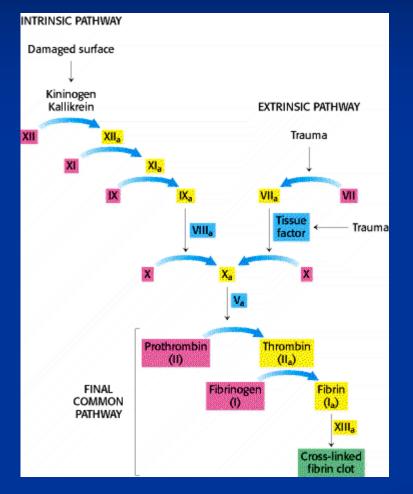
Evaluation of the Invader® assay platform for molecular analysis of the Factor V (G1691A) and Factor II (G20210A) mutations.

O. N. Wood, D. J. Bunyan, J. F. Harvey, NCP Cross

Wessex Regional Genetics Laboratory and National Genetics Reference Laboratory.

Introduction:

Blood clotting cascade:



- Activated Factor V (FVa) is involved in the conversion of prothrombin to thrombin.
- Thrombin then acts on fibrinogen to form fibrin.
- Fibrin forms the main constituent of the blood clot.

Thrombophilia:

- Pathological activation of the clotting cascade leading to venous thromoboembolism (VTE).
- Incidence = 1/ 1000.

<u>Clinical manifestations:</u>

Deep vein thrombosis (DVT) of the lower limbs and pulmonary embolism.

Inherited	acquired	Mixed
Anti-thrombin deficiency	Age	Hyperhomocysteinemia
Protein C deficiency	Immobilisation	Increased Factor VII levels
Factor V Leiden	Surgery	Increased Factor XI levels
Factor II G20210A	Malignancy	Increased factor IX levels
	Pregnancy	Increased Fibrinogen levels
	Oral contraceptives	
	HRT	

Genetic, acquired and mixed risk factors for thrombosis:

Genetic thrombophilia:

 Individuals with genetic thrombophilia show an increased RISK of recurrent thrombosis with an earlier onset (<45 yrs).

Factor V (Proaccelerin):

- Factor V Leiden mutation (Arg506Glu) affects an activated protein C (APC) cleavage site and causes APC resistance.
- Pathology = lowered turnover of FVa and an increased conversion of prothrombin to thrombin.
- Heterozygous = 5% of general population and 18% of thrombophilia patients. Increased risk of thrombosis = 2 to 7-fold higher
- Homozygous mutations carriers have increased risk of 40-80 fold higher.

Cont: <u>Factor II (prothrombin):</u>

- The prothrombin mutation G20210A locates to the 3'untranslated region and causes hyperthrombinemia.
 - It is present in 2% of the population and 7% of individuals with thrombosis.
 - FII (G20210A) is linked to a 2 to 5-fold increase in risk. of thrombosis, homozygosity of the mutation is associated with a further increase in risk of thrombosis.

Co-inheritance of FVL and FII mutations:

- Compound heterozygosity for FVL (G1691A) and the Factor II (G20210A) mutations occurs in 1/1000.
 - This is associated with a 20-fold increase in risk of thrombosis.

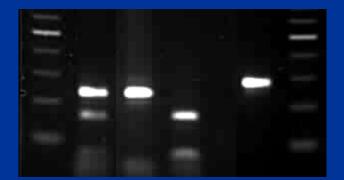
Methodology:

The RFLP method (PCR based):

Factor V Leiden:

Restriction enzyme = Mnl I

(loss of restriction site)



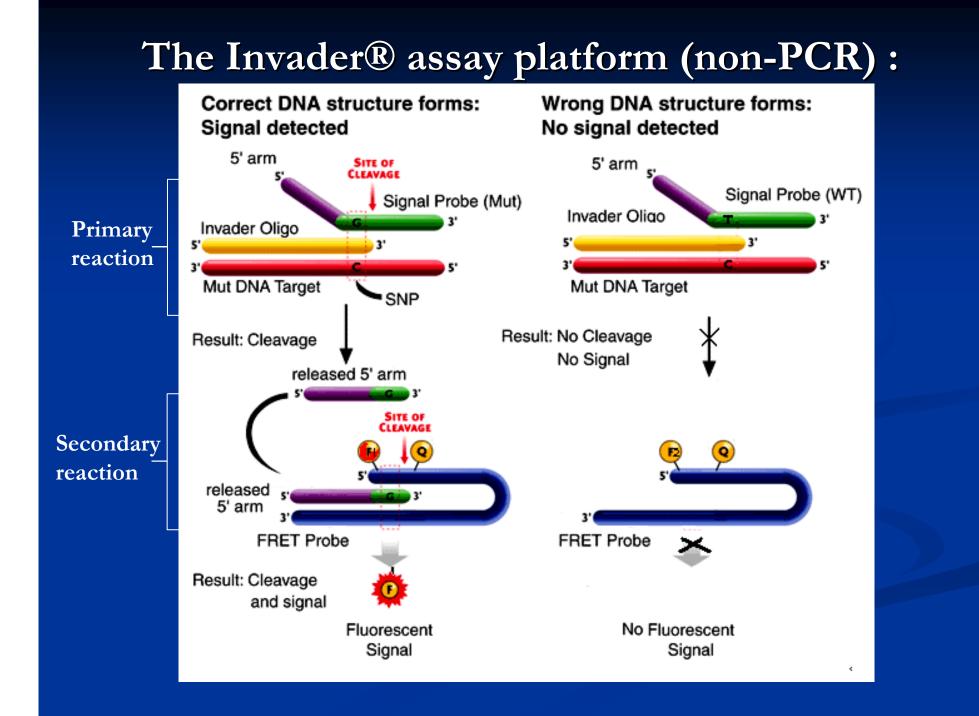
Undigested No DNA Normal Homozygous Heterozygous Factor II:

Restriction enzyme = Hind III

(Use of mutagenic primer and G > A creates restriction site)



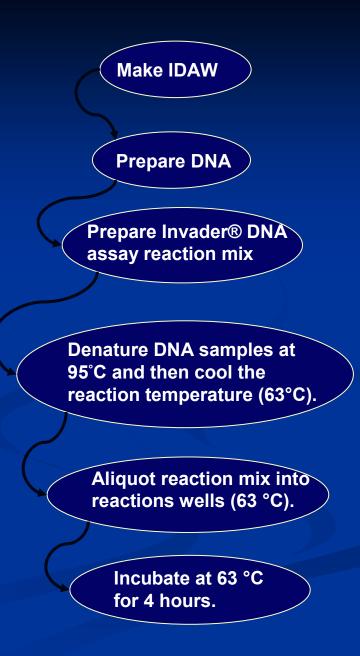
Undigested No DNA Heterozygous Normal



Invader® assay platform:

(Third Wave technologies)

- >100ng of DNA is needed
- 96 well plate format.
- biplex format F (WT) and R (Mut) signal
- Controls include a Normal, Heterozygote and Homozygote
- Fluorescence analysed using a 96 well plate reader (CytoFluor 96 well plate reader).
- An excel worksheet (IDAW) is used to calculate the net signal/ background or net fold over zero (FOZ).
- Ratio of the WT reaction to the mutant reaction.
 - Heterozygous = >0.3 to <3
 - Homozygous = <0.2
 - Normal = >5
- Total assay time = ~ 5 hours (hands on time = 30-45min)



Aim:

- To evaluate the Third WaveTM Invader® DNA assay for the detection of the FVL (G1691A) and Factor II (G20210A) mutations.
- Test 100 samples where the genotype is known for the FV and FII mutations as determined by the RFLP method.
- Compare and contrast the two methods for use in a diagnostic setting.

Results:

IDAW:

Data Filo	Date Stamp:					Raw Data					
F Signal	Date Stamp:					Kaw Data					
(Mut)	1	2	3	4	5	6	7	8	9	10	11
AB	259 684										
č	909	232									
D	294 349	217 199									
E	318										
G	1508	285									
н	352	417									
						1					
R Signal (WT)	1 534	2 1678	3	4	5	6	7	8	9	10	11
A B	540	227									
С	245	2210									
DE	253 400	911 1026									
F	686	1174									
G	1374 1302										
Н	1302	04/									
	D. I.					Lot Numbers		ET D 0		FVL (1691) Control 1 (V	
Operator: oly2	Date: 30/01/2004	DNA Reactio FVL (1691)						ET_R Cassette (R) ET_F Cassette (F)		FVL (1691) Control 2 (H FVL (1691) Control 3 (N	
	0010112001	FVL (1691)						zyme 40 ng/µl (E)		Control 4 (No Target Bla	
			Invade	r Data Analy	sis - FVL (G1	1691A) Biple	x Assay			Version 040202	
	Invader					Net F Signal	Net R Signal				
Sample	Genotype										
	senotype	F Signal	R Signal	F Signal FOZ	R Signal FOZ	FOZ	FOZ	RATIO	Data	Action	
FVL (1691)	WT	F Signal	R Signal	F Signal FOZ	R Signal FOZ	FOZ	FOZ	27.767	Data VALID	Action	
FVL (1691) Control 1											
FVL (1691) Control 1 FVL (1691)											
FVL (1691) Control 1 FVL (1691) Control 2	WT	259	534	0.88	2.11	0.04	1.11	27.767	VALID	NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691)	WT	259	534	0.88	2.11	0.04	1.11	27.767	VALID	NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3	WT HET	259 684 909	534 540 245	0.88	2.11 2.13	0.04	1.11	27.767 0.855	VALID VALID VALID	NONE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4	WT HET MUT	259 684 909 294	534 540 245 253	0.88 2.33 3.09	2.11 2.13 0.97	0.04 1.33 2.09	1.11 1.13 0.04	27.767 0.855 0.019	VALID VALID VALID VALID	NONE NONE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul)	WT HET MUT EQ1	259 684 909 294 349	534 540 245 253 400	0.88 2.33 3.09 1.19	2.11 2.13 0.97 1.58	0.04 1.33 2.09 0.19	1.11 1.13 0.04 0.58	27.767 0.855 0.019 3.106	VALID VALID VALID VALID INVALID	NONE NONE NONE NONE REPEAT SAMPLE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul)	WT HET MUT EQ1 WT	259 684 909 294 349 318	534 540 245 253 400 686	0.88 2.33 3.09 1.19 1.08	2.11 2.13 0.97 1.58 2.71	0.04 1.33 2.09 0.19 0.08	1.11 1.13 0.04 0.58 1.71	27.767 0.855 0.019 3.106 20.965	VALID VALID VALID VALID INVALID VALID	NONE NONE NONE NONE REPEAT SAMPLE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9	WT HET MUT EQ1 WT HET	259 684 909 294 349 318 1508	534 540 245 253 400 686 1374	0.88 2.33 3.09 1.19 1.08 5.13	2.11 2.13 0.97 1.58 2.71 5.43	0.04 1.33 2.09 0.19 0.08 4.13	1.11 1.13 0.04 0.58 1.71 4.43	27.767 0.855 0.019 3.106 20.965 1.073	VALID VALID VALID VALID INVALID VALID VALID	NONE NONE NONE NONE REPEAT SAMPLE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10	WT HET MUT EQ1 WT HET WT	259 684 909 294 349 318 1508 352	534 540 245 253 400 686 1374 1302	0.88 2.33 3.09 1.19 1.08 5.13 1.20	2.11 2.13 0.97 1.58 2.71 5.43 5.15	0.04 1.33 2.09 0.19 0.08 4.13 0.20	1.11 1.13 0.04 0.58 1.71 4.43 4.15	27.767 0.855 0.019 3.106 20.965 1.073 21.017	VALID VALID VALID VALID INVALID VALID VALID VALID	NONE NONE NONE REPEAT SAMPLE NONE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11	WT HET MUT EQ1 WT HET WT WT	259 684 909 294 349 318 1508 352 211	534 540 245 253 400 686 1374 1302 1678	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810	VALID VALID VALID VALID INVALID VALID VALID VALID VALID	NONE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11 11	WT HET MUT EQ1 WT HET WT WT	259 684 909 294 349 318 1508 352 211 285	534 540 245 253 400 686 1374 1302 1678 227	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72 0.97	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63 0.90	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63 0.04	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810 1.000	VALID VALID VALID VALID INVALID VALID VALID VALID VALID INVALID	NONE NONE NONE REPEAT SAMPLE NONE NONE NONE NONE REPEAT SAMPLE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11 11 12 13	WT HET MUT EQ1 WT HET WT WT WT	259 684 909 294 349 318 1508 352 211 285 232	534 540 245 253 400 686 1374 1302 1678 227 2210	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72 0.97 0.79	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63 0.90 8.74	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04 0.04 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63 0.04 7.74	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810 1.000 193.379	VALID VALID VALID VALID INVALID VALID VALID VALID VALID VALID VALID	NONE NONE NONE REPEAT SAMPLE NONE NONE NONE REPEAT SAMPLE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11 12 12 13 19	WT HET MUT EQ1 WT HET WT WT WT WT	259 684 909 294 349 318 1508 352 211 285 232 217	534 540 245 253 400 686 1374 1302 1678 227 2210 911	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72 0.97 0.79 0.74	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63 0.90 8.74 3.60	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04 0.04 0.04 0.04 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63 0.04 7.74 2.60	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810 1.000 193.379 65.020	VALID VALID VALID VALID INVALID VALID VALID VALID VALID VALID VALID VALID VALID	NONE NONE NONE REPEAT SAMPLE NONE NONE NONE REPEAT SAMPLE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11 12 13 19 15	WT HET MUT EQ1 WT HET WT WT WT WT	259 684 909 294 349 318 1508 352 211 285 232 217 199	534 540 245 253 400 686 1374 1302 1678 227 2210 911 1026	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72 0.97 0.79 0.74 0.68	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63 0.90 8.74 3.60 4.06	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04 0.04 0.04 0.04 0.04 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63 0.04 7.74 2.60 3.06	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810 1.000 193.379 65.020 76.383	VALID VALID VALID VALID INVALID VALID VALID VALID VALID VALID VALID VALID VALID VALID	NONE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11 12 13 19 15 16	WT HET MUT EQ1 WT HET WT WT WT WT WT	259 684 909 294 349 318 1508 352 211 285 232 217 199 212	534 540 245 253 400 686 1374 1302 1678 227 2210 911 1026 1174	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72 0.97 0.79 0.74 0.68 0.72	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63 0.90 8.74 3.60 4.06 4.64	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04 0.04 0.04 0.04 0.04 0.04 0.04 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63 0.04 7.74 2.60 3.06 3.64	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810 1.000 193.379 65.020 76.383 91.008	VALID VALID VALID VALID INVALID VALID VALID VALID VALID VALID VALID VALID VALID VALID VALID	NONE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE NONE NONE	
FVL (1691) Control 1 FVL (1691) Control 2 FVL (1691) Control 3 Control 4 66(4ul) 6(4ul) 9 10 11 12 13 19 15	WT HET MUT EQ1 WT HET WT WT WT WT	259 684 909 294 349 318 1508 352 211 285 232 217 199	534 540 245 253 400 686 1374 1302 1678 227 2210 911 1026	0.88 2.33 3.09 1.19 1.08 5.13 1.20 0.72 0.97 0.79 0.74 0.68	2.11 2.13 0.97 1.58 2.71 5.43 5.15 6.63 0.90 8.74 3.60 4.06	0.04 1.33 2.09 0.19 0.08 4.13 0.20 0.04 0.04 0.04 0.04 0.04 0.04	1.11 1.13 0.04 0.58 1.71 4.43 4.15 5.63 0.04 7.74 2.60 3.06	27.767 0.855 0.019 3.106 20.965 1.073 21.017 140.810 1.000 193.379 65.020 76.383	VALID VALID VALID VALID INVALID VALID VALID VALID VALID VALID VALID VALID VALID VALID	NONE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE REPEAT SAMPLE NONE NONE NONE	

Factor V and Factor II Invader results:

	Factor V	Factor II
Number of samples	110	110
Normal	71	98
Heterozygous	33	9
Homozygous	2	X
% Concordance	100%	100%
% Repeated	5.5%	3.6%
% Fail	3.6%	2.7%

Discussion:

The genotypes obtained from the Invader® assay showed 100% concordance to the RFLP method showing that it is suitable for use in diagnostic molecular genetics.

<u>Repeated samples:</u> Factor V 5.5% and Factor II 3.6%.

Possible reasons:

- Low signal as a result of low DNA concentration meaning the patient sample doesn't exceed the background fluorescence seen in the no target blank control.
 - when repeated with more DNA the correct genotype was obtained.
- Failed samples: Factor V 3.6% and Factor II 2.7%.
- The samples that could not be genotyped were due to a low DNA concentration.

- 50 /110 samples tested were from Southampton Human genetics unit (total volume 10-15µl).
- All failed samples were from this source and could not be quantified or genotyped due to sample being depleted.

Comparison of Invader and RFLP:

	RFLP	Invader platform
Total time	7-25 hours	4-5 hours
Hands on time	2-3 hours	<45 mins
Number of steps	8	4
	1: Prepare sample	1: Prepare sample
	2: Make master mix	2: Make master mix
	3: Make digest mix	3: Add master mix to plate
	4: Add digest mix to samples	4: Read plate
	5: Restriction digest	
	6: Pour gel	
	7: Load gel	
	8: Image gel	
Analysis	Gel (subjectivity)	Excel spreadsheet (IDAW)
Visualisation	EtBr (mutagenic)	FRET (fluorescence)

Cost per test:

Invader assay platform = $\pounds 8$ per result

 $RFLP = Approx. \pounds 2-3$

Other applications of the Invader assay platform:

- Cystic fibrosis testing
- Conexin 26
- MTHFR (methylenetetrahydrofolate reductase)
- ApoE
- Rett syndrome
- Prenatal chromosomal analysis

Conclusion:

- The invader offers cheap rapid detection of SNP's
- Highly reproducible results with 100% concordance to existing methods.
- It is non-PCR based.
- Wide applications to other areas of molecular diagnostics.
- Highly dependant on template concentration as it affects the reaction dynamics and overall signal strength.
- More expensive than the existing RFLP method but is less labour intensive and is more rapid with results in ~ 5 hours.

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