Two human cDNA molecules coding for the Duchenne muscular dystrophy (DMD) locus are highly homologous

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Recently, Koenig et al. have reported the complete sequence (**A**) of the human fetal cDNA coding for the Duchenne muscular dystrophy (DMD) locus and predicted a 3685 amino acid long, rod-shaped cytoskeletal protein (dystrophin) as the protein product[1]. Independently, we have isolated and sequenced different DMD cDNA molecules from human adult and fetal muscle[2,3]. The complete 12.5 kb long sequence (**B**) of all our cDNA clones has now been determined and we report here the nucleotide (nt) and amino acid (aa) differences between the sequences of both groups.

Our cDNA sequence comprises the whole coding region but lacks the first 110 nt from the 5'-untranslated region and the last 1417 nt of the 3'-untranslated region. We have found altogether 11 nt differences (approximately 99.9 % homology) from which 7 occured at the aa level:

	sequence **A**			sequence **B**		
	nt position	nt	and aa	nt position	nt	and aa
1.	606	A	Q	496	C	P
2.	1882	T		1772	G	
3.	2075	C	L	1965	A	I
4.	2559	C	A	2449	G	G
5.	3797	G	V	3687	T	F
6.	4339	A	K	4229	T	N
7.	4614	T	L	4504	A	Q
8.	5185	C		5075	T	
9.	5442	G		5332	A	
10.	5740	A		5630	C	
11.	7304	C	Q	7194	A	K

There are no differences at the nt or aa level from the position 7305 (7195) to the 3'-end. We have found one variation (nt position: 606 (496), nt: A → C, aa: Q → P) in the first domain, the putative actin-binding site. All the other variations were observed in the second domain which has been predicted to be rod-shaped and formed by 26 repeats.[1] It is interesting to note that a substantial amount of aa variation is allowed for the dystrophin protein. These variations are not predicted to substantially alter the secondary structure of the protein.

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