

FUNCTIONAL CHARACTERIZATION OF THREE NOVEL MUTATIONS IN THE *IGF1R* GENE

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Introduction

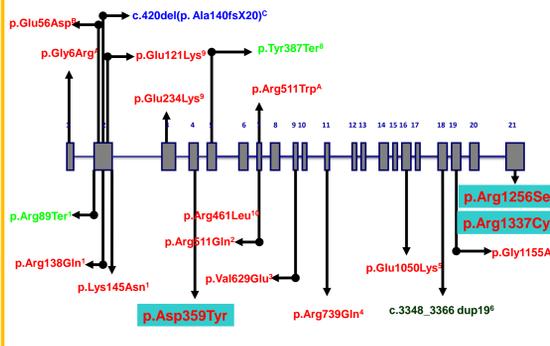
Components of the IGF system are ubiquitously expressed throughout pre- and postnatal life regulating the development of most, if not all, tissues and organs.

Since 2003, several *IGF1R* gene mutations have been associated with varying degrees of intrauterine and postnatal growth retardation and microcephaly due to IGF1 insensitivity in humans.

We have previously reported three novel variants in the *IGF1R* gene: *de novo* p.Arg1256Ser, *de novo* p.Asn359Tyr and p.Tyr865Cys (ENDO 2013, OR20-2)

Aim: To characterize the functional effects of the novel *IGF1R* gene allelic variants.

Gene and Mutations



- (1) Abuzzahab M et al. NEJM 2003 (A) Leal AC et al. ENDO 2010
 (2) Inagaki K et al. JCEM 2007 (B) Volkmann J et al. ENDO 2011
 (3) Wallborn T et al. JCEM 2010 (C) Choi JH et al. LWPESESPE 2009
 (4) Kawashima Y et al. JCEM 2005 (D) Radermacher E et al. ENDO 2012
 (5) Walenkamp MJ et al. JCEM 2006 (E) Fujimoto M et al. ENDO 2012
 (6) Fang P et al. JCEM 2009
 (7) Kruis T et al. JCEM 2010
 (8) Mohn A et al. Horm Res Ped 2011
 (9) Fang P et al. JCEM 2012
 (10) Kawashima Y et al. Clin Endocrinol 2012
 (11) Labarta J.I et al Clin Endocrinol 2012
- nonsense * homozygous
 ■ missense
 ■ duplication
 ■ small deletion

Study Population

Of 74 SGA patients without catch-up growth, we selected 28 unrelated Argentinean children suspected of having IGF-1 insensitivity according to the following criteria:

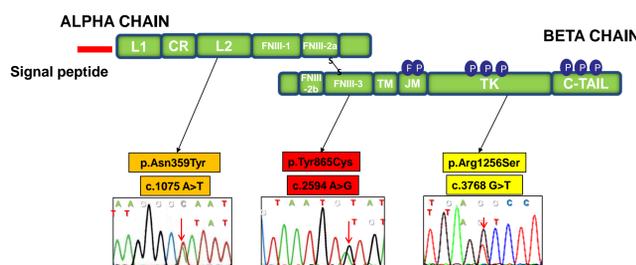
1. Being born SGA
2. Postnatal growth failure
3. Normal karyotype
4. Microcephaly

Cases reports

Molecular Studies

AT BIRTH	P1	P2	P3	P3 Mother
SEX	male	male	female	female
Gestational Age wk	37	38	38.5	at term
Weight Kg (SDS)	1.9 (-2.98)	2.37 (-2.05)	2.23 (-2.31)	not available
Length cm (SDS)	42 (-4.77)	48 (-1.44)	43 (-3.9)	not available
Head Circumference (HC) cm (SDS)	not available	not available	31 (-2.6)	not available
ON ADMISSION				
Chronological Age yr	1.49	2.8	1.9	35
Bone Age yr	1.4	1.49	1.5	
Length / Height cm (SDS)	74 (-2.17)	81.2 (-3.19)	77.7 (-2.25)	161 (0)
Weight Kg (SDS)	7.75 (-3.33)	10.5 (-2.56)	7.91 (-2.97)	
HC cm (SDS)	42.5(-4)	46.2 (-3) [#]	43 (-2.89)	52.2 (-2.1)
MENTAL DEVELOPMENT	Mild delay	Normal	Normal	
ADDITIONAL FINDINGS	Clinodactyly	Forehead		
	Triangular face	Broad nasal bridge		
	Thin lips			
	Long filtrum			
	Forehead			
KARYOTYPE	46 XY	46 XY	46 XX	
LABORATORY FINDINGS				
IGF1 ng/ml (SDS)	231 (+2.94)	58 (+0.54)	211 (+2.43)	
IGFBP3 mg/l (SDS)	5.2 (+3.37)	2.6 (-0.20)	4.7 (+2.76)	
Basal serum GH ng/ml	8	0.27	1.18	
Maximun GH peak ng/ml #		9.6		
OGTT	normal	normal	normal	
HOMA	0.4	0.18	0.89	

* at 3.2 yr chronological age # after Arginine stimulation



Species	Patient 2	Patient 3	Patient 1
Human	QMLGGCTIFKGNLLINIRRG	EPENPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Mutated	QMLGGCTIFKGYLLINIRRG	EPENPNGLILMCEIKYQSGSQ	WRMCWQYNPKMRPSFL
Chimp	QMLGGCTIFKGNLLINIRRG	EPENPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Rhesus	QMLGGCTIFKGNLLINIRRG	EPENPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Mouse	QMLGGCTIFKGNLLINIRRG	EPENPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Chicken	QMLGGCTIFKGNLLINIRRG	EPTNPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Xenopus	NLQLNIRRG	EPKRNPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Zebrafish	VYGGNLLINIRRG	EPILPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL
Fugu	TYIDNLLINIRRG	EPITPNGLILMYEIKYQSGSQ	WRMCWQYNPKMRPSFL

In silico tools were applied to predict the functional effects of the novel variants.

Variant	PolyPhen-2	SIFT	MutationTaster
p.Asn359Tyr P2	PROBABLY DAMAGING (score of 1.000)	PREDICTED TO BE TOLERATED (Score of 0.14)	DISEASE CAUSING (AA change score: 3.90)
p.Tyr865Cys P3	PROBABLY DAMAGING (score of 1.000)	AFFECT PROTEIN FUNCTION (Score of 0.00)	DISEASE CAUSING (AA change score: 5.29)
p.Arg1256Ser P1	PROBABLY DAMAGING (score of 1.000)	AFFECT PROTEIN FUNCTION (Score of 0.00)	DISEASE CAUSING (AA change score: 3.00)

Functional Studies (*in vitro* assays)

Fibroblast cell primary culture

Fibroblast cultures were established from skin biopsies obtained from the abdomen zone from patients affected by the variations (P1, P2 and P3) and two control subjects (C1 and C2). Cell cultures were maintained in Dulbecco's modified Eagle medium and F12 (DMEM/F12, SIGMA, Buenos Aires, Argentina) containing 10 or 20% fetal bovine serum (FBS), at 37 °C in a humidified atmosphere with 5% CO₂. Fibroblasts were subcultured for 3 passages and then stored in liquid N until the time of performing the assay. Finally, all fibroblasts were subcultured once more to collect the necessary cell number for the study. All studies were performed at passage 4. Fibroblasts were stimulated with different concentrations of IGF-1, and the highest response was observed at 50 ng/ml.

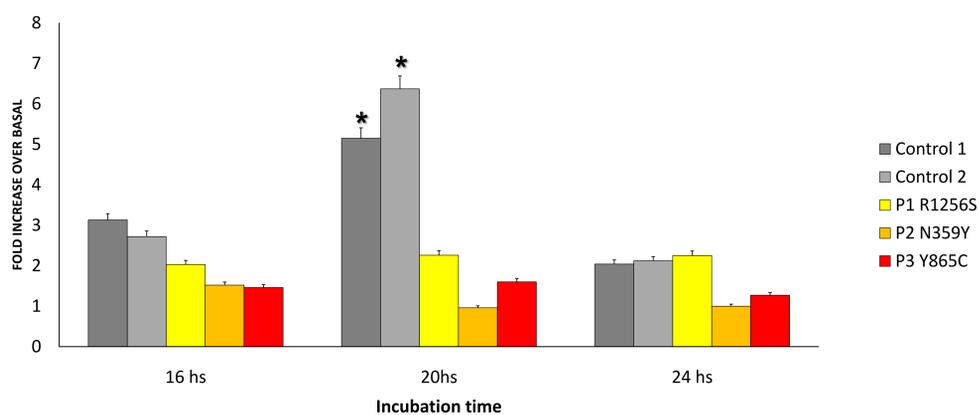
IGF1-dependent DNA synthesis assay (3[methyl-³H] Thymidine incorporation)

Fibroblasts were stimulated with 50 ng/ml of IGF-1 for 16, 20, and 24 h. [Methyl- ³H] thymidine (1 mCi/ml) was added for 4 h prior to basal conditions and to 12, 16, 20 h of IGF-1 treatment.

A significant increase of ³[H] thymidine incorporation was observed after 20 hours of IGF-1 treatment in C1 and C2 (p<0.05 by ANOVA and Student's t Test). No significant increase was observed in P1, P2, and P3.

Results are expressed as fold increase over basal X ± SD.

*P < 0.05 20 h vs 16 and 24 h.



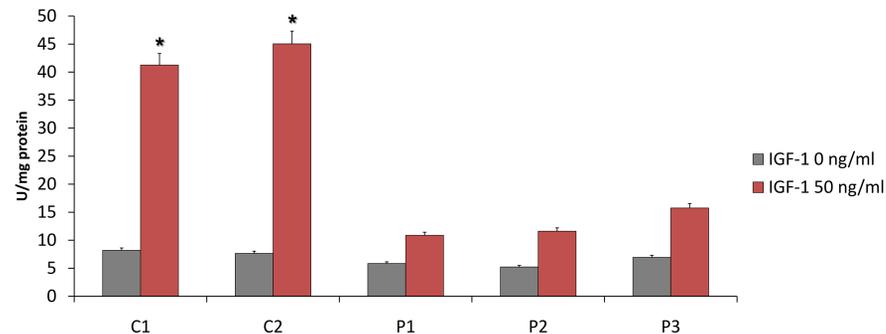
AKT phosphorylation stimulation by IGF-1 (Phospho-Akt (Ser473) STAR ELISA Kit (Millipore))

A total of 80000 cells/wells were incubated in 24-well plates and stimulated with 50 ng/ml of IGF-1. The fibroblasts were lysed and the protein concentration was measured by Bradford assay.

AKT phosphorylation was measured with phospho-Akt (Ser473) STAR ELISA Kit (Merk Millipore, Tecnolab, Buenos Aires, Argentina). The entire assay was performed in duplication. Results are expressed as units per mg of protein.

Akt phosphorylation was significantly stimulated in the control subjects by IGF-1 (P < 005 by ANOVA and Bonferroni tests). No significant stimulation in the PI3K/Akt pathway was observed in P1, P2 and P3.

*P < 005 vs basal conditions.



Discussion

We characterized three novel heterozygous mutations, *de novo* p.Arg1256Ser (P1), *de novo* p.Asn359Tyr (P2), and familial p.Tyr865Cys (P3) in the *IGF1R* gene that inhibit cell proliferation induced by IGF-1 and affect IGF1R signal transduction in patients' fibroblast cultures. These findings strongly suggest that these mutations lead to failure of the IGF1R and cause the phenotype of pre- and postnatal growth retardation and microcephaly.

Using this approach, we found 3/28 affected patients with mutations in the *IGF1R* (estimated frequency 10.7%), which reinforces the importance of measuring head circumference in the evaluation of SGA and short-statured patients.