



## Presence of 'ACKR1/DARC null' polymorphism in Arabs from Jisr az-Zarqa with Benign Ethnic Neutropenia

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 We describe the presence of the ACKR1 (rs2814778) polymorphism within a socially closed Arab community in Israel.
 To our knowledge this is the FIRST documentation of Duffy-null genotype in the Arab-Israeli

population.

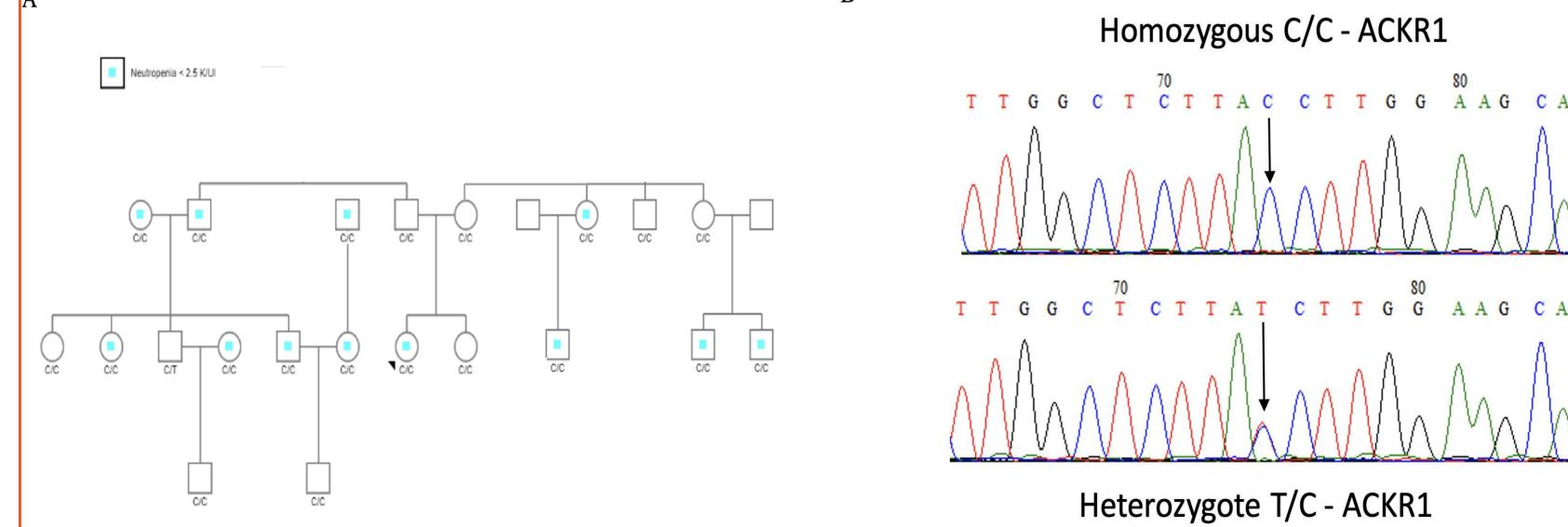
We observed a strong correlation

	T/C –	C/C –	D
Characteristics	heterozygous	homozygous	P- value
	(N=4)	(N=26)	varac
WBC Count (K/ul)			
Mean (SD)	8.35 (0.83)	5.68 (1.57)	<0.
Median (IQR)	8.20 (1.5)	5.20 (1.5)	001
Range	7.5-9.5	3.6-11.2	
Neutrophil count (K/ul)			
Mean (SD)	3.80 (1.87)	2.20 (0.733)	
Median (IQR)	4.65 (3.00)	2.10 (1.20)	
Range	1.0-4.9	0.9-3.4	
Neutrophilic			
Count <i>,</i> % (n/N) >	75% (3/4)	34.6% (9/26)	
2.5 k/uL			
Relative			
Neutropenia, %			
(n/N)	0% (0/4)	42.3% (11/26)	< 0.01
between 2.5-1.5			
k/uL			
Neutropenia, %			
(n/N)	25% (1/4)	23.1% (6/26)	
< 1.5 k/uL			
Hemoglobin Count (g/dl)			
Mean (SD)	13.65 (2.83)	12.51 (1.88)	
Median (IQR)	12.80 (5.2)	12.40 (2.9)	
Range	11.4-17.6	9.1-17.1	
Platelets Count (K/ul)			
Mean (SD)	244.25 (53.98)	258.46 (49.06)	
Median (IQR)	232 (101)	260 (60)	
Range	195-318	140-362	
Age (years) ***			
Mean (SD)	15.5 (13.9)	28.3 (17.6)	
Median (IQR)	16.0 (25)	27.0 (26)	
Range	2.0-28.0	2.0-60.0	
Gender, % (n/N)			
		46.15%	
Female	75% (3/4)	(12/26)	
		53.85%	
Male	25% (1/4)	(14/26)	
Table 1: Patients	characteristic		0

between low neutrophil counts and the ACKR1 null- genotype.
Within the ACKR1-null genotype (C/C) subgroup, the mean neutrophil count was decreased while 35% of individuals displayed normal neutrophil counts. Interestingly, this is about 3.5-fold more common in our cohort than previously described studies.

A higher awareness of benign ethnic neutropenia within specific populations could prevent such investigations and minimize management setbacks in neutropenic patients.

**Table 1**: Patients characteristics according to ACKR1 genotype SD, standard deviation; IQR, interquartile range; WBC, white blood cell Statistically significant values are in bold



**Figure 1** (A) Family pedigree analysis of Child A. Homozygous C/C - ACKR1 null genotype. (B) Sanger sequencing validation of the two detected ACKR1 genotypes in the studied family.