



Development and Characterization of Microsatellite Loci in the Endangered Catpaw, *Epioblasma Obliquata* (Bivalvia:Unionidae)

Authors: Ortiz, Katlyn, Jones, Jess W., and Hallerman, Eric M.

Source: Freshwater Mollusk Biology and Conservation, 25(1) : 1-6

Published By: Freshwater Mollusk Conservation Society

URL: <https://doi.org/10.31931/fmbc-d-21-00002>

BioOne Complete (complete.BioOne.org) is a full-text database of 200 subscribed and open-access titles in the biological, ecological, and environmental sciences published by nonprofit societies, associations, museums, institutions, and presses.

Your use of this PDF, the BioOne Complete website, and all posted and associated content indicates your acceptance of BioOne's Terms of Use, available at www.bioone.org/terms-of-use.

Usage of BioOne Complete content is strictly limited to personal, educational, and non - commercial use. Commercial inquiries or rights and permissions requests should be directed to the individual publisher as copyright holder.

BioOne sees sustainable scholarly publishing as an inherently collaborative enterprise connecting authors, nonprofit publishers, academic institutions, research libraries, and research funders in the common goal of maximizing access to critical research.

REGULAR ARTICLE

DEVELOPMENT AND CHARACTERIZATION OF MICROSATELLITE LOCI IN THE ENDANGERED CATSPAW, *EPIOBLASMA OBLIQUATA* (BIVALVIA:UNIONIDAE)

Katlyn Ortiz¹, Jess W. Jones^{1,2*}, and Eric M. Hallerman¹

¹ Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061 USA

² U.S. Fish and Wildlife Service, Department of Fish and Wildlife Conservation, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061 USA

ABSTRACT

The endangered Catspaw, *Epioblasma obliquata*, is restricted to one known reproducing population in Killbuck Creek, Coshocton County, Ohio. Little is known about the genetic diversity of this small population, and such information is needed to help inform recovery planning. We nonlethally sampled 44 individuals of *E. obliquata* using buccal swabs, from which we developed and characterized 14 polymorphic microsatellite loci. Significant deviations from Hardy–Weinberg Equilibrium (HWE), showing deficiencies in heterozygotes, were observed at 6 of the 14 loci, and linkage disequilibrium (LD) was observed at 9 (~10%) of 91 possible pairwise comparisons among loci. Allelic diversity ranged from 2 to 15 alleles per locus and averaged 7.6 alleles per locus. Observed heterozygosity per locus ranged from 0.091 to 1.000 and averaged 0.674. Possible explanations for deviations from HWE and LD could be from loci located close together on the same chromosome, segregation of null alleles, family structure within the small population, population bottlenecks, inbreeding, hermaphroditic reproduction, or some combination of these factors. Managers can use these microsatellite markers to assess and monitor genetic diversity in the remaining wild population in Killbuck Creek, prospective broodstock, hatchery-reared progeny, and reintroduced populations founded to promote recovery of the species.

KEY WORDS: Catspaw, *Epioblasma obliquata*, freshwater mussel, DNA microsatellite loci, primers, genetic diversity

INTRODUCTION

The Catspaw, *Epioblasma obliquata*, was listed as endangered under the U.S. Endangered Species Act in 1990; at that time, two isolated nonreproducing populations were known, one in the Green River in Kentucky and the other in the Cumberland River in Tennessee (USFWS 1990). These two populations now are considered extirpated. However, in 1994, a population of reproducing *E. obliquata* was discovered in a short reach of Killbuck Creek, a tributary of the Walhonding River in the Muskingum River watershed in

Coshocton County, Ohio (Hoggarth et al. 1995). State and federal agencies are using this population as a source of broodstock for captive propagation in an attempt to recover the species.

Given the single-source population, genetic variation in hatchery progeny is a concern. Potential genetic threats to survival of the species include loss of within-population genetic variation from nonrepresentative sampling or low numbers of broodstock and family-size variation in the hatchery (Jones et al. 2006; Cooper et al. 2009). Microsatellites, or simple sequence repeats, are tandemly repeated motifs of multiple bases of nuclear DNA found in all eukaryotic genomes (Zane et al. 2002). Microsatellites are highly

*Corresponding Author: Jess_Jones@fws.gov

polymorphic loci that are ideally suited for genetic monitoring of wild and captive populations. The goal of this study was to develop and evaluate a set of microsatellite DNA PCR primers to analyze the genetic variation of the small source population in Killbuck Creek and any progeny produced in hatcheries.

METHODS

We obtained DNA samples from 44 adult *Epioblasma obliquata* that originally were collected from Killbuck Creek, Coshocton County, Ohio. These adults represented all individuals found at multiple sites and during multiple visits to the creek to collect broodstock in 2016–17. Adults were transported to and held at the Kentucky Department of Fish and Wildlife Resources' Minor E. Clark Fish Hatchery as part of the recovery program for the species. We nonlethally sampled these 44 individuals from the hatchery in the fall of 2018 by gently opening each mussel and vigorously swabbing the foot with a buccal swab (Kit DDK-50, Isohelix, Harrietsham, UK). From the buccal swab, DNA was isolated and extracted using an Isohelix DNA isolation kit, and its concentration and purity were assessed by using a μ Lite PC spectrophotometer (Biodrop, Cambridge, UK). In addition to morphological identification, the identification of all individuals as *E. obliquata* was confirmed using the mitochondrial DNA sequence from the first subunit of NADH dehydrogenase (*ND1*), a protein-encoding gene amplified by PCR using primers and conditions reported by Serb et al. (2003).

The Savannah River Ecology Laboratory at the University of Georgia developed a microsatellite library. Genomic DNA used to isolate the microsatellite loci was extracted from two individuals collected from the wild in 2016, utilizing a DNEasy Blood and Tissue Kit (Qiagen, Germantown, MD, USA). A genomic library was prepared with inserts size-selected to range from 300 to 600 bp. Paired-end reads were sequenced on an Illumina HiSeq sequencer. Using the program MSATCOMMANDER (Faircloth 2008), 463,713 reads containing 3–6 bp repeat motifs were identified. Primer3 (Untergasser et al. 2012) was used for PCR primer design. Initially, we screened 60 primer pairs on a panel of eight *E. obliquata* individuals and narrowed our evaluation to a set of 14 microsatellite polymorphic primer pairs. The criteria used to select these primer pairs were polymorphism of the loci amplified (i.e., observation of more than one allele), tri- or tetranucleotide repeat motif, and annealing temperature close to 59°C for use in subsequent multiplexing. Forward primers were labelled with fluorescent markers as noted in Table 1. Four sets of loci were coamplified in multiplex PCR—*Eoo11* and *Eoo20*; *Eoo16* and *Eoo19*; *Eoo22* and *Eoo24*; *Eoo8*, *Eoo9*, and *Eoo10*; other loci were amplified individually. PCR conditions consisted of H₂O, 5× PCR buffer (Promega, Madison, WI, USA), 2.5 mM MgCl₂ (Promega), 2.5 mM deoxynucleotide triphosphate (dNTPs) (ThermoFisher Scientific, Waltham, MA, USA), 1 mg/mL bovine serum albumin (BSA) (ThermoFisher Scientific), 5 μ M of each primer, 0.1 μ L GoTaq Polymerase (New England Biolabs, Ipswich, MA,

USA), and 1 μ L of genomic DNA at 50 ng/ μ L, in a total reaction volume of 22 μ L. PCR thermal cycling conditions were as follows: 94°C for 3 min, followed by 35 cycles of 94°C for 40 s, 59°C for 40 s, and 72°C for 1 min; a final extension at 72°C for 5 min; and a hold at 4°C. Amplification of PCR products was verified by visualization under ultraviolet light in an ethidium bromide-stained agarose gel. PCR products were sent to the Institute of Biotechnology at Cornell University, Ithaca, New York, for DNA fragment-size analysis. Microsatellites were scored for length using GeneMarker (SoftGenetics, State College, PA, USA). Arlequin v3.0 (Excoffier et al. 2005) was used to assess heterozygosity, number of observed alleles per locus, conformance to Hardy–Weinberg equilibrium (HWE), and linkage disequilibrium (LD). Testing for HWE and LD used Arlequin and a critical type I error rate = 0.05. Evidence for a bottleneck at each locus was tested using the Garza–Williamson index (*M*-ratio, the ratio of the number of alleles observed to the number of alleles possible within the observed range in allele sizes) using Arlequin; values of *M* below 0.7 suggest the occurrence of a bottleneck (Garza and Williamson 2001). MICROCHECKER 2.2.3 (Van Oosterhout et al. 2004) was used to assess the possibility of segregation of null alleles.

RESULTS AND DISCUSSION

Allelic diversity ranged from 2 to 15 alleles per locus and averaged 7.6 alleles per locus, while observed heterozygosity per locus ranged from 0.091 to 1.000 and averaged 0.674 (Table 1). Significant deviations from HWE, showing deficiencies in heterozygotes, were observed at 6 of the 14 loci, and LD was observed at 9 (~10%) of the 91 pairwise comparisons among loci and involved 12 of the 14 total loci sampled (*Eoo9* and *Eoo19*; *Eoo11* and *Eoo19*; *Eoo9* and *Eoo22*; *Eoo20* and *Eoo22*; *Eoo16* and *Eoo24*; *Eoo11* and *Eoo31*; *Eoo8* and *Eoo44*; *Eoo31* and *Eoo38*; *Eoo11* and *Eoo60*). The *M*-ratios for six loci were below 0.70, suggesting recent loss of allelic diversity at these loci. Possible segregation of null alleles was detected at loci *Eoo16*, *Eoo20*, *Eoo22*, and *Eoo38*. Because of the small size of the population sampled, deviations from HWE and LD could result from loci being closely located on the same chromosome, segregation of null alleles, family structure, population bottlenecks, inbreeding, hermaphroditic reproduction (van der Schalie 1970), or some combination of these factors. Appendix A1 lists individual genotypes at the 14 loci.

These primer pairs are the third set of microsatellite primers developed for the genus *Epioblasma*. The first set of primers was developed for *Epioblasma capsaeformis* (Jones et al. 2004) and the second for *Epioblasma rangiana* (Zanatta and Murphy 2006). We did not test primers developed for *E. capsaeformis* and *E. rangiana* on *E. obliquata*, but allelic diversity of *E. obliquata* was lower than in those two species. For the 10 loci developed for *E. capsaeformis* ($n = 20$ individuals assessed/locus), allelic diversity ranged from 5 to 17 alleles/locus and averaged 9.7 alleles/locus. For the six loci

Table 1. Characteristics of 14 microsatellite loci developed using DNA obtained in 2016 and 2017 from 44 individuals of the Catspaw (*Epioblasma obliquata*) from Killbuck Creek, Coshocton County, Ohio. H_O and H_E are observed and expected heterozygosity, respectively. Statistically significant deviations from Hardy–Weinberg Equilibrium (HWE) are denoted by an asterisk (*). M -ratio is the Garza–Williamson index. Individual genotypes at the 14 loci are reported in Appendix A1.

Locus	Primer Sequence (5'–3') and Fluorescent Label	Melting Temperature (°C)	Repeat Motif	Allele Size Range (bp)	No. of Alleles/ Locus	H_O	H_E	HWE P Value	M -Ratio
<i>Eoo8*</i>	F:TATCCCTCCGCTGCTGTAAG – PET R:CCCTGGCCTGTAACAATCTTG	59.7 59.7	ACT ₍₁₆₎	125–173	5	1.000	0.586	0.000*	0.714
<i>Eoo9</i>	F:CTCTCCGTGATGTTTGCTCC – VIC R:TTCCATTCCAAGCACGTACG	59.3 59.7	AAT ₍₂₉₎	110–197	4	0.477	0.512	0.081	1.000
<i>Eoo10*</i>	F:CTGGTTGTTCTGGTCTTGTGG – NED R:ACTTTACATCCTGTCCAACCTGC	59.4 59.8	ATC ₍₈₎	137–161	13	0.864	0.815	0.019*	0.867
<i>Eoo11</i>	F:GCCGCCATGAATAGCCTATC – 6FAM R:TCTCCCATCAACCAACATTGTC	59.4 59.4	AAC ₍₁₀₎	197–227	2	0.455	0.505	0.556	0.667
<i>Eoo16*</i>	F:TGGGTAGTCTCTGTCTGATGC – NED R:AATGGCGCTAATCCACAAC	59.7 59.7	ACAT ₍₁₁₎	132–176	8	0.477	0.597	0.021*	0.363
<i>Eoo19</i>	F:CCTAGGCAGCAAACAGTTCG – 6FAM R:GCGGCCAGTATTAATGGTGG	59.8 59.9	AGAT ₍₁₀₎	109–149	13	0.977	0.900	0.137	0.541
<i>Eoo20</i>	F:ACTACAGTACACGACCAGGC – PET R:ACCCATGACCTTCCGTATCC	59.6 59.9	ACAT ₍₁₉₎	74–150	15	0.786	0.921	0.050	0.789
<i>Eoo22*</i>	F:CAGTCCAAGTCATCTCTCAGG – VIC R:GCATACGTGTAGCTTTATCGTG	58.4 58.2	AGAT ₍₁₅₎	91–151	12	0.750	0.894	0.003*	0.923
<i>Eoo24</i>	F:TCACAAGTCCTACACCCTCTC – PET R:TCTTATCAGTTGGGTTTGGTGG	59.0 59.2	AATC ₍₆₎	169–193	2	0.500	0.471	0.748	1.000
<i>Eoo31</i>	F:CAGTCGGGCGTCATCATTCCCTAGCAA – PET R:GTTTGGTGTAGTGCTCGGAAAC	59.7 58.9	ATC ₍₉₎	205–232	6	0.591	0.651	0.314	0.500
<i>Eoo38*</i>	F:CAGTCGGGCGTCATCAGCTAACTCCA – 6FAM R:GTTTCGCCACCTGAACAGCATATG	59.4 60.1	AAG ₍₁₁₎	101–134	13	0.659	0.882	0.000*	0.722
<i>Eoo44*</i>	F:CAGTCGGGCGTCATCACCATTAACT – VIC R:GTTTGGGCATCAACGACTTTCATTC	59.8 58.6	AAC ₍₈₎	84–108	2	1.000	0.506	0.000*	0.667
<i>Eoo46</i>	F:CAGTCGGGCGTCATCACTGTAACGAG – NED R:GTTTGTAGTTGGGCGGATGGTTG	58.9 59.9	ATCC ₍₆₎	223–247	2	0.091	0.088	1.000	0.500
<i>Eoo60</i>	F:GTTTGTCTGCGGTATGTGCTG – VIC R:CAGTCGGGCGTCATCACCATCTTCAAG	60.5 59.0	AATC ₍₁₀₎	167–207	10	0.818	0.845	0.814	0.714
Mean					7.6	0.675	0.655		0.712

developed for *E. rangiana* ($n = 73$ –86 individuals/locus), allelic diversity ranged from 12 to 28 alleles/locus and averaged 19.3 alleles/locus. After careful screening for null alleles, HWE, and LD, some of our microsatellite loci developed for *E. obliquata* may prove useful for cross-species amplification in other species, especially other *Epioblasma*. Likewise, future studies could screen the microsatellite loci developed by Jones et al. (2004) and Zanatta and Murphy (2006) to determine whether additional loci are suitable for cross-species amplification in *E. obliquata*.

Sampling more individuals of *E. obliquata* for further population genetic analysis would benefit conservation management. The screening of more wild individuals and any other populations that may be found could provide insight into the population genetic diversity and natural history of this species. Given the isolation and small size of the remaining

known population of *E. obliquata*, these microsatellite loci and other genetic markers will be valuable for monitoring the effects of propagation and management practices seeking to maintain or increase genetic diversity in hatchery stocks and wild populations receiving stocked individuals. For example, if hatchery technology improves to allow for the long-term holding, spawning, and fertilization of broodstock in captivity, the loci developed in this study will be useful for monitoring genetic diversity and inbreeding in parental stocks and progeny, which will be critical for maintaining healthy captive and wild populations of *E. obliquata* (Jones et al. 2020).

ACKNOWLEDGMENTS

The U.S. Fish and Wildlife Service (USFWS), Frankfort, Kentucky, provided support for this project. We thank Dr.

Monte McGregor, Kentucky Department of Fish and Wildlife Resources, and Leroy Koch, USFWS, for their assistance in collecting mussel tissue samples from Killbuck Creek, Ohio, and Minor Clark Fish Hatchery, Kentucky. The participation of E. M. Hallerman was supported in part by the U.S. Department of Agriculture through the National Institute of Food and Agriculture. The findings and conclusions in this article are those of the authors and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

LITERATURE CITED

- Cooper, A. M., L. M. Miller, and A. R. Kapuscinski. 2009. Conservation of population structure and genetic diversity under captive breeding of remnant coaster brook trout, *Salvelinus fontinalis*, populations. *Conservation Genetics* 11:1087–1093.
- Excoffier, L., G. Laval, and S. Schneider. 2005. Arlequin ver. 3.0: An integrated software package for population genetics data analysis. *Evolutionary Bioinformatics Online* 1:47–50.
- Faircloth, B. C. 2008. MSATCOMMANDER: Detection of microsatellite repeat arrays and automated, locus-specific primer design. *Molecular Ecology Resources* 8:92–94.
- Garza, J. C., and E. G. Williamson. 2001. Detection of reduction in population size using data from microsatellite loci. *Molecular Ecology* 10:305–318.
- Hoggarth, M. A., D. L. Rice, and D. M. Lee. 1995. Discovery of the federally endangered freshwater mussel, *Epioblasma obliquata obliquata* (Rafinesque, 1820) (Unionidae), in Ohio. *The Ohio Journal of Science* 4:298–299.
- Jones, J. W., M. Culver, V. David, J. Struthers, N. A. Johnson, R. J. Neves, S. J. O'Brien, and E. M. Hallerman. 2004. Development and characterization of microsatellite loci in the endangered oyster mussel *Epioblasma capsaeformis* (Bivalvia:Unionidae). *Molecular Ecology Notes* 4:649–652.
- Jones, J. W., E. M. Hallerman, and R. J. Neves. 2006. Genetic management guidelines for captive propagation of freshwater mussels (Unionoidea). *Journal of Shellfish Research* 25:527–535.
- Jones, J. W., W. F. Henley, A. J. Timpano, E. Frimpong, and E. M. Hallerman. 2020. Spawning and gravidity of the endangered freshwater mussel *Epioblasma capsaeformis* (Bivalvia: Unionidae) in captivity for production of glochidia. *Invertebrate Development and Reproduction* 64:312–325.
- Serb, J. M., J. E. Buhay, and C. Lydeard. 2003. Molecular systematics of the North American freshwater bivalve genus *Quadrula* (Unionidae: Ambloeminae) based on mitochondrial *ND1* sequences. *Molecular Phylogenetics and Evolution* 28:1–11.
- Untergasser, A., I. Cutcutache, T. Koressaar, J. Ye, B. C. Faircloth, M. Remm, and S.G. Rozen. 2012. Primer3—New capabilities and interfaces. *Nucleic Acids Research* 40(15):e115.
- USFWS (U.S. Fish and Wildlife Service). 1990. Purple cat's paw pearlymussel determined to be an endangered species. *Federal Register* 55:28209–28213.
- van der Schalie, H. 1970. Hermaphroditism among North American freshwater mussels. *Malacologia* 10:93–112.
- Van Oosterhout, C., W. F. Hutchinson, D. P. Wills, and P. Shipley. 2004. MICROCHECKER: software for identifying and correcting genotyping errors in microsatellite data. *Molecular Ecology Notes* 4:535–538.
- Zanatta, D. T., and R. W. Murphy. 2006. Development and characterization of microsatellite markers for the endangered northern riffleshell mussel *Epioblasma torulosa rangiana* (Bivalvia: Unionidae). *Molecular Ecology Notes* 6:850–852.
- Zane, L., L. Bargelloni, and T. Patarnello. 2002. Strategies for microsatellite isolation: a review. *Molecular Ecology* 11:1–16.

Appendix A1. Scored microsatellite genotypes of 44 individuals of the Catspaw (*Epioblasma obliquata*) from Killbuck Creek, Coshocton County, Ohio, at 14 loci. Microsatellite amplicons were scored for length using Genemarker software (SoftGenetics, State College, PA, USA). Individuals and loci without a scored allele (—) indicate that no allele product was observed at that locus. Columns with either 1 or 2 designate alleles per locus.

Loci	Eoo8 ACT(16)	Eoo9 AAT(29)	Eoo10 ATC(8)	Eoo11 AAC(10)	Eoo16 ACAT(11)	Eoo19 AGAT(10)	Eoo20 ACAT(19)	Eoo22 AGAT(15)	Eoo24 AATC(6)	Eoo31 ATC(9)	Eoo38 AAG(11)	Eoo44 AAC(8)	Eoo46 ATCC(6)	Eoo60 AATC(10)
Individual	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Wildstock1	169	184	182	188	199	211	260	266	224	236	189	201	—	—
Wildstock2	169	184	182	185	211	217	260	266	240	240	197	213	—	—
Wildstock3	169	184	179	179	211	220	266	266	240	240	193	197	294	294
Wildstock4	169	184	182	185	205	205	266	266	228	228	185	201	282	298
Wildstock5	169	184	182	182	199	199	260	266	240	240	193	201	254	326
Wildstock6	169	184	182	182	199	211	266	266	240	240	193	197	282	298
Wildstock7	169	184	182	182	199	220	260	266	240	240	177	205	282	298
Wildstock8	169	184	179	182	190	211	266	266	240	244	185	225	302	326
Wildstock9	169	184	185	185	190	199	266	266	240	240	201	217	282	302
Wildstock10	169	184	182	185	190	199	260	266	240	240	197	205	306	326
Wildstock11	169	184	182	188	202	211	266	266	228	240	185	189	254	294
Wildstock12	169	184	182	182	190	208	260	260	240	240	193	205	278	278
Wildstock13	169	184	182	182	190	199	266	266	228	240	185	201	298	314
Wildstock14	169	184	182	185	199	199	260	260	240	240	185	205	282	314
Wildstock15	169	181	182	182	193	211	266	266	232	240	177	205	278	298
Wildstock16	169	184	182	182	187	208	260	266	240	240	193	201	310	326
Wildstock17	169	184	179	185	190	202	260	260	232	232	193	213	254	314
Wildstock18	169	181	182	182	199	220	260	266	240	240	133	189	262	286
Wildstock19	169	184	182	188	199	199	260	260	240	240	193	213	286	326
Wildstock20	169	184	182	185	202	211	260	266	240	240	185	201	282	306
Wildstock21	169	184	182	182	190	190	260	266	232	240	177	181	282	318
Wildstock22	169	187	179	179	199	211	260	266	240	240	197	201	254	294
Wildstock23	169	184	182	185	190	199	260	266	228	228	133	201	314	314
Wildstock24	169	184	182	185	196	220	260	260	232	236	181	205	298	310
Wildstock25	169	184	182	185	190	199	260	266	232	240	133	201	278	314
Wildstock26	169	184	182	185	190	199	260	260	240	240	181	205	302	322
Wildstock27	169	184	182	185	190	199	260	260	240	240	189	197	254	254
Wildstock28	169	181	179	185	190	199	266	266	240	240	209	209	314	322
Wildstock29	169	184	182	188	199	211	260	266	228	240	185	189	254	314
Wildstock30	169	184	182	182	190	199	266	266	168	240	197	201	306	306
Wildstock31	169	181	179	182	208	217	260	266	232	240	189	201	278	290
Wildstock32	169	184	182	188	196	220	260	260	240	240	133	193	282	290
Wildstock33	169	184	182	182	190	208	260	266	168	240	133	197	282	302
Wildstock34	169	184	182	182	199	211	260	266	168	240	133	197	282	294
Wildstock35	169	184	182	182	211	220	260	260	168	240	185	193	278	298

Appendix A1. Scored microsatellite genotypes of 44 individuals of the Catspaw (*Epioblasma obliquata*) from Killbuck Creek, Coshocton County, Ohio, at 14 loci. Microsatellite amplicons were scored for length using Genemarker software (SoftGenetics, State College, PA, USA). Individuals and loci without a scored allele (—) indicate that no allele product was observed at that locus. Columns with either 1 or 2 designate alleles per locus.

Loci	<i>Eoo8</i> ACT(16)	<i>Eoo9</i> AAT(29)	<i>Eoo10</i> ATC(8)	<i>Eoo11</i> AAC(10)	<i>Eoo16</i> ACAT(11)	<i>Eoo19</i> AGAT(10)	<i>Eoo20</i> ACAT(19)	<i>Eoo22</i> AGAT(15)	<i>Eoo24</i> AATC(6)	<i>Eoo31</i> ATC(9)	<i>Eoo38</i> AAG(11)	<i>Eoo44</i> AAC(8)	<i>Eoo46</i> ATCC(6)	<i>Eoo60</i> AATC(10)														
Wildstock36	169	184	182	185	199	205	260	266	168	168	197	217	302	302	185	201	171	175	199	232	256	289	253	259	124	136	202	218
Wildstock37	169	178	182	182	199	214	260	266	168	240	133	193	310	310	185	221	175	175	199	217	253	292	253	259	124	124	246	254
Wildstock38	169	178	182	182	199	211	260	266	232	240	133	193	282	282	189	193	175	175	199	199	259	265	253	259	124	136	234	246
Wildstock39	169	178	182	182	199	199	266	266	240	240	185	201	302	314	185	201	171	175	199	217	277	289	253	259	124	124	202	218
Wildstock40	169	184	182	185	202	214	260	266	236	240	133	185	294	302	185	205	171	175	199	211	256	289	253	259	124	124	218	234
Wildstock41	169	184	182	182	199	211	266	266	160	232	189	201	278	306	209	221	175	175	199	199	241	259	253	259	124	124	234	234
Wildstock42	169	184	182	182	199	211	260	260	168	232	193	205	310	310	189	193	171	171	199	211	256	256	253	259	124	124	218	238
Wildstock43	169	184	182	182	193	199	260	260	168	240	197	205	294	302	201	201	171	175	211	232	265	280	253	259	124	124	218	226
Wildstock44	169	184	182	182	178	199	266	266	160	228	133	197	254	298	205	217	171	175	199	199	262	289	253	259	124	124	234	246