



---

## Faculty Scholarship

---

2002

# Rapid communication: Thirty-eight polymorphic microsatellite markers for mapping in rainbow trout.

C E Rexroad

R L Coleman

W K Hershberger

J Killefer

Follow this and additional works at: [https://researchrepository.wvu.edu/faculty\\_publications](https://researchrepository.wvu.edu/faculty_publications)

---

### Digital Commons Citation

Rexroad, C E; Coleman, R L; Hershberger, W K; and Killefer, J, "Rapid communication: Thirty-eight polymorphic microsatellite markers for mapping in rainbow trout." (2002). *Faculty Scholarship*. 305.

[https://researchrepository.wvu.edu/faculty\\_publications/305](https://researchrepository.wvu.edu/faculty_publications/305)

This Article is brought to you for free and open access by The Research Repository @ WVU. It has been accepted for inclusion in Faculty Scholarship by an authorized administrator of The Research Repository @ WVU. For more information, please contact [ian.harmon@mail.wvu.edu](mailto:ian.harmon@mail.wvu.edu).

# Rapid communication: Thirty-eight polymorphic microsatellite markers for mapping in rainbow trout<sup>1</sup>

C. E. Rexroad III<sup>\*2</sup>, R. L. Coleman<sup>\*</sup>, W. K. Hershberger<sup>\*</sup>, and J. Killefer<sup>†</sup>

<sup>\*</sup>National Center for Cool and Cold Water Aquaculture, USDA-ARS, Leetown, WV and

<sup>†</sup>Division of Animal and Veterinary Sciences, West Virginia University, Morgantown

*Species.* *Oncorhynchus mykiss*.

*Source and Description.* Microsatellite repeats were identified by sequencing clones from microsatellite-enriched libraries constructed from genomic DNA. Microsatellite markers were developed by designing primers to amplify the repeats.

*Primer Sequences.* See Table 1.

*Method of Detection.* PCR conditions were optimized using rainbow trout DNA (Kamloop strain) and mini-prep DNA from the clone used to develop the marker. PCR reactions included 25 ng of DNA, 1.5 to 2 mM MgCl<sub>2</sub>, 1× manufacturer's reaction buffer (Applied Biosystems, Foster City, CA), 2 mM dNTPs, 1 μM each of forward and reverse primer, and 0.05 units of AmpliTaq Gold (Perkin-Elmer, Norwalk, CT). Reactions were thermocycled as follows: 10 min at 94°C, 35 cycles of 94°C for 30 s, annealing temperature for 30 s, and 72°C for 30 s, and a final extension at 72°C for 5 min. PCR

products were analyzed by electrophoresis in 3% agarose stained with ethidium bromide and viewed using a ChemImager (Alpha Innotech, San Leandro, CA). Forward primers of successfully optimized primer pairs were resynthesized labeled with FAM, HEX, or NED fluorescein dyes. PCR was done to amplify the National Center for Cool and Cold Water Aquaculture "Polymorphism Identification and Mapping Panel" of 45 DNA samples that included 25 unrelated rainbow trout (OSU, Arlee, Swanson, Hot Creek, Clearwater, Housecreek, Kamloop, Redband, and Steelhead) and 20 representatives of other salmonids (two to four each, Cutthroat Trout, Sockeye Salmon, Chinook Salmon, Atlantic Salmon, Brown Trout, Brook Trout, and Arctic Char). PCR products were then combined for capillary electrophoresis on an ABI3700. Results were analyzed using Genotyper (ABI, Foster City, CA).

*Description of Polymorphism.* See Table 1.

*Comments.* OMM1032 had a 171-bp fragment for all rainbow trout genotyped. Two clones contained more than one microsatellite repeat and each was given an independent designation (OMM1101 and OMM1102, OMM1116 and OMM1117).

---

<sup>1</sup>Mention of trade names or commercial products in this publication is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the USDA.

<sup>2</sup>Correspondence: P.O. Box 100, Kearneysville, WV 25430 (phone: 304-876-7723; fax: 304-876-7262; E-mail: crexroad@afrs.ars.usda.gov).

Received March 9, 2001.

Accepted October 23, 2001.

Key Words: Mapping, Microsatellites, Rainbow Trout

---

J. Anim. Sci. 2002. 80:541–542

Table 1. Microsatellite marker information for mapping in rainbow trout

Marker	Library	Repeat	Forward primer sequence	Reverse primer sequence	AT <sup>a</sup>	MgCl <sub>2</sub> mM	No. of alleles	Size range	% Het <sup>b</sup>	GenBank
OMM1032	TAGA	(AG) <sup>22</sup>	GCGAGGAAGAGAAAGTAGTAG	CCCATCTCTCTCTGATTATG	58	2	9	200–222	5	AF352737
OMM1053	TAGA	(TAGA) <sup>15</sup>	GACTGACAGGGTATTGAA	TATGTATATACCCAGCGTGTG	56	2	15	247–357	33	AF352738
OMM1054	TAGA	(TATC) <sup>38</sup>	AGCCCTTATCTTATGAC	ACATCAGTACCCGCTG	60	2	26	190–325	70	AF352739
OMM1055	TAGA	(AC) <sup>14</sup>	GGCCAAAGCTTTTAGTGTG	GCCAGCTTACTCATTACC	58	2	4	213–220	26	AF352740
OMM1058	TAGA	(TAGA) <sup>18</sup>	GTGTGTATGTGGTTCCAC	CCAATGAGAAGCGTTAC	60	2	1	174–227	45	AF352741
OMM1059	ATG	(CAT) <sup>9</sup>	CGCCAGATGATTAACGA	GGGTATTTACACACGTTCA	58	2	6	182–193	35	AF352742
OMM1061	ATG	(ATC) <sup>8</sup>	GCGGTCACTGTCAAGA	GGGAGACATGGATCATA	62	2	4	222–275	12	AF352743
OMM1064	TAGA	(GATA) <sup>19</sup>	AGAATGCTACTGTGGTGTATTGTGA	TCTGAAAGCAGGTGGATGGTTCC	60	2	12	146–199	68	AF352744
OMM1073	ATG	(GTGA) <sup>13</sup>	CATATGTCAAAGTGTGTGCTCCA	CTATCAGTCAGCAGGCTTTCATGATC	58	2	6	134–174	24	AF352745
OMM1075	TAGA	(TATC) <sup>7</sup>	ACGCAACCAGACAGTTAAGAA	GCGCTGACAAGAACAAC	58	2	13	203–284	74	AF352746
OMM1076	TAGA	(TATC) <sup>26</sup>	AACCCGACACCTAGGACACCT	CTTACACCATGCCACGGAAAGTTA	64	1.5	15	171–277	55	AF352747
OMM1077	TAGA	(GATA) <sup>9</sup>	GGCTGACCAGAGAAAGACTAGTTC	TGTTACGGTGTCTGACATGC	58	2	3	225–262	0	AF352748
OMM1078	TAGA	(TAGA) <sup>24</sup>	AACTCACGCCCTGACCAACCTAAC	GATTTCAAGTATTTGGTCCGAGCC	64	2	20	184–298	65	AF352749
OMM1080	TAGA	(GATA) <sup>14</sup>	GAGACTGACACGGGTATTGA	GTTATGTTGTCATGCGCTAGGG	58	2	15	206–303	52	AF352750
OMM1081	TAGA	(TATC) <sup>17</sup>	CCGTTGTATAACAGGTATGAC	TCTTTACACAGAGGGTCTTAC	56	2	16	151–258	78	AF352751
OMM1082	TAGA	(GATA) <sup>17</sup>	CAAGAGCACTAACAGCACATGT	CGCAAGCAAGCTAACACA	58	2	13	166–223	86	AF352752
OMM1083	TAGA	(GATA) <sup>26</sup>	GCCCTGACCAACCTAACACA	TGCTGACATTTGGTTAGTAGTGG	58	2	17	122–282	41	AF352753
OMM1084	TAGA	(GATA) <sup>20</sup>	CGAGACAAGCAGCCAGATAGAG	CACCTGACTGTCTGCTTTGGCTATC	58	2	10	198–242	71	AF352754
OMM1086	TAGA	(TATC) <sup>7</sup>	GTATGCTTTCACAAATGCACTG	CTGTTTCAGCTCAAACTCAC	64	2	9	186–223	45	AF352755
OMM1087	TAGA	(TCTA) <sup>13</sup>	GACGCAGAAAGTTTAGCTCT	TTACTGTCTTCTGCGCAGCA	58	2	13	237–291	71	AF352756
OMM1088	TAGA	(GATA) <sup>12</sup>	CTACAGGCCAACACTACAATC	CTATAAAGGGAATAGGCACTT	58	2	12	111–170	78	AF352757
OMM1089	TAGA	(GATA) <sup>13</sup>	GCAGCTCCTGTTTCTATGTG	CTGAGATGCAGTCCCTTAGAC	58	2	17	111–238	26	AF352758
OMM1090	TAGA	(AG) <sup>90</sup> (TAGA) <sup>10</sup>	TGCGGTAGGAAGGCTTTTAGTG	AAATGGAGCAGCGCTGGTAT	64	2	11	253–394	26	AF352759
OMM1093	TAGA	(TO) <sup>26</sup>	CCGTTATCTGCCAGTTCACCTCTC	CGGCTGCACTGTGAGATAGAGA	58	2	10	269–303	16	AF352761
OMM1096	TAGA	(TATC) <sup>34</sup>	CTCGCTTTATTTGATCATGTTCTACTG	AGAGATCAGTGGCAGCTTAGGG	64	1.5	19	124–275	48	AF352762
OMM1097	TAGA	(GATA) <sup>26</sup>	CTAGCCATCGGAACACTG	AGAAATAGGGTGCCTGTATCTC	64	2	20	201–304	68	AF352763
OMM1100	TAGA	(GATA) <sup>14</sup>	AGCTTGTCCCTTATCCTT	GCCCATAGTTATGATCC	58	2	11	193–229	65	AF352764
OMM1101	TAGA	(ATAG) <sup>31</sup>	CTGCCCTCTGATTTGAGAACCATAATC	CCGTGTCAGATGAATGGG	62	2	15	139–228	68	AF352765
OMM1102	TAGA	(ATAG) <sup>31</sup> (AC) <sup>19</sup>	CGGCCCTGTGCTGTGATCCAAATAT	CTGACTTCAATCTGAGCCGATGAG	64	2	14	261–298	32	AF352765
OMM1104	TAGA	(GATA) <sup>15</sup>	AACAGGCCCTGATGAGTTTC	CTCTCTGTCTCGCTCCTATTG	58	2	15	166–227	77	AF352767
OMM1105	TAGA	(AGAC) <sup>23</sup> (GATA) <sup>16</sup>	GCACACTGTCTGGTTAAAGAGA	GCCAGGCCACACTAAACCA	62	2	12	131–200	36	AF352768
OMM1108	TAGA	(TCTA) <sup>14</sup>	CACAGCTGTGAGAACATGCGGTAAT	TCACAGCGGACAAATGTGACAGATAGA	58	2	12	141–191	43	AF352769
OMM1109	TAGA	(AC) <sup>30</sup>	GGCAACAACCCACCCAAACCAATCTA	TACAGCTCCGTCCAGTCTCG	62	2	10	160–203	29	AF352770
OMM1116	TAGA	(GA) <sup>11</sup> (GATA) <sup>19</sup>	GACAAAGACAGAGAGGGACGA	AGCACCAAGATCGAACTCC	58	2	3	113–119	9	AF352771
OMM1117	TAGA	(GATA) <sup>19</sup>	AAGCCAGAGGGGATAAGATG	GCAATGGGCTCTATGACTGAT	62	2	12	183–223	59	AF352771
OMM1120	TAGA	(GATA) <sup>11</sup>	TTGAAGACAAGTGAAGCGAGAG	TTGGTGTTCACAGGACAGTAA	62	2	8	217–251	19	AF352772
OMM1122	TAGA	(TAGA) <sup>9</sup>	TACATCAACAGGTCATTTGTG	CCTGCTATTTGTCACATGCTAC	58	2	1	121	0	AF352773
OMM1125	TAGA	(AC) <sup>41</sup> (GT) <sup>12</sup> (AG) <sup>49</sup>	GGAGATTTGGGTGAGAGCTAAA	TTCTCATCCCATCTACCATCC	64	2	8	117–132	39	AF352774

<sup>a</sup>Annealing temperature.<sup>b</sup>Heterozygosity.