Use of the Systems D1S80, D17S30, ApoB, TC11, VWA, and SE33 for Zygosity Determination - Letter to the Editor

H.-G. Scheil¹, W. Huckenbeck²

¹Institute of Human Genetics and Anthropology; ²Institute of Legal Medicine, Heinrich-Heine-University, Düsseldorf, Germany

Abstract. The usefulness of PCR systems (D1S80, D17S30, ApoB, TC11, VWA, and SE33) is discussed. The statistical evaluation shows that these systems – together with other systems – are well suited for zygosity testing.

Key words: Zygosity testing in twins, Systems D1S80, D17S30, ApoB, TC11, VWA and SE33.

In Vol. 44 (1995: 25-30) of this journal, an article [2] discussed the use of single—and multi-locus and PCR-systems for zygosity determination. Unfortunately, the authors do not say anything about the genotypes and frequencies of the PCR-systems (D1S80, D17S30, ApoB, TC11, VWA, and SE33) whose effectiveness in zygosity determination their study tested. Moreover, the authors' conclusion that their results prove monozygosity from the fact that the twins they studied were identical in all systems, is incorrect. And their statistical interpretation is somewhat curious in its neglect of the parents' genotypes and the differing respective frequencies of the genotypes.

There are three basic methods for determining zygosity in twins; tests involving parents (cf. [1]), tests excluding parents (cf. [6]) and tests using questionnaires (cf. [7], [11]). Due to the missing parental data in the paper cited, we tested zygosity by the second method see ([6] and [9] for details of this technique) in three ways: the twins show the rarest, the most frequent or medium-frequent genotypes respectively in all systems. As can be seen from Tables 1-3, the minimum probability for monozygosity of 99.9% required by the forementioned coauthors [2] was only obtained by using the rarest genotypes, while the value obtained by using the most frequent genotypes in each system (97.27%) is below this required minumum. It is evident that these cases are very rare. Normally there will be a mixture of more or less frequent genotypes. The genotypes which occur with medium frequency result in a probability of just 98.99%. Generalizing,

Table 1 - Zygosity determination using the rarest genotypes of the systems D1S80, D17S30, ApoB, TC11, VWA and SE33*

System	Genotype	Expected frequency (%)	Monozygosity probability for each system	Bibliography of data used
D1S80	16-34	0.003	61.69	[3]
D17S30	13-13	0.002	76.13	[8]
ApoB	2-2	0.002	76.16	[8]
TC11	11-11	0.010	75.95	[4]
VWA	13-13	0.002	76.13	[5]
SE33	V12-V12	0.0004	76.23	[10]
		Combined:	99.94	•

^{*}The nomenclature of systems and genotypes is that of the authors cited.

Table 2 - Zygosity determination using the most frequent genotypes of the systems D1S80, D17S30, ApoB, TC11, VWA and SE33

System	Genotype	Expected frequency (%)	Monozygosity probability for each system	Bibliography of data used
	_			
D1S80	18-24	17.354	59.70	[3]
D17S30	2-4	12.484	60.25	[8]
ApoB	4-5	20.775	59.33	[8]
TC11	6-10	11.633	60.34	[4]
VWA	16-17	12.946	60.19	[5]
SE33	V18-V19	1.456	61.52	[10]
		Combined:	97.27	

Table 3 - Zygosity determination using medium-frequent genotypes of the systems D1S80, D17S30, ApoB, TC11, VWA and SE33

System	Genotype	Expected frequency (%)	Monozygosity probability for each system	Bibliography of data used
D1S80	18-18	6.401	67.22	[3]
D17S30	2-2	5.808	67.65	[8]
ApoB	4-4	7.673	66.38	[8]
TC11	6-7	5.873	61.00	[4]
VWA	15-17	6.069	60.98	[5]
SE33	V19-V33	0.717	61.60	[10]
		Combined:	98.99	. •

it is clear that in most cases, the six systems studied will not give sufficient statistical results. In their paper, the same group of authors [2] emphasize the importance of an appropriate determination of zygosity for clinical studies of twins and for genetic counselling. Regrettably, they did not they did not keep to this requirement in their study. However, we agree with the authors that the six PCR-systems (D1S80, D17S30, ApoB, TC11, VWA and SE33) – together with other systems – are well suited for zygosity testing.

One final remark seems worth making: the probabilities of the most frequent and medium-frequent genotypes of the six combined systems are only slightly higher than those which can be achieved by the much cheaper method of questionnaires [11].

REFERENCES

- 1. Emery AEH (1976): Methodology in medical genetics. Edinburgh, London & New York: Churchill Livingstone.
- 2. Eufinger H, Rand SP, Schütte U (1995): Use of single- and multi-locus and polymerase chain reaction systems for zygosity determination clinical application in twins with clefts of the lip and palate. Acta Genet Med Gemellol 44: 25-30.
- 3. Huckenbeck W, Scheil H-G, Stancu V, Bonte, W (1996): VNTR locus D1S80: Allele frequencies and genotype distribution in the region of Düsseldorf. Anthrop Anz 54: in press.
- 4. Huckenbeck W, Scheil H-G, West S, Kanja J, Bonte W (1996): Northrhine Westphalian data on the HumTHO1 locus. Anthrop Anz 54: in press.
- Huckenbeck W, Scheil H-G, West S, Demir K, Kanja J, Kaiser A, Hees V, Meyer W, Scholten D, Stancu V, Bronczek M, Bonte W (1996): German data on the PCR based loci Hum VWA31, HumTH01, HumFES/FPS, HumF13B and D1S80. Adv Forens Haemogenet 6: in press.
- 6. Maynard Smith S, Penrose LS (1955): Monozygotic and dizygotic twin diagnosis. Ann Hum Genet 19: 273-289.
- Ooki S, Yamada K, Asaka A (1993): Zygosity diagnosis of twins by questionnaire for twins' mothers. Acta Genet Med Gemellol 42: 17-22.
- 8. Pascal O, Levayer T, Aubert D, Peneau A, Markey P, Moisan JP (1994): French population data of 6 AMPFL's. Adv Forens Haemogenet 5: 542-544.
- 9. Scheil H-G, Koppatz K (1991): Tabellen zur Eiigkeitsdiagnose bei Zwillingen anhand hämogenetischer Polymorphismen. Anthrop Anz 49: 161-175.
- 10. Schwartz DWM, Jungl EM, Krenek OR, Mayr WR (1994): Typing for STR-loci by electrophoresis on rehydratable polyacrylamide gels: phenotype and allele frequencies of SE33 and TC11 in an Austrian population sample. Adv Forens Haemogenet 5: 581-583.
- 11. Torgersen S (1979): The determination of twin zygosity by means of a mailed questionnaire. Acta Genet Med Gemellol 28: 225-236.

Correspondence: Dr. Hans-Georg Scheil, Institute of Human Genetics and Anthropology, Heinrich-Heine-University, Universitätssta β e 1, D-40225 Düsseldorf, Germany.