characteristics to sexually-compatible species outside the trial area is estimated as very low. Camelina seeds are moderate in size and not normally dispersed by wind. Management measures including netting when the Camelina is in flower and the use of gas guns and hawk kites will be employed to mitigate the risk of seed removal by birds. Management procedures to minimize the spread of seeds or pollen (such as insect-excluding netting) will further reduce the probability of these events occurring. There will be no compatible species grown for 1000 meters from the boundary of the site and no sexually-compatible wild relatives of *C. sativa* exist in the vicinity of the Rothamsted farm. In the unlikely event of a hybrid being generated, the presence of EPA and DHA in the seed oil of any such progeny will not convey a selectable advantage and most likely the omega-3 trait would not be retained.

The risk of non-sexual, horizontal gene transfer to other species is extremely low. In the event of horizontal gene transfer to bacteria, neither the trait genes nor the marker genes would be expected to confer a selective advantage in the field environment under consideration. The genes introduced in Camelina have been inserted via *Agrobacterium tumefaciens*-mediated gene transfer, and in one iteration (B) the insertion contains the bacterial *nptII* gene from *E. coli*, which is already widely present in the environment. The *nptII* gene expressed in the Camelina plants imparts resistance to certain antibiotics, of value only during the selection process in culture. This confers no selective advantage in the field and has been considered safe for such use by the European Food Safety Authority and it has a 15 year history of use with transgenic crops for this purpose. We estimate the likelihood of horizontal gene transfer as low and the consequences, were it to occur, as negligible. The area proposed to be planted with GMOs is small and temporary (lasting between 3 and 5 months).

Bearing in mind its limited scope, overall risk of harm to human health or the environmental arising from this trial is assessed as very low.

**B7 The methods and plans for monitoring the genetically modified organisms and for responding to an emergency.**

The release site will be visited by trained laboratory personnel who are working on the project at no less than weekly intervals (and at some periods, daily) during the growing season of each year of the trial. Any unexpected occurrences that could potentially result in adverse environmental effects or the possibility of adverse effects on human health will be notified to the Defra

immediately. Should the need arise to terminate the release at any point the emergency plans detailed below will be followed.

At the end of each season, the plot will remain in stubble and monitored for volunteers during the remainder of the year and the following season. Any volunteers identified will be destroyed by herbicide treatment (e.g. glyphosate) or removed by hand and destroyed.

Following completion of the four-year trial the release site will remain fallow for a further season to enable easy identification of volunteers. The site will be inspected regularly and any volunteers identified will be immediately destroyed either by application of a systematic broad leaf herbicide.

**Emergency procedures:** In the unlikely event that the integrity of the site is seriously compromised, the trial will be terminated and all plants, (including GM and control Camelina plots, and cereal separator) will be destroyed using a suitable herbicide or harvesting as deemed appropriate. All harvested material will be removed from the site and disposed of by incineration or deep burial at a local authority-approved landfill site using an approved contractor. Transportation of waste materials will be in secure containers. The phone numbers of all key staff will be available to site security and farm.