

Environmental Protection Agency

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and microorganism identity information required for MCANs in § 725.155(c), (d)(1), and (d)(2).

(d) Persons applying for a TME must submit phenotypic and ecological characteristics information required in § 725.155(d)(3) as it relates directly to the conditions of the proposed test marketing activity.

(e) Persons applying for a TME must also submit the following information about the proposed test marketing activity:

(1) *Proposed test marketing activity.* (i) The maximum quantity of the microorganism which the applicant will manufacture or import for test marketing.

(ii) The maximum number of persons who may be provided the microorganism during test marketing.

(iii) The maximum number of persons who may be exposed to the microorganism as a result of test marketing, including information regarding duration and route of such exposures.

(iv) A description of the test marketing activity, including its duration and how it can be distinguished from full-scale commercial production and research and development activities.

(2) *Health and environmental effects data.* All existing data regarding health and environmental effects of the microorganism must be reported in accordance with § 725.160.

§ 725.370 EPA review of the TME application.

General procedures for review of all submissions under this part are contained in §§ 725.28 through 725.60. In addition, the following procedures apply to EPA review of TME applications submitted under this subpart:

(a) No later than 45 days after EPA receives a TME, the Agency will either approve or deny the application.

(b) A submitter may only proceed with test marketing activities after receipt of EPA approval.

(c) In approving a TME application, EPA may impose any restrictions necessary to ensure that the microorganism will not present an unreasonable risk of injury to health and the environment as a result of test marketing.

Subpart G—General Exemptions for New Microorganisms

§ 725.400 Scope and purpose.

(a) This subpart describes exemptions from reporting under subpart D of this part, and from review under this part altogether, for manufacturing and importing of certain new microorganisms for commercial purposes.

(b) Recipient microorganisms eligible for the tiered exemption from review under this part are listed in § 725.420.

(c) Criteria for the introduced genetic material contained in the new microorganisms are described in § 725.421.

(d) Physical containment and control technologies are described in § 725.422.

(e) The conditions for the Tier I exemption are listed in § 725.424.

(f) In lieu of complying with subpart D of this part, persons using recipient microorganisms eligible for the tiered exemption may submit a Tier II exemption request. The limited reporting requirements for the Tier II exemption, including data requirements, are described in §§ 725.450 and 725.455.

(g) EPA review procedures for the Tier II exemption are set forth in § 725.470.

(h) Subparts A through C of this part apply to any submission under this subpart.

§ 725.420 Recipient microorganisms.

The following recipient microorganisms are eligible for either exemption under this subpart:

(a) *Acetobacter aceti.*

(b) *Aspergillus niger.*

(c) *Aspergillus oryzae.*

(d) *Bacillus licheniformis.*

(e) *Bacillus subtilis.*

(f) *Clostridium acetobutylicum.*

(g) *Escherichia coli* K-12.

(h) *Penicillium roqueforti.*

(i) *Saccharomyces cerevisiae.*

(j) *Saccharomyces uvarum.*

§ 725.421 Introduced genetic material.

For a new microorganism to qualify for either exemption under this subpart, introduced genetic material must meet all of the criteria listed in this section.

(a) *Limited in size.* The introduced genetic material must consist only of the following:

- (1) The structural gene(s) of interest.
- (2) The regulatory sequences permitting the expression of solely the gene(s) of interest.
- (3) Associated nucleotide sequences needed to move genetic material, including linkers, homopolymers, adaptors, transposons, insertion sequences, and restriction enzyme sites.
- (4) The nucleotide sequences needed for vector transfer.
- (5) The nucleotide sequences needed for vector maintenance.

(b) *Well-characterized.* For introduced genetic material, well-characterized means that the following have been determined:

- (1) The function of all of the products expressed from the structural gene(s).
- (2) The function of sequences that participate in the regulation of expression of the structural gene(s).
- (3) The presence or absence of associated nucleotide sequences and their associated functions, where associated nucleotide sequences are those sequences needed to move genetic material including linkers, homopolymers, adaptors, transposons, insertion sequences, and restriction enzyme sites.

(c) *Poorly mobilizable.* The ability of the introduced genetic material to be transferred and mobilized is inactivated, with a resulting frequency of transfer of less than 10⁻⁸ transfer events per recipient.

(d) *Free of certain sequences.* (1) The introduced genetic material must not contain a functional portion of any of the toxin-encoding sequences described in this paragraph (d).

(i) For the purposes of this section, a functional portion of a toxin-encoding sequence means any sequence which codes for a polypeptide that has one of the following effects:

(A) It directly or indirectly contributes to toxic effects in humans. Directly contributes to toxic effects in humans means those sequences encoding polypeptides that have direct toxicity to target cells. An example of a sequence which directly contributes to toxic effects in humans is one which encodes the portion of diphtheria toxin, listed in paragraph (d)(2) of this

section, capable of interacting with elongation factor 2, leading to inhibition of protein synthesis in target respiratory, heart, kidney, and nerve tissues. Indirectly contributes to toxic effects in humans means a sequence whose encoded polypeptide is not directly toxic to target cells, yet still adversely affects humans. An example of a sequence which indirectly contributes to toxic effects is the sequence which encodes the portion of the botulinum toxin, listed in paragraph (d)(3) of this section, capable of blocking the release of acetylcholine from gangliosides. Botulinum toxin affects neuromuscular junctions by its blockage of acetylcholine release, leading to irreversible relaxation of muscles and respiratory arrest.

(B) It binds a toxin or toxin precursor to target human cells.

(C) It facilitates intracellular transport of a toxin in target human cells.

(ii) While these toxins are listed (with synonyms in parentheses) in paragraphs (d)(2) through (d)(7) of this section according to the source organism, it is use of the nucleotide sequences that encode the toxins that is being restricted and not the use of the source organisms. The source organisms are listed to provide specificity in identification of sequences whose use is restricted. Although similar or identical sequences may be isolated from organisms other than those listed below in paragraphs (d)(2) through (d)(7) of this section, these comparable toxin sequences, regardless of the organism from which they are derived, must not be included in the introduced genetic material.

(2) *Sequences for protein synthesis inhibitor.*

Sequence Source	Toxin Name
<i>Corynebacterium diphtheriae</i> & <i>C. ulcerans</i>	Diphtheria toxin
<i>Pseudomonas aeruginosa</i>	Exotoxin A
<i>Shigella dysenteriae</i>	Shigella toxin (Shiga toxin, Shigella dysenteriae type I toxin, Vero cell toxin)
<i>Abrus precatorius</i> , seeds	Abrin
<i>Ricinus communis</i> , seeds	Ricin

(3) *Sequences for neurotoxins.*

Sequence Source	Toxin Name
<i>Clostridium botulinum</i>	Neurotoxins A, B, C1, D, E, F, G (Botulinum toxins, botulin toxins)

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Sequence Source	Toxin Name
<i>Clostridium tetani</i>	Tetanus toxin (tetanospasmin)
<i>Proteus mirabilis</i>	Neurotoxin
<i>Staphylococcus aureus</i>	Alpha toxin (alpha lysin)
<i>Yersinia pestis</i>	Murine toxin
Snake toxins	
<i>Bungarus caeruleus</i>	Caeruleotoxin
<i>Bungarus multicinctus</i>	Beta-bungarotoxin (phospholipase)
<i>Crotalus</i> spp.	Crotoxin (phospholipase)
<i>Dendroaspis viridis</i>	Neurotoxin
<i>Naja naja</i> varieties	Neurotoxin
<i>Notechia scutatus</i>	Notexin (phospholipase)
<i>Oxyuranus scutellatus</i>	Taipoxin
Invertebrate toxins	
<i>Chironex fleckeri</i>	Neurotoxin
<i>Androctonus australis</i>	Neurotoxin
<i>Centruroides sculpturatus</i>	Neurotoxin

(4) Sequences for oxygen labile cytolyins.

Sequence Source	Toxin Name
<i>Bacillus alve</i>	Alveolysin
<i>Bacillus cereus</i>	Cereolysin
<i>Bacillus laterosporus</i>	Laterosporolysin
<i>Bacillus thuringiensis</i>	Thuringiolysin
<i>Clostridium bifermentans</i>	Lysin
<i>Clostridium botulinum</i>	Lysin
<i>Clostridium caproicum</i>	Lysin
<i>Clostridium chauvoei</i>	Delta-toxin
<i>Clostridium histolyticum</i>	Epsilon-toxin
<i>Clostridium novyi</i>	Gamma-toxin
<i>Clostridium oedematiens</i>	Delta-toxin
<i>Clostridium perfringens</i>	Theta-toxin (Perfringolysin)
<i>Clostridium septicum</i>	Delta-toxin
<i>Clostridium sordellii</i>	Lysin
<i>Clostridium tetani</i>	Tetanolysin
<i>Listeria monocytogenes</i>	Listeriolysin (A B)
<i>Streptococcus pneumoniae</i>	Pneumolysin
<i>Streptococcus pyogenes</i>	Streptolysin O (SLO)

(5) Sequences for toxins affecting membrane function.

Sequence Source	Toxin Name
<i>Bacillus anthracis</i>	Edema factor (Factors I II); Lethal factor (Factors II III)
<i>Bacillus cereus</i>	Enterotoxin (diarrheagenic toxin, mouse lethal factor)
<i>Bordetella pertussis</i>	Adenylate cyclase (Heat-labile factor); Pertussigen (pertussis toxin, islet activating factor, histamine sensitizing factor, lymphocytosis promoting factor)
<i>Clostridium botulinum</i>	C2 toxin
<i>Clostridium difficile</i>	Enterotoxin (toxin A)
<i>Clostridium perfringens</i>	Beta-toxin; Delta-toxin
<i>Escherichia coli</i> & other Enterobacteriaceae spp.	Heat-labile enterotoxins (LT); Heat-stable enterotoxins (STa, ST1 subtypes ST1a ST1b; also STb, STII)
<i>Legionella pneumophila</i>	Cytolysin
<i>Vibrio cholerae</i> & <i>Vibrio mimicus</i>	Cholera toxin (choleraegen)

(6) Sequences that affect membrane integrity.

Sequence Source	Toxin Name
<i>Clostridium bifermentans</i> & other <i>Clostridium</i> spp	Lecithinase
<i>Clostridium perfringens</i>	Alpha-toxin (phospholipase C, lecithinase); Enterotoxin
<i>Corynebacterium pyogenes</i> & other <i>Corynebacterium</i> spp.	Cytolysin (phospholipase C), Ovis toxin (sphingomyelinase D)
<i>Staphylococcus aureus</i>	Beta-lysin (beta toxin)

(7) Sequences that are general cytotoxins.

Sequence Source	Toxin Name
<i>Adenia digitata</i>	Modeccin
<i>Aeromonas hydrophila</i>	Aerolysin (beta-lysin, cytotoxic lysin)
<i>Clostridium difficile</i>	Cytotoxin (toxin B)
<i>Clostridium perfringens</i>	Beta-toxin; Epsilon-toxin; Kappa-toxin
<i>Escherichia coli</i> & other Enterobacteriaceae spp.	Cytotoxin (Shiga-like toxin, Vero cell toxin)
<i>Pseudomonas aeruginosa</i>	Proteases
<i>Staphylococcus aureus</i>	Gamma lysin (Gamma toxin); Enterotoxins (SEA, SEB, SEC, SED SEE); Pyrogenic exotoxins A B; Toxic shock syndrome toxins (TSST-1)
<i>Staphylococcus aureus</i> & <i>Pseudomonas aeruginosa</i>	Leucocidin (leukocidin, cytotoxin)
<i>Streptococcus pyogenes</i>	Streptolysin S (SLS); Erythrocytic toxins (scarlet fever toxins, pyrogenic exotoxins)
<i>Yersinia enterocolitica</i>	Heat-stable enterotoxins (ST)

§ 725.422 Physical containment and control technologies.

The manufacturer must meet all of the following criteria for physical containment and control technologies for any facility in which the new microorganism will be used for a Tier I exemption; these criteria also serve as guidance for a Tier II exemption.

(a) Use a structure that is designed and operated to contain the new microorganism.

(b) Control access to the structure.

(c) Provide written, published, and implemented procedures for the safety of personnel and control of hygiene.

(d) Use inactivation procedures demonstrated and documented to be effective against the new microorganism contained in liquid and solid wastes prior to disposal of the wastes. The inactivation procedures must reduce viable microbial populations by at least 6 logs in liquid and solid wastes.

(e) Use features known to be effective in minimizing viable microbial populations in aerosols and exhaust gases released from the structure, and document use of such features.