A STUDY ON THE SHORT TANDEM REPEAT SYSTEM ACTBP2 (SE33) IN AN AUSTRIAN POPULATION SAMPLE USING NON-DENATURING ELECTROPHORESIS AND A SEQUENCED ALLELIC LADDER

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System and locus: SE33 (ACTBP2) (Polymeropoulos et al.1992)

Population and sample size: Austria, 100 individuals.

MATERIALS AND METHODS:

Amplification and electrophoresis were performed according to Wiegand et al 1993. Typing was performed by comparison with a sequenced allelic ladder (Möller and Brinkmann 1994)
As suggested by Rand et al. 1992 the alleles were pooled into 4 groups before testing for Hardy-Weinberg equilibrium using chi^2 tests. The mean exclusion chance (ME) was calculated according to Krüger et al. 1968 and the discriminating power was calculated as 1-S (expected phenotype frequencies)^2 (Fisher 1951).

RESULTS:

A total of 70 genotypes corresponding to 21 alleles (Table 1) were found in the 100 subjects tested. 25 alleles migrated differently from the alleles in the ladder. Accordingly they were assigned the letter "A" if migrating anodal, or "C" if migrating cathodal of the closest allele. The inclusion of these interalleles resulted in a summ of 79 genotypes (Table 2). No significant deviations from Hardy Weinberg deviations were found. The heterocygosity rate was 97%, the mean exclusion chance (ME) was 0.87, and the discriminating power (PD) was 0.98. exclusion chance (ME) was calculated according to Krüger et al. 1968 and the discriminating power was calculated as 1-S (expected phenotype frequencies)2 (Fisher 1951).

Allele	Frequency	Allele	Frequency	Allele	Frequency	Allele	Frequency
12	0,011	18	0,113	24	0,016	29	0,086
13	0,022	19	0,016	25	0,048	30	0,043
14	0,048	20	0,022	26	0,065	31	0,043
15	0,027	21	0,038	27	0,081	32	0,016
16	0,065	22	0,027	28	0,091	33	0,000
17	0,097	23	0,027				

Tab 1. Allele frequencies in percent

Gen.	Obs.	Gen.	Obs.	Gen.	Obs.	Gen.	Obs.
13//17	1	17//18	3	19//28	2	24//31	1
13//20	1	17//19	1	19//28C	1	24A//31A	1
13//24	1	17//21	1	19//28A	1	25//26	1
14//17	1	17//22	1	19//29	4	25A//29A	1
14//17	1	17//23	2	19//30	2	25//29	1
14//19	1	17//28	1	19//30A	2	26//28	1
14//30	1	17//31	2	20//26	1	26//29	1
14//31A	1	17A//32	1	20//27	1	26//31A	1
15//18	2	18//19	2	20//30A	1	27//28C	1
15//19	1	18//22	1	21//27	1	27//29	2
15//27	2	18//26A	1	21//29	2	27//29A	1
15//28	1	18//27	2	22//27	1	28//29	2
15//30A	1	18//28	2	22//29	1	28//30A	1
15//32	1	18//28A	2	22//31	2	29//30A	1
15//33	1	18//29A	1	22//31A	1	30//30	1
16//18	1	18//30	2	23//26	1	30//32	1
16//19	1	18//30A	1	23A//28	1	30//33	1
16//27	1	19//19	1	23A//29	1	31//33	1
16//28	1	19//24	1	23A//30	1	32//32	1
16//32	1	19//26	1	24A//26	1		

Table 2. Observed genotypes

COMMENTS:

Despite-or because-of its outstanding polymorphicity, the STR system ACTBP2 (Se33) is problematic due to difficulties in typing, influence of the electrophoretic setup, or the allelic ladder used. This is confirmed by the fact that, as opposed to several other STRs, no commercial kits are available at the moment. The usage of a sequenced allelic ladder allows a nomenclature corresponding to the number of repeats (Möller and Brinkmann 1994). However, a standardized electrophoretic system would be necessary to allow inter-laboratory controls for such a complicated STR system.

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