Report of the 1st UCLA International MICA Exchange

May 15, 2007

We thank the reference laboratories that participated in the first UCLA International MICA Exchange program. Four DNA samples (MICA#001-#004) were shipped to 7 laboratories that are actively involved in MICA genotyping studies. Six laboratories submitted MICA typing results. Four laboratories used a Luminex-based sequence-specific oligonucleotide probe hybridization method (SSOP) and 2 laboratories used in-house direct DNA sequencing methods. The 2 laboratories that used sequencing methods reported the number of GCT-triplet repeats in exon 5.

We encourage the participating laboratories to resolve the discrepancies so that the information can be shared to improve the reliability and resolution of MICA typing systems.

Thanks again for your participation in this important program.

Best regards,

Marie Lau, Arlene Locke, Qiuheng Zhang, Raja Rajalingam, and Elaine F. Reed

MICA exchange sample: MICA#001

This sample was from a Caucasian individual. MICA*010 was assigned by 67% of the laboratories. Two laboratories reported MICA*016/19 by either SSOP or SBT methods. MICA*010 differs from MICA*016 in the alpha 1 chain at position 6 (exon 2), where MICA*010 has a proline while MICA*016 has an arginine. MICA*010 is relatively common in Caucasians and Asians, but not in African Americans (*1-3*). The amino acid change at codon 6 results in the loss of cell surface expression of MICA*010 (*4*). MICA*010 also differs from MICA*016 in the alpha 3 chain at position 221 (exon 4), where a valine in MICA*010 is replaced by leucine in MICA*016. Based upon the GCT repeats in exon 5, MICA alleles can be grouped into 8 categories that differ in the number of GCT repeats at position 296 (*4*). MICA*010, MICA*016 and MICA*019 all have 5 GCT repeats.

MICA*004 were detected by 100% of the laboratories. MICA*004 has 6 GCT repeats in exon 5. MICA*004 is common in African Americans, Caucasians and Asians (*1-3*). MICA*004 has been shown to have a strong association with HLA-B*44 in these populations (*2, 5, 6*).

MICA exchange sample: MICA#002

This DNA was derived from an African-American donor. MICA*008 and MICA*011 were assigned by 100% of the laboratories. MICA*008 is the most common allele, with allele frequencies of 55% (*7*) and 42.6% (*3*). MICA*008 has the same nucleotide sequence in exons 2, 3, and 4 as MICA*027. MICA*008 belongs to the A5.1 group with a G insertion after the second GCT repeat which results in a stop codon at position 304. MICA*008 is reported to be aberrantly transported to the apical cell surface (*8*). MICA*027 alleles can be mistyped for MICA*008 if only exons 2-4 are studied.

MICA*011 is relatively uncommon, with an allele frequency less than 5% in most of the populations (*1-3, 6, 7*).

MICA exchange sample: MICA#003

The ethnic origin of this donor was Hispanic. MICA*008 and MICA*027 were assigned by 100% of the laboratories. MICA*008 has the same nucleotide sequence in exons 2, 3, and 4 as MICA*027; therefore, MICA*008 and MICA*027 can be mistyped if only these exons are studied. Currently, MICA*027 is found with an allele frequency of over 30% in American Indians (*9*), but less than 5% among other populations (*1-3, 6*). MICA*00801 differs from MICA*00804 at the leader sequence with a synonymous mutation. MICA*00801 differs from MICA*048 at codon 318 in the transmembrane domain, where a glycine in MICA*00801 is replaced by a tryptophan in MICA*048.

MICA exchange sample: MICA#004

This DNA was obtained from an Asian donor. MICA*010 was assigned by 67% of the laboratories. One laboratory reported MICA*016/19 by SSOP and another lab reported MICA*019 by sequence based typing. MICA*019 differs from MICA*010 only in the alpha 1 chain at position 6 (exon 2) where MICA*010 has a proline while MICA*016 has an arginine. MICA*016 differs from MICA*019 in the alpha 3 chain at position 221 (exon 4), where MICA*016 has a leucine, but MICA*019 has a valine.

MICA*027 was assigned by 100% of the laboratories. MICA*027 can be mistyped for MICA*008 if only exons 2-4 are studied. Currently, MICA*027 is found with an allele frequency of over 30% in American Indians (*9*), but less than 5% among other populations (*1-3, 6*).

References

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	MICA#001				
CTR	**Investigator Name**	**MICA**	**MICA***	**OTHERS**	**METHOD**
3625	Darke,Christophe	NT			
713	Jackson,Annette	*004	*010		RVSSO
278	Lee,Jar-How	*004	*016/*019		RVSSO
5142	Little,Ann-Margar	*004	*010		SBT ex2-5
8049	Lopez-Larrea,Car	*004	*016/*019		RVSSO
3753	Reed,Elaine	*004	*010		RVSSO
791	Stastny,Peter	*004	*010	*004/A6, *010/A5	SBT
	MICA#002				
CTR	**Investigator Name**	**MICA**	**MICA***	**OTHERS**	**METHOD**
3625	Darke,Christophe	NT			
713	Jackson,Annette	*008	*011		RVSSO
278	Lee,Jar-How	*008	*011		RVSSO
5142	Little,Ann-Margar	*00801/*00804	*011	*027,*048; ex5-A5.1/A6 excluded	SBT ex2-5
8049	Lopez-Larrea,Car	*00801	*011		RVSSO
3753	Reed,Elaine	*008	*011		RVSSO
791	Stastny,Peter	*008	*011	*008/A5.1, *011/A6	SBT
	MICA#003				
CTR	**Investigator Name**	**MICA**	**MICA***	**OTHERS**	**METHOD**
3625	Darke,Christophe	NT			
713	Jackson,Annette	*008	*008/*027		RVSSO
278	Lee,Jar-How	*008	*027		RVSSO
5142	Little,Ann-Margar	*008/*00804/*027/*048	*00801/*00804/*027/*048		SBT ex2-5
8049	Lopez-Larrea,Car	*00801	*027		RVSSO
3753	Reed,Elaine	*008	*008/*027		RVSSO
791	Stastny,Peter	*008	*027	*008/A5.1, *027/A5, *048/A5	SBT
	MICA#004				
CTR	**Investigator Name**	**MICA**	**MICA***	**OTHERS**	**METHOD**
3625	Darke,Christophe	NT			
713	Jackson,Annette	*010	*027		RVSSO
278	Lee,Jar-How	*010	*027		RVSSO
5142	Little,Ann-Margar	*019	*027/*048	*00801/*00804;ex5-A5 only excluded	SBT ex2-5
8049	Lopez-Larrea,Car	*016/*019	*027		RVSSO
3753	Reed,Elaine	*010	*027		RVSSO
791	Stastny,Peter	*010	*027	*010/A5, *027/A5, *048/A5	SBT