

EVALUATION OF MALE INFERTILITY MOLECULAR ASPECTS IN LATVIAN POPULATION

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Background

Some aspects of male infertility could be explained analysing Y-chromosomal and autosomal genes that are involved in spermatogenesis process.

The aim

To study molecular-genetic aspects of idiopathic male infertility in Latvian population.

Materials and methods

A study encompassed 100 idiopathic infertile men and 153 individuals of control group.

Y chromosome microdeletions were analysed by two multiplex PCR. Y chromosome haplogroups (Y-Hg) were detected using appropriate biallelic markers. CFTR gene mutations delF508, R117H and IVS8 polymorphisms (poly-T and poly-TG) analysis was performed by PCR and followed by RFLP and sequencing.

Results

Y-chromosome microdeletions were detected in 5% (5 cases of 100: 3 cases AZFc; 2 cases AZFa+b+c) (Figure 1).

Y-Hg analysis showed that Hg N3a1 and Hg R1a1 were less frequent in infertile male group compared to control group, however Hg K* was predominantly found in infertile male ($p < 0.001$; Bonferroni correction) (Table 1).

Analysis of CFTR gene mutations delF508 and R117H and IVS8 polymorphisms (Figure 2) could not confirm association with infertility.

Conclusions

1. Frequency of Y chromosome microdeletions in males with idiopathic infertility is 5%.
2. Y chromosome Hg K* may be associated with male infertility.
3. CFTR gene mutations delF508, R117H, and IVS8 polymorphisms do not affect process of spermatogenesis directly.

Figure 1. Data of Y chromosome microdeletion analysis in patients with AZF region microdeletions

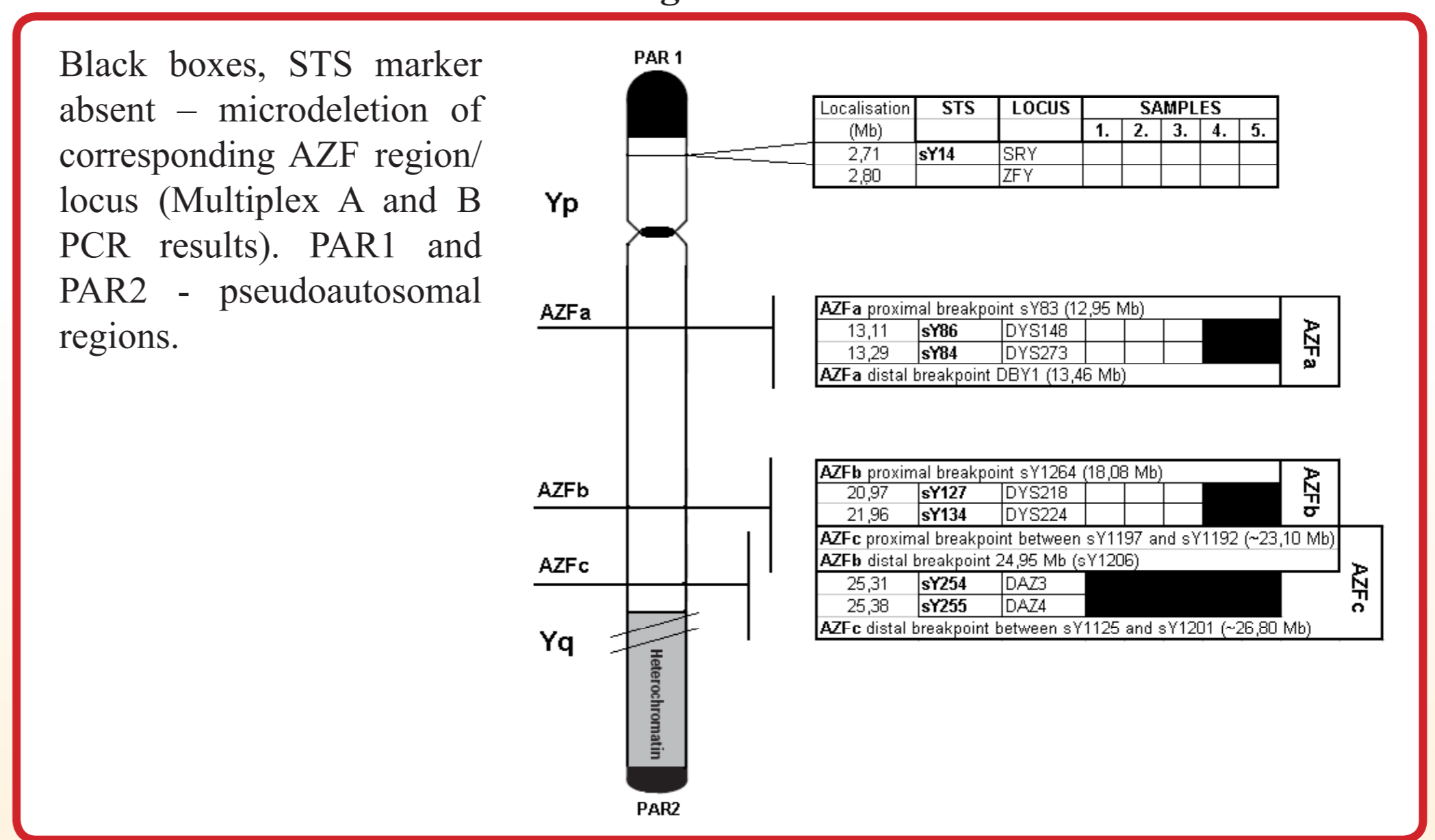


Table 1. Incidence of Y chromosome haplogroups among infertile males and control group

Haplogroups (Hg)	Incidence of haplogroups (%)		p
	Infertile males n = 79	Control group n = 153	
N3a1	24 (30.4%)	65 (42.5%)	0.223
R1a1	12 (15.2%)	60 (39.2%)	0.005
I	2 (2.5%)	13 (8.5%)	0.097
K* (without N3 and R1a)	20 (25.3%)	10 (6.5%)	< 0.001
Other (M9 C; DE* and F*:G, J)	21 (26.6%)	5 (3.3%)	< 0.001

Figure 2. Polymorphisms of CFTR gene poly-T and poly-TG variants in the analysed samples

