Identification of the PvuII RFLPs from the switch human immunoglobulin alpha (IGSA) regions

G.Keyeux*, N.Ghanem⁺, G.Lefranc and M.-P.Lefranc

Laboratoire d'Immunogénétique Moléculaire, URA CNRS 199, Université des Sciences et Techniques du Languedoc, Place E. Bataillon, 34060 Montpellier Cedex 1, France

SOURCE/DESCRIPTION : A specific human immunoglobulin switch alpha ($S\alpha$ or IGSA) probe, pS α HS2.1 corresponding to a 2.1 kb HindIII-SacI fragment from the clone λ TOU ϵ - α (1), subcloned into pUC.

POLYMORPHISM : PvuII (CAG $\downarrow$ CTG) identifies four polymorphic $S\alpha$ 1 fragments (IGSA1*B1 to B4) and ten polymorphic $S\alpha$ 2 fragments (IGSA2*B1 to B10) in the Black African, Tunisian, French and Lebanese populations.

	kb	African	French (34)	Lebanese (36)	Tunisian
FREQUENCY :					
IGSA1*B1	3.3	N.D.	0.68	0.67	N.D.
*B2	3.25	"	0.15	0.19	"
*B3	3.2	"	0.17	0.08	"
*B4	3.35	"	-	0.06	"
		(28)	(58)	(62)	(54)
IGSA2*B1	7.6	0.29	0.90	0.68	0.80
*B2	7.65	-	0.03	0.10	0.04
*B3	7.8	0.11	-	0.08	0.06
*B4	8.1	0.14	-	0.05	0.05
*B5	7.75	0.18	-	-	-
*B6	7.5	0.07	0.02	-	0.05
*B7	7.7	0.30	-	0.06	-
*B8	6.6	-	0.02	-	-
*B9	7.4	-	0.03	-	-
*B10	7.9	0.18	-	0.03	-

Number of chromosomes are given in brackets

pS α HS2.1 Probe

CHROMOSOMAL LOCALISATION : 14q32

MENDELIAN INHERITANCE : Codominant segregation

PROBE AVAILABILITY : Available from Dr. M.-P. Lefranc

OTHER COMMENTS : The Black African population shows the highest IGSA2 polymorphic variation, despite the low number of individuals tested. The incidence of rare alleles present at the homozygous state in the Lebanese and Tunisian populations might be explained by a higher degree of consanguinity observed in these populations. A previous report (2), using a 16 kb probe, assigned the polymorphic $S\alpha$ 1 region to a 4.6 or 5.1 kb PvuII fragment. Although detected with the switch alpha probe pS α HS2.1, these fragments hybridize only weakly under high stringency washing conditions (0.05xSSC).

Permanent addresses: *Unidad de Genética Clínica, Facultad de Medicina, Universidad Javeriana, Bogotá, Colombia and ⁺Université Libanaise, Faculté des Sciences Médicales, Beyrouth, Lebanon

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