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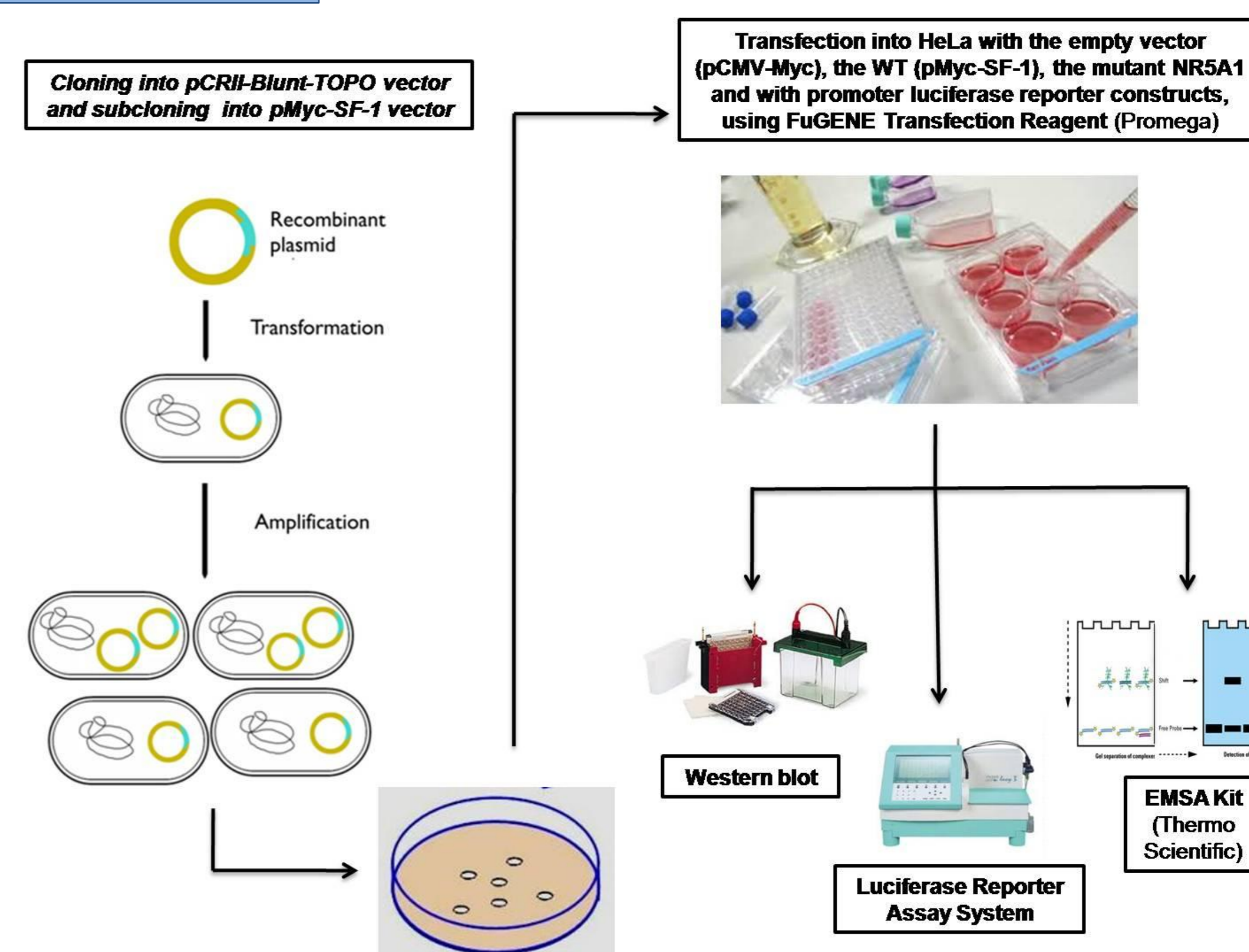
Introduction:

Steroidogenic factor-1 (SF-1), encoded by *NR5A1* gene, is a key regulator of steroidogenesis and reproductive development¹. *NR5A1* mutations found in 46,XY patients with disorder of sex development (DSD), are associated with a range of conditions within the spectrum of phenotypes, including testicular dysgenesis, hypospadias and male infertility².



Fig. 1: Structure of human SF-1 is characterized by a DNA-binding domain (DBD) containing two zinc fingers, an accessory hinge region, a ligand-binding domain (LBD), and two functional activation domains, AF-1 and AF-2, located at the hinge region and at the C-terminal in LBD, respectively³.

Methods:



Results:

Two mutations (p.C247* and p.K396Rfs*34), identified in the SF-1 ligand domain (LBD) have been analyzed to estimate their functional influence on SF-1 transcriptional activity. Luciferase reporter gene expression was reduced for both p.C247* and p.K396Rfs*34 when tested on *AHM* and *STAR* promoters. Whereas the transactivation activity for p.K396Rfs*34 was completely null, p.C247* retained a very low activity. Western blot showed that normal and mutant proteins were expressed in similar amounts. EMSA was also performed to analyze if those mutations would disturb SF-1 DNA binding ability. Results showed that the mutation p.K396Rfs*34 abolished the ability to bind DNA, whereas the formation of a protein-DNA complex was still observed for p.C247*. Clinical data of the patients are detailed in Table 1.

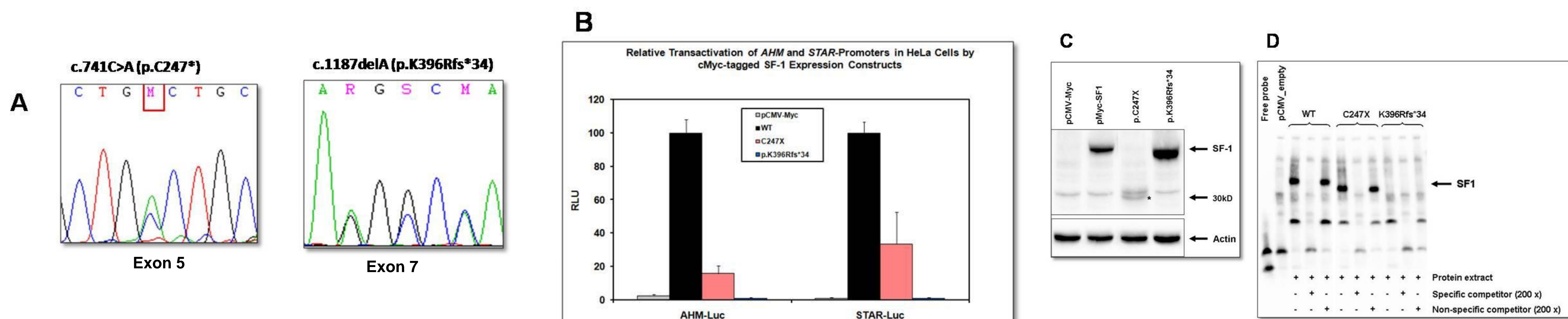


Fig. 2: A) Part of electropherogram sequences showing the mutations c.741C>A in exon 5 and c.1187delA within exon 7. B) Transactivation of *AHM* and *STAR* Promoters in HeLa cells, showing no activity of the mutant p.K396Rfs*34 and low activity of p.C247*. C) Expression levels of SF-1 protein in the Western Blot. D) EMSA assays revealed that only the SF-1 mutant p.C247* was able to bind to an SF-1 specific DNA sequence, whereas the p.K396Rfs*34, lost this ability.

Table 1: Clinical data of the patients with *NR5A1* mutations.

<i>NR5A1</i> gene mutation	Karyotype/Assigned sex	PHENOTYPE							Family
		Age at first visit	Urethral opening	Gonadal location (R/L)	Basal gonadotrophins	Basal testosterone	Testosterone response to hCG testing	Gonadal histology (R/L)	
p.C247*	46,XY/Female to male	20 years	Penoscrotal	IC / LSF	Elevated FSH, normal-high LH	Normal	NP	N/A	NP
p.K396Rfs*34	46,XY/ Male	7.8 years	Perineal	LSF / LSF	Prepubertal	Prepubertal	No response	Dysgenetic testes bilaterally	M=N

R, Right; L, Left; IC, Inguinal Channel; LSF, Labioscrotal folds; NP, Not performed; M, Mother; N, Normal.

DISCLOSURE STATEMENT: The authors have nothing to disclose.

REFERENCES: ¹Luo X, Ikeda Y, Parker KL. A cell-specific nuclear receptor is essential for adrenal and gonadal development and sexual differentiation. *Cell* 1994;77(4):481-90. ²Pedace L, Laino L, Preziosi N, Valentini MS, Scommegna S, et al. Longitudinal hormonal evaluation in a patient with disorder of sexual development, 46,XY karyotype and one *NR5A1* mutation. *Am. J. Med. Genet. Part A* 2014;164(August):2938-2946. ³Hoivik EA, Lewis AE, Aumo L, Bakke M. Molecular aspects of steroidogenic factor 1 (SF-1). *Mol. Cell. Endocrinol.* 2010;315(1-2):27-39. ⁴Camats N, Pandey A, Fernández-Cancio M, Andaluz P, et al. Ten novel mutations in the *NR5A1* gene cause disordered sex development in 46,XY and ovarian insufficiency in 46,XX individuals. *J. Clin. Endocrinol. Metab.* 2012;97(7):E1294-306.

Supported by:

Conclusion:

It is already known that, mutations at SF-1 LBD, may result in variable effects depending on their location and alterations in the ligand specificity/recognition⁴. This was also observed here, once both mutations localized in the LBD had completely different effects on DNA binding. However, both patients present partial gonadal dysgenesis, suggesting that the genotype-phenotype correlation, especially for mutations within the LBD, remains elusive. SF-1 function/regulation is very complex and must be increasingly studied, mainly because the number of different phenotypes correlated with mutations on this gene has been constantly increased.