

Revised Deletion Process for the Site-Specific Recalculation Procedure for Aquatic Life Criteria

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Foreword

This guidance on deriving water quality criteria provides scientific recommendations to states and tribes authorized to establish water quality standards under the Clean Water Act (CWA). Under the CWA, states and tribes are to establish water quality criteria to protect designated uses. State and tribal decision makers retain the discretion to adopt appropriate approaches that differ from those recommended here. While this updated guidance constitutes United States Environmental Protection Agency (EPA) scientific recommendations regarding one possible approach for deriving site-specific criteria that protect aquatic life, this update does not substitute for the CWA or EPA's regulations; nor is it a regulation itself. Thus, it cannot impose legally binding requirements on EPA, states, tribes, or the regulated community, and might not apply to a particular situation based upon the circumstances. EPA may change this guidance in the future, as new scientific information becomes available This document has been approved for publication by the Office of Science and Technology, Office of Water, U.S. Environmental Protection Agency. Mention of trade names or commercial products does not constitute endorsement or recommendation for use.

Acknowledgment

This document was prepared by Charles G. Delos, Office of Science and Technology, Office of Water. This was done in consultation with Charles E. Stephan, Midcontinent Ecology Division, Office of Research and Development, who devised the underlying concept of the approach and produced Appendix 2. The document was peer reviewed by Alex M. Barron, Virginia Department of Environmental Quality, Steven P. Canton, GEI Consultants, Inc., and Jerome M. Diamond, Tetra Tech, Inc. Submit questions to Charles Delos at: delos.charles@epa.gov.

Purpose

The Recalculation Procedure involves editing the composition of a Species Sensitivity Distribution of tested species used to derive a site-specific aquatic life criterion in order to allow it to better reflect the taxonomy of species that reside at the site. This document presents a revision of the Deletion Process of the Recalculation Procedure.

Background

U.S. EPA (1984) described three procedures that can be used to derive a site-specific aquatic life water quality criterion: (1) the Recalculation Procedure, a taxonomic composition adjustment, (2) the Indicator Species Procedure, a bioavailability adjustment now called the Water-Effect Ratio Procedure, and (3) the Resident Species Procedure, a little-used approach effectively superseded by combined application of the Recalculation and Water-Effect Ratio procedures.

The Recalculation Procedure is used to edit the taxonomic composition of the toxicity dataset used for the Species Sensitivity Distribution (SSD) upon which a site-specific criterion is based, in order to better match the assemblage that resides at the site. The Recalculation Procedure is intended to provide flexibility to States to derive site-specific criteria that best reflect the species that reside at a site.

The underlying premise of the Recalculation Procedure is that taxonomy has value in predicting sensitivity, such that a site-specific SSD can be adjusted to reflect the taxonomy of species that reside at a site. The core of the procedure is the Deletion Process, which involves removing tested species from the SSD. The recommended procedure allows deletion of nonresident tested species if and only if they are not appropriate surrogates of resident untested species – based on taxonomy.

The use of taxonomy, while reasonable and systematically straightforward, is not the only conceivable basis for weighing how well a tested species represents untested species at a site. Possibly a system could be developed using ecological traits: that is, morphological, behavioral, and functional characteristics of an organism. Although USGS (2013) offers an invertebrate trait database, and U.S. EPA (2013) suggests some uses, no system involving its use for site-specific criteria exists at this time.

Based on taxonomy, U.S. EPA (1994) provided the Recalculation Procedure with a step-by-step protocol for deciding which nonresident tested species to retain or delete. For any particular nonresident tested species, the decision process begins at the genus level: the species is either (a) deleted, (b) retained as a surrogate for resident untested species in the genus, or (c) a decision is postponed. If the decision is postponed, then the next higher taxonomic level is considered. For a nonresident tested species, this hierarchical process stops once the decision to delete or retain is made – that is, the decision to delete or retain is not reconsidered or reversed at a higher taxonomic level.

U.S EPA (1997) modified the procedure in response to issues raised about its behavior with a particular configuration of tested and resident species. Likewise, the current guidance has been prepared in response to apparent conflicts between the results of the step-by-step protocol applied to certain datasets, and the stated goals of the 1997 procedure. Although the 1997 revision had corrected unintended behavior of the 1994 procedure at the genus and family levels, it did not eliminate the possibility that certain data configurations could produce unintended retention of inappropriate potential surrogates at the order, class, or phylum levels.

The purpose of this document is to update and supersede the guidance on applying the Deletion Process of the Recalculation Procedure presented in U.S. EPA (1984, 1994, and 1997). The principles underlying this revised procedure are identical to those applied at the genus and family level in the 1997 revision. It now extends those principles to the order, class, and phylum levels.

Concept of the Procedure

The concept of the Recalculation Procedure remains unchanged: to create a site-specific toxicity dataset (Species Sensitivity Distribution) that is appropriate for deriving a site-specific aquatic life criterion, by modifying the national toxicity dataset for the pollutant of concern by correcting, adding, and/or deleting test results. Deletion is based on taxonomic composition of the site under consideration.

Because some tested species might be needed to represent untested species that occur at the site, the deletion procedure does not provide for simplistic deletion of all species that do not occur at the site. Rather the concept is to consider which tested species are most closely related to those occurring at the site, and delete those for which another tested species would better represent the species occurring at the site.

The Deletion Process is designed to ensure that:

- Each species, genus, family, order, class, and phylum that occurs both at the site and in the national toxicity dataset is retained in the site-specific toxicity dataset.
- Each species, genus, family, order, class, and phylum that occurs at the site but not in the national toxicity dataset is represented in the site-specific dataset by at least one species most closely related to it from the national dataset.

The underlying principle of the Deletion Process has been and continues to be as follows:

- 1. Looking within a genus, are all of its resident species tested? (That is, are they in the national toxicity dataset?) If so, then delete the nonresident tested species in that genus. If not, retain them as surrogates.
- 2. Moving up to the family level, does every resident genus in a family contain at least one tested species? (That is, are all of its resident genera tested?) If so, then delete the tested

- species in the family's nonresident genera. If not, retain them. (Note that this is not asking whether every resident *species* in the family is tested. Rather it asks whether every resident *genus* in the family appears in the national toxicity dataset.)
- 3. Moving up each subsequent level, to order, class, and phylum, the concept remains parallel. Does every resident family in an order contain at least one tested species? Does every resident order in a class contain at least one tested species? Does every resident class in a phylum contain at least one tested species? In each case, if so, delete the nonresident. If not, retain as surrogates.

It is at the order, class, and phylum levels that the exact wording of the 1997 step-by-step process did not match the underlying concept. This revision of the guidance corrects that problem.

Review of Several Key Provisions from Previous Guidance

Because the Deletion Process is taxonomy based, it is important that one taxonomic system be used consistently in the derivation of national and site-specific criteria. The system that U.S. EPA uses is the Integrated Taxonomic Information System (ITIS; www.itis.gov). However, the only ITIS taxonomic levels that are used by the Deletion Process are the traditional and universally recognized levels of species, genus, family, order, class, and phylum. (That is, subdivisions such as subclass, infraclass, and superorder are not used.)

Following the 1994 Recalculation Procedure guidance, the equivalent terms "resident" or "occur at the site" includes life stages and species that:

- a. are usually present at the site,
- b. are present at the site only seasonally due to migration,
- c. are present at the site intermittently because they periodically return to or extend their ranges into the site,
- d. were present at the site in the past, are not currently present at the site due to degraded conditions, but are expected to return to the site when conditions improve, or
- e. are present in nearby bodies of water, are not currently present at the site due to degraded conditions, but are expected to be present at the site when conditions improve.

The terms "resident" or "occur at the site" do *not* include life stages and species that:

a. were once present at the site but cannot exist at the site now due to permanent alterations of the habitat or other conditions that are not likely to change within reasonable planning horizons, or

b. are still-water life stages or species that are found in a flowing-water site solely and exclusively because they are washed through the site by stream flow from a still-water site.

The definition of the "site" is important when the Deletion Process is used. For example, the number of taxa that occur at the site will generally decrease as the size of the site decreases. However, if the site is defined to be very small, a permit limit might be controlled by a criterion that applies outside (e.g., downstream of) the site. Use of the Recalculation Procedure does not sidestep the need to protect downstream uses.

Resident "critical species" merit one special provision, per EPA (1994). A critical species is a resident species that (a) is commercially or recreationally important at the site, or (b) is listed as threatened or endangered under section 4 of the Endangered Species Act, or (c) is a species for which there is firm evidence that its loss would yield an unacceptable impact on the site's commercially or recreationally important species, endangered species, abundances of a variety of other species, or structure or function. The Deletion Process should not be undertaken unless toxicity data are available for at least one species in each *class* of aquatic plants or animals that contains a critical species. Thus for example, if the site has an amphibian that fits the designation of a critical species, the Deletion Process should not be undertaken unless toxicity data for a species in class Amphibia are available (possibly via new testing).

Although the scope of this update is limited – to fulfill a change that was intended by the U.S. EPA (1997) guidance – analysts experienced with application of the procedure have reported some other issues (ERG 2013). The comprehensiveness of the list of resident species is influenced by the quality of the biological survey of the site water body and of comparable water bodies. Although greater or lesser comprehensiveness does not inherently bias a criterion recalculation either upward or downward, lesser comprehensiveness increases the uncertainty in the appropriateness of the recalculated criterion. Uncertainties in the process of identifying species occurring at the site have been reported as impediments to the acceptance of recalculations proposed to states (ERG 2013). It is thus important to fully document the effort put into compiling the list of resident species.

ERG (2013) also reported issues about sites having limited diversity – for example, sites that cannot support fish. For deriving *national* criteria, tests with three families of fish are called for (unless an amphibian is substituted for one of them). For site-specific recalculations, the underlying concept of having tests for a diversity of species is more fundamental than having tests for particular taxonomic groups that may be irrelevant to the site.

Explanatory Example of the Deletion Process

The underlying concept may be illustrated through a hypothetical example. In the following simple case, the class Actinopterygii (ray-finned fishes) has only four species to consider: two are resident at the site, and three are tested.

Phylum	Class	Order	Family	Genus	Species	Resident?	Tested?	Retain?	Why?
Chord.	Actinopterygii	Perciformes	Percidae	Etheostoma	nigrum	Yes	No	No	1
Chord.	Actinopterygii	Perciformes	Centrarchidae	Lepomis	cyanellus	Yes	Yes	Yes	2
Chord.	Actinopterygii	Perciformes	Moronidae	Morone	saxatilis	No	Yes	Yes	3
Chord.	Actinopterygii	Salmoniformes	Salmonidae	Oncorhynchus	mykiss	No	Yes	No	4

- (1) The one species in family Percidae, although *resident*, is *not tested* and so obviously cannot be in the site-specific toxicity dataset.
- (2) The one species in family Centrarchidae is both *resident and tested* and so is retained in the site-specific dataset.
- (3) The one species in family Moronidae is *not resident* but is *tested*. The question is whether it should be retained as a surrogate. Here order Perciformes has two resident families, Percidae and Centrarchidae. Of these two only Centrarchidae is tested. Consequently, family Moronidae is retained so that it can serve along with Centrarchidae as surrogates equally closely related to the untested resident family Percidae.
- (4) Order Salmoniformes is *not resident* but has a *tested* species. Again the question is whether to retain it as a surrogate. In this case it is deleted because the site has no resident untested fish order needing a surrogate. That is, the only resident order, Perciformes, is tested (that is, Perciformes contains at least one tested species), making it unnecessary for anything in Salmoniformes to serve as a surrogate. In contrast, if the dataset had contained an untested third order, say Cypriniformes, essentially equally closely related to the tested Perciformes and Salmoniformes, then the tested Salmoniformes would be retained to share the surrogacy.

The Deletion Process itself is presented in Appendix 1 and Appendix 2. These two appendices represent two different ways of setting forth the procedure. Nevertheless, they are logically equivalent such that they yield identical results. Appendix 3 provides a number of examples illustrating the results of applying the Deletion Process.

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Appendix 1. Shorter Statement of the Deletion Process

This version is identical to the EPA 1997 guidance in Steps 1 and 2, and extends the concept of Steps 1 and 2 (genus and family) to Steps 3, 4, and 5 (order, class, and phylum).

In the (possibly updated) national toxicity dataset, circle each species that either satisfies the definition of "occur at the site". Then use the following step-wise process to determine which of the uncircled (i.e., nonresident) species are to be deleted.

1. Does a species in the genus occur at the site?

If "No", go to step 2.

If "Yes", are there one or more species in the genus that occur at the site but are not in the national toxicity dataset?

If "No", delete the uncircled species.*

If "Yes", retain the uncircled species.*

2. Does a species in the family occur at the site?

If "No", go to step 3.

If "Yes", are there one or more genera in the family that occur at the site but are not in the national toxicity dataset?

If "No", delete the uncircled species.*

If "Yes", retain the uncircled species.*

3. Does a species in the order occur at the site?

If "No", go to step 4.

If "Yes", are there one or more families in the order that occur at the site but are not in the national toxicity dataset?

If "No", delete the uncircled species.*

If "Yes", retain the uncircled species.*

4. Does a species in the class occur at the site?

If "No", go to step 5.

If "Yes", are there one or more orders in the class that occur at the site but are not in the national toxicity dataset?

If "No", delete the uncircled species.*

If "Yes", retain the uncircled species.*

5. Does a species in the phylum occur at the site?

If "No", delete the uncircled species.*

If "Yes", are there one or more classes in the phylum that occur at the site but are not in the national toxicity dataset?

If "No", delete the uncircled species.*

If "Yes", retain the uncircled species.*

* = Continue the deletion process by starting at step 1 for another uncircled species unless all uncircled species in the national toxicity dataset have been addressed.

Appendix 2. Longer Statement of the Deletion Process

In contrast to the Appendix 1 version, which operates on the list of tested species, comparing it to the list of resident species, this version operates on a single combined list. Use of a single list was found to have certain advantages, which furthered the development of an automated spreadsheet for determining retention or deletion of tested species. Appendices 1 and 2 are intended to yield identical results.

Steps A through J are performed sequentially so that the appropriate entry is made in the site-specific toxicity dataset column for each species; the entry indicates whether the species is or is not included in the site-specific toxicity dataset. This version of the Deletion Process is organized so that, beginning with Step D, each species that does not have an entry in the site-specific toxicity dataset column is addressed at the genus level before any species is addressed at the family level. Then, the order, class, and phylum taxonomic levels are addressed sequentially. The number of species that need to be addressed decreases as higher and higher taxonomic levels are addressed.

- Step A: Make a table that lists all of the species in the (possibly modified) national toxicity dataset, all of the species that occur at the site, and all surrogates that are used for critical species at the site in taxonomic order by species, genus, family, order, class, and phylum using the current version of ITIS. If a surrogate species is listed in the table, the species that it is a surrogate for should not be listed in the table. Fill in each column for each species, except do not put anything in the last column on the right, which is titled "In site-specific toxicity dataset?"
- Step B: For each species that has a "No" in the national toxicity dataset column, enter "N-1" in the site-specific toxicity dataset column.
 - 1. N = "No" and means that the species is not in the site-specific toxicity database.
- Step C: For each species that has a "Yes" in the "Occur at the site?" column and a "Yes" in the national toxicity dataset column, enter "Y-2" in the site-specific toxicity dataset column.

Each species that does not yet have an entry in the site-specific toxicity dataset column has a "No" in the "Occur at the site?" column and a "Yes" in the national toxicity dataset column.

- Step D: Look down the column titled "Genus" and every time a genus name appears more than once, draw a circle around all of the multiple entries for that one genus. The species in the circled genera are the only species that will be addressed in this Step D. For each species that is in a circled genus and does not already have an entry in the site-specific toxicity dataset column, look at the circled genus that that species is in and do one of the following regarding the site-specific toxicity dataset column:
 - 1. Enter "N-3" if all of the <u>species</u> in that genus that occur at the site are already in the site-specific toxicity dataset.
 - 2. Enter "Y-4" if one or more of the <u>species</u> in that genus that occur at the site are not in the <u>site-specific</u> toxicity dataset.

This step will not result in an entry for tested species in genera having no species occurring at the site.

- Step E: Look down the column titled "Family" and every time a family name appears more than once, draw a circle around all of the multiple entries for that one family. The species in the circled families are the only species that will be addressed in this Step E. For each species that is in a circled family and does not already have an entry in the site-specific toxicity dataset column, look at the circled family that that species is in and do one of the following regarding the site-specific toxicity dataset column:
 - 1. Enter "N-5" if all of the <u>genera</u> in that family that occur at the site are already represented in the <u>site-specific</u> toxicity dataset.
 - 2. Enter "Y-6" if one or more of the <u>genera</u> in that family that occur at the site are not represented in the <u>site-specific</u> toxicity dataset.

This step will not result in an entry for tested species in families having no species occurring at the site.

- Step F: Look down the column titled "Order" and every time an order name appears more than once, draw a circle around all of the multiple entries for that one order. The species in the circled orders are the only species that will be addressed in this Step F. For each species that is in a circled order and does not already have an entry in the site-specific toxicity dataset column, look at the circled order that that species is in and do one of the following regarding the site-specific toxicity dataset column:
 - 1. Enter "N-7" if all of the <u>families</u> in that order that occur at the site are already represented in the <u>site-specific</u> toxicity dataset.
 - 2. Enter "Y-8" if one or more of the <u>families</u> in that order that occur at the site are not represented in the <u>site-specific</u> toxicity dataset.

This step will not result in an entry for tested species in orders having no species occurring at the site.

- Step G: Look down the column titled "Class" and every time a class name appears more than once, draw a circle around all of the multiple entries for that one class. The species in the circled classes are the only species that will be addressed in this Step G. For each species that is in a circled class and does not already have an entry in the site-specific toxicity dataset column, look at the circled class that that species is in and do one of the following regarding the site-specific toxicity dataset column:
 - 1. Enter "N-9" if all of the <u>orders</u> in that class that occur at the site are already represented in the <u>site-specific</u> toxicity dataset.
 - 2. Enter "Y-10" if one or more of the <u>orders</u> in that class that occur at the site are not represented in the <u>site-specific</u> toxicity dataset.

This step will not result in an entry for tested species in classes having no species occurring at the site.

Step H: Look down the column titled "Phylum" and every time a phylum name appears more than once, draw a circle around all of the multiple entries for that one phylum. The species in the circled phyla are the only species that will be addressed in this Step H. For each species that is in a circled phylum and does not already have an entry in the

site-specific toxicity dataset column, look at the circled phylum that that species is in and do one of the following regarding the site-specific toxicity dataset column:

- 1. Enter "N-11" if all of the <u>classes</u> in that phylum that occur at the site are already represented in the <u>site-specific</u> toxicity dataset.
- 2. Enter "Y-12" if one or more of the <u>classes</u> in that phylum that occur at the site are not represented in the <u>site-specific</u> toxicity dataset.

Step I: For each species for which no entry has been made in the site-specific toxicity dataset column, enter "N-13" because the phylum does not occur at the site.

Aspects of a completed table that are easy to review.

- a. Every "N" should have an odd number after it.
- b. Every "Y" should have an even number after it.
- c. Every species that has "No" in the national toxicity database column should have "N-1" in the site-specific database column.
- d. Every species that has "Y-2" in the site-specific toxicity database column should have "Yes" in the "Occur at the site?" column and in the national toxicity dataset column.

Appendix 3. Table of Hypothetical Examples Illustrating Results of the Deletion Process

The hypothetical *input* data constitute all but the last column (Phyla Pa – Pi, Classes Ca – Cq, ..., Species Sa – Sbk), as would be arranged for the procedure's "Longer Statement" (Appendix 2). The last column shows the result of applying the Deletion Process; its numeric codes correspond to those of Appendix 2, thereby indicating the step at which the decision was made to include (Y) or not include (N) the species in the site-specific Species Sensitivity Distribution (SSD).

The table is intended to represent numerous individual examples rather than a single complete dataset. It begins by examining behavior at the genus through family levels. Later portions of the table illustrate decisions made at higher taxonomic levels. The table illustrates various cases where tested species that do not occur at the site are either retained as surrogates for untested species that do occur at the site, or are deleted as less representative than the tested species retained.

						Occurs at	In national	Include in
Phylum	Class	Order	Family	Genus	Species	the site?	SSD?	site SSD?
Pa	Ca	Oa	Fa	Ga	Sa	Yes	Yes	Y-2
Pa	Ca	Oa	Fb	Gb	Sb	Yes	No	N-1
Pa	Ca	Oa	Fb	Gb	Sc	Yes	No	N-1
Pa	Ca	Oa	Fc	Gc	Sd	No	Yes	N-3
Pa	Ca	Oa	Fc	Gc	Se	Yes	Yes	Y-2
Pa	Ca	Oa	Fd	Gd	Sf	Yes	No	N-1
Pa	Ca	Oa	Fd	Gd	Sg	No	Yes	Y-4
Pa	Ca	Oa	Fd	Gd	Sh	Yes	Yes	Y-2
Pa	Ca	Oa	Fe	Ge	Si	No	Yes	Y-4
Pa	Ca	Oa	Fe	Ge	Sj	Yes	No	N-1
Pa	Ca	Oa	Fe	Ge	Sk	No	Yes	Y-4
Pa	Ca	Oa	Fe	Ge	Sl	Yes	No	N-1
Pa	Ca	Oa	Ff	Gf	Sm	No	Yes	N-3
Pa	Ca	Oa	Ff	Gf	Sn	Yes	Yes	Y-2
Pa	Ca	Oa	Ff	Gf	So	No	Yes	N-3
Pa	Ca	Oa	Ff	Gf	Sp	No	Yes	N-3
Pa	Ca	Oa	Fg	Gg	Sq	Yes	Yes	Y-2
Pa	Ca	Oa	Fg	Gg	Sr	No	Yes	N-3
Pa	Ca	Oa	Fg	Gh	Ss	Yes	No	N-1
Pa	Ca	Oa	Fg	Gi	St	No	Yes	Y-6
Pa	Ca	Oa	Fh	Gj	Su	No	Yes	N-5
Pa	Ca	Oa	Fh	Gk	Sv	No	Yes	N-5
Pa	Ca	Oa	Fh	Gl	Sw	Yes	Yes	Y-2
Pa	Ca	Oa	Fi	Gm	Sx	No	Yes	Y-6
Pa	Ca	Oa	Fi	Gn	Sy	No	Yes	Y-6
Pa	Ca	Oa	Fi	Go	Sz	Yes	No	N-1

						Occurs at	In national	Include in
Phylum	Class	Order	Family	Genus	Species	the site?	SSD?	site SSD?
Pb	Cb	Ob	Fj	Gp	Saa	Yes	No	N-1
Pb	Cc	Oc	Fk	Gq	Sab	No	Yes	Y-12
Pc	Cd	Od	Fl	Gr	Sac	No	Yes	N-13
Pd	Ce	Oe	Fm	Gs	Sad	No	Yes	N-11
Pd	Cf	Of	Fn	Gt	Sae	Yes	Yes	Y-2
Pd	Cf	Of	Fn	Gu	Saf	Yes	No	N-1
Pd	Cf	Of	Fn	Gu	Sag	No	Yes	Y-4
Pd	Cf	Of	Fn	Gu	Sah	No	Yes	Y-4
Pd	Cf	Of	Fn	Gv	Sai	Yes	Yes	Y-2
Pd	Cf	Of	Fn	Gv	Saj	No	Yes	N-3
Pd	Cf	Of	Fn	Gw	Sak	No	Yes	N-5
Pd	Cf	Of	Fo	Gx	Sal	Yes	No	N-1
Pd	Cf	Of	Fo	Gy	Sam	No	Yes	Y-6
Pd	Cf	Og	Fp	Gz	San	Yes	No	N-1
Pd	Cf	Og	Fq	Gaa	Sao	No	Yes	Y-8
Pd	Cf	Oh	Fr	Gab	Sap	Yes	Yes	Y-2
Pd	Cf	Oh	Fr	Gab	Saq	Yes	No	N-1
Pd	Cf	Oh	Fr	Gab	Sar	No	Yes	Y-4
Pd	Cf	Oh	Fs	Gac	Sas	No	Yes	N-7
Pd	Cg	Oi	Ft	Gad	Sat	Yes	No	N-1
Pd	Cg	Oj	Fu	Gae	Sau	No	Yes	Y-10
Pe	Ch	Ok	Fv	Gaf	Sav	Yes	Yes	Y-2
Pe	Ci	Ol	Fw	Gag	Saw	No	Yes	N-11
Pf	Cj	Om	Fx	Gah	Sax	Yes	Yes	Y-2
Pf	Cj	On	Fy	Gai	Say	No	Yes	N-9
Pg	Ck	Oo	Fz	Gaj	Saz	Yes	Yes	Y-2
Pg	Ck	Oo	Fz	Gaj	Sba	No	Yes	N-3
Pg	Ck	Oo	Fz	Gak	Sbb	No	Yes	N-5
Pg	Ck	Op	Faa	Gal	Sbc	No	Yes	N-9
Pg	Cl	Oq	Fab	Gam	Sbd	No	Yes	Y-12
Pg	Cm	Or	Fac	Gan	Sbe	Yes	No	N-1
Ph	Cn	Os	Fad	Gao	Sbf	No	Yes	Y-12
Ph	Cn	Os	Fad	Gao	Sbg	No	Yes	Y-12
Ph	Cn	Os	Fad	Gap	Sbh	No	Yes	Y-12
Ph	Co	Ot	Fae	Gaq	Sbi	Yes	No	N-1
Pi	Ср	Ou	Faf	Gar	Sbj	No	Yes	N-13
Pi	Cq	Ov	Fag	Gas	Sbk	No	No	N-1