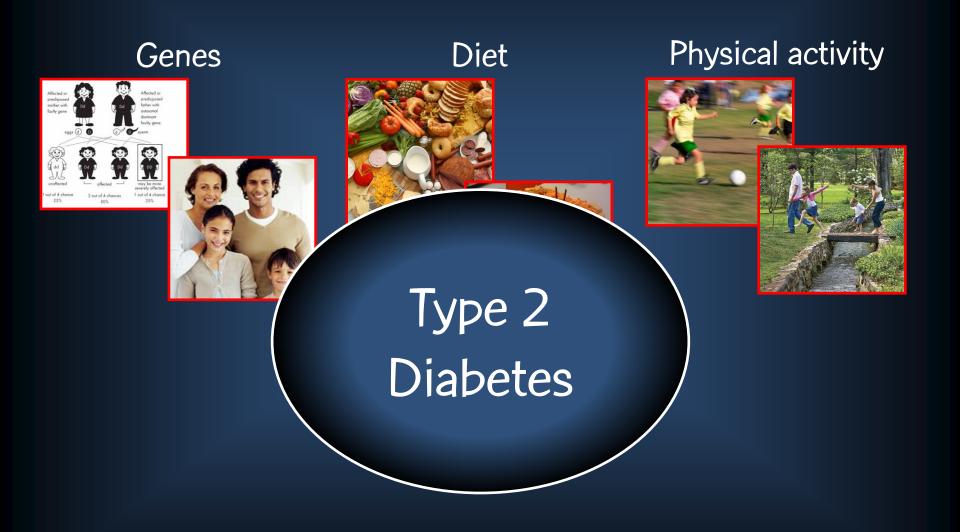
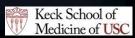
# Human Genomic Analysis of Type 2 Diabetes and its Translation to Clinical Care

# Keck School of Medicine of **USC**

Richard M. Watanabe, Ph.D.

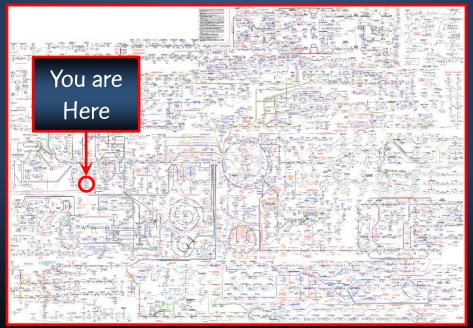
Depts. of Preventive Medicine and Physiology & Biophysics USC Diabetes and Obesity Research Institute



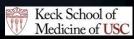


#### Glucose is only a convenient end—point

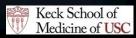
- Diagnostic criteria is population—based and examines risk for retinopathy
- Clinical cut—offs ignore the continuous nature of glucose
- Fundamentally not a good indicator of a trajectory towards T2DM
- There are many ways to get to hyperglycemia.



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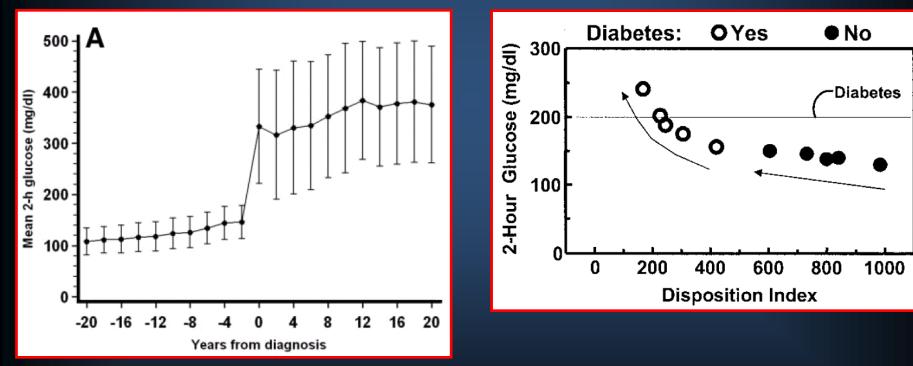


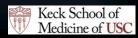
- Clinical diagnosis does not recognize that "diabetes" is a cluster of different diseases that manifest in hyperglycemia
- T2DM is fundamentally a disease of the pancreatic  $\beta$ -cell
- Most physicians still use mono—therapy with the goal of reducing glycemia or HbA1c



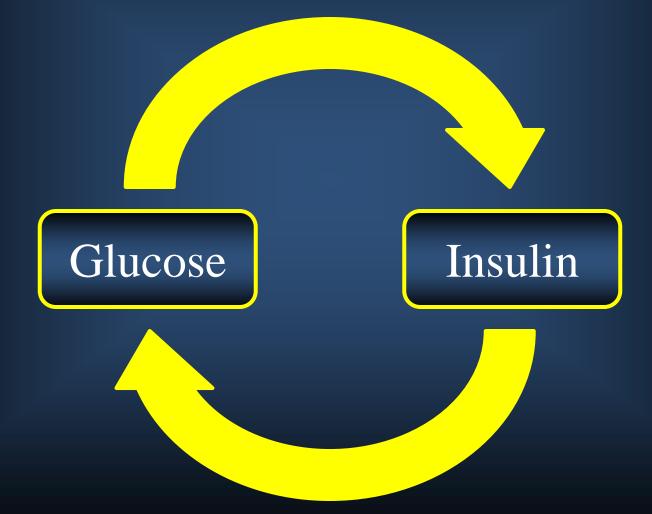
#### Data from Pima Indians Mason *et al.,* Diabetes 56:2054–2061, 2007

#### Data from Latinas Buchanan *et al.,* Diabetes Care 30:S105–S111, 2007

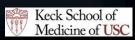




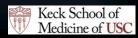
Need to consider the regulatory feedback nature of glucose and insulin

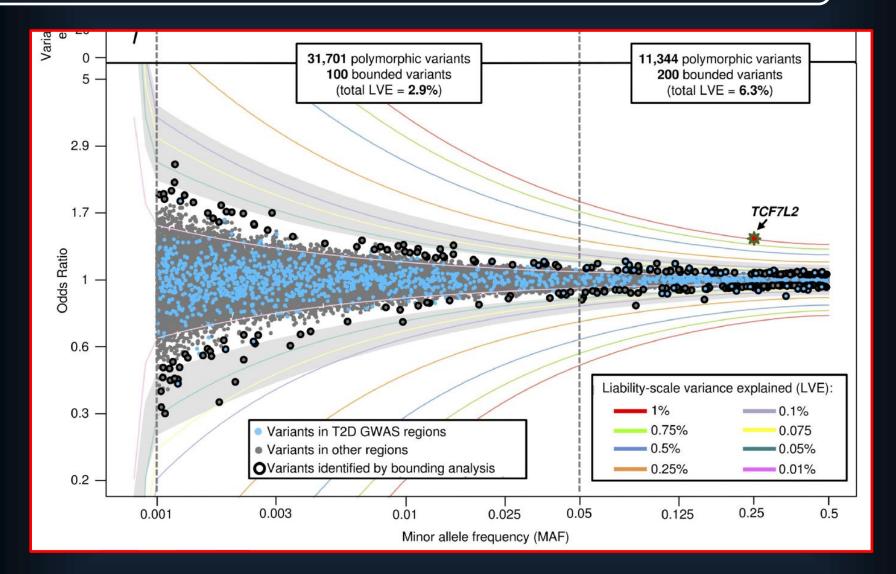


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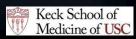


- Genome—wide association (GWA) studies have identified
  - Over 80 loci associated with risk for T2DM
  - "Hundreds" of loci associated with variation in T2DM—related traits
    - Glycemia/insulinemia
    - Obesity/adiposity
    - Lipids/lipoproteins
    - Related metabolic disorders
- Recent whole—exome and whole—genome studies revealed new insights
  - There appear to be few rare variants of large effect
  - Most rare variants have effect sizes similar to common variants
  - Not likely to explain the so—called "missing" heritability

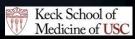




Taken from Fuchsberger et al., Nature 536:41-47, 2016



- Question: So how should we think about the role of genetic variation in the pathogenesis of type 2 diabetes?
- Most variants are in intergenic or intronic regions
  - Suggests transcriptional regulation or gene splicing may be important
- Most associations are only landmarks, so fine—mapping to identify "the" variant will be key
- Much work to do . . .



- An alternative view . . .
- While reductionist science is important, many times small molecular changes do not manifest themselves in a clinical phenotype
- Physiologic regulation can mask the small effects engendered by some genetic variants
- Some effects may not manifest in a phenotype for prolonged periods of time

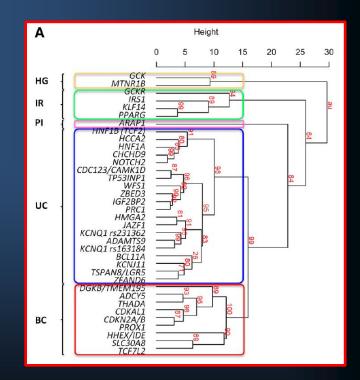
#### Translating Genetics

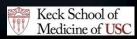
Two important observations:

- First, majority of type 2 diabetes susceptibility loci appear to map to the pancreatic  $\beta$ -cell
  - But difficult to map loci back to phenotypes
- Second, β–cell preservation appears to be one of the keys to prevention of type 2 diabetes
  - Supported by two key studies (in addition to others)

#### **Translating Genetics**

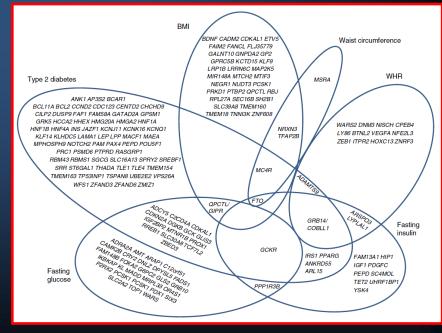
- MAGIC (Dimas *et al.*, Diabetes 63:2158–2171, 2014)
- Associate 37 type 2 diabetes loci with physiologic phenotypes
- Major outcomes:
  - Cluster analysis identified 5 groupings
    - Insulin secretion with hyperglycemia (HG)
    - Insulin resistance (IR)
    - Proinsulin processing (PI)
    - β–cell without hyperglycemia (BC)
    - Uncategorized (UC)
  - Based on association with phenotypes most loci fell into "uncategorized", despite known biology related to pancreas

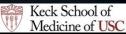




#### Translating Genetics

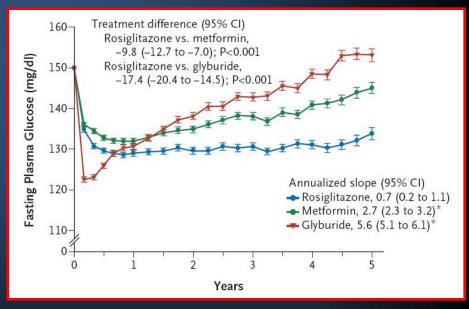
- Lack of overlap in loci across phenotypes (Grarup *et al.*, Diabetologia 57:1528–1541, 2014)
- Assessed the overlap in loci across GWAS for type 2 diabetes and diabetes—related phenotypes
- Major outcome:
  - Almost no overlap in loci across phenotypes
  - Greatest overlap with fasting glucose

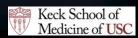




#### **Diabetes Prevention**

- The ADOPT Study (Kahn *et al.*, New Engl J Med 355:2427–2443, 2006)
- Compared "durability" of different mono-therapies
- Major outcomes:
  - Mono–therapy failure:
    - 15% with rosiglitazone
    - 21% with metformin
    - 34% with glyburide
  - Risk reduction:
    - 32% rosiglitazone *vs.* metformin
    - 63% rosiglitazone *vs.* glyburide



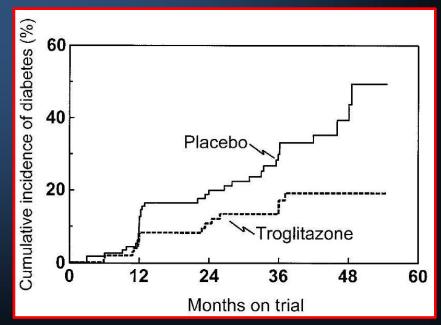


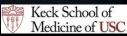
#### **Diabetes Prevention**

- The TRIPOD Study (Buchanan *et al.*, Diabetes 51:2796–2803, 2002)
- First study to assess whether improving insulin sensitivity to preserve  $\beta$ -cell function can reduce risk for type 2 diabetes

#### Major outcomes:

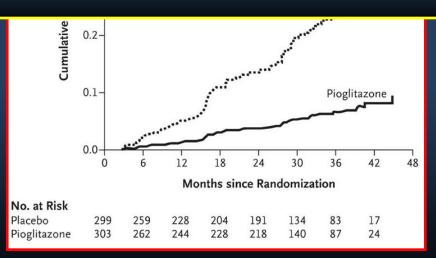
- Troglitazone mono-therapy reduced risk of future type 2 diabetes by >50%
- Degree of reduction was related to degree of improvement in β–cell function

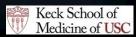




#### **Diabetes Prevention**

- TRIPOD results have been replicated in larger trials using both rosiglitazone and pioglitazone
- Example: ACT NOW showed 72% reduction in risk for type 2 diabeted with piedliterone more therapy (DeFrence et al., New Engl Suggests focusing on pancreatic β–cell and β–cell function is the key to "preventing" type 2 diabetes

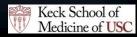




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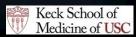
#### **Translation of Genetics**

- Question: So how can we translate GWAS and sequencing findings for use in clinical care?
- Prediction of diabetes: Nice public relations reasons, but not particularly need
  - Family history currently used to identify at—risk individuals
  - Most studies show that including variants does not significantly improve prediction
  - Could be useful in the absence of family history information
- Identification of additional disease classes: Fewer studies, but possible that unique variants might help discriminate different subsets of diabetes



## **Translation of Genetics**

- Lifestyle response: Potential for an individual to respond to lifestyle modification
  Likely to have limited efficacy
- New therapeutics
  - Potential pharmaceutical targets, but much work required
  - Gene therapy hopefully in the near future
- Pharmacogenetics/genomics: Area of great promise, but many facets
  - Susceptibility to adverse events/side effects
  - Responders *vs.* non–responders
  - How to define "response"
  - Focus on individual drugs?



- Success stories for rare variants (not quite pharmacogenetics)
- Best example: Rare variants in *KCNJ11* and *ABCC8* and neonatal diabetes (Pearson *et al.*, New Engl J Med 355:467–477, 2006)
  - Infants presented as type 1 diabetes, treated with insulin
  - Actually had rare inactivating mutations in KCNJ11 and ABCC8
  - Treatable with sulphonylureas

Examples for type 2 diabetes and common variants are rare and many times not strongly convincing

#### See review by Ivan Tkac (Curr Diab Rep 15:43, 2015) (3

	Study drug [reference]	No. of patie	nts SNP	Gene	Reduction in HbA1c (%) major (reference) vs. minor allele	р	
	Metformin [16••]	1024	rs11212617 (A→C)	ATM	AA: reference; per C allele: +0.18 %	$1.8 \cdot 10^{-5}$	
	Metformin [17•]	4443	rs11212617 (A→C)	ATM	AA: reference; per C allele: +0.05 %	0.020	
	Metformin [18]	277	rs11212617 (A→C)	ATM	AA: reference; AC: +0.81 %, CC: +0.92 %	0.048	
	Metformin [30•]	118	rs2289669 (G→A)	SLC47A1	GG: reference; GA: +0.32 %, AA: +0.66 %	0.005	
oglitazone	[64] 250	1.40	rs1801282 (P12A)	PPARG	P12P: reference; P12A: +0.22 %	0.010	0.00
siglitazon	e [65] 198		rs1801282 (P12A)	PPARG	P12P: reference; P12A: +0.84 %		0.01
	Sulfonylureas [46]	101	rs5219 (E23K)	KCNJ11	E23E: reference; E23K + K23K: +0.25 %	0.036	
	Repaglinide [47]	100	rs5219 (E23K)	KCNJ11	E23E: reference; K23K: + 1.13 %	0.022	
	Sulfonylurea [54••]	901	rs1225372 (G→T)	TCF7L2	GG: reference; TT: -0.33 %	0.032	
			rs7903146 (C→T)		CC: reference; TT: -0.31 %	0.039	
	Sulfonylureas [55•]	101	rs7903146 (C→T)	TCF7L2	CC: reference; CT + TT: -0.35 %	0.006	
	Sulfonylureas [59••]	1073	rs1799853 *2(R144C) rs1057910 *3(I359L)	CYP2C9	*1/*1: reference; *2/*2, *2/*3 or *3/*3: +0.50 %	0.0009	
	Pioglitazone [64]	250	rs1801282 (P12A)	PPARG	P12P: reference; P12A: +0.22 %	0.004	
	Rosiglitazone [65]	198	rs1801282 (P12A)	PPARG	P12P: reference; P12A: +0.84 %	0.015	
	Linagliptin [80••]	961	rs7903146 (C→T)	TCF7L2	CC: reference; TT: -0.26 %	0.0182	
	Gliptins [81••]	354	rs7202877 (T→G)	CTRB1/2	TT: reference; TG + GG: $-0.51$ %	0.0015	

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#### Other studies examining PPARG Pro12Ala

Author	Drug	Response	Associated?
Bluher <i>et al.</i>	Pioglitazone	Glucose or HbA1c	No
Kang <i>et al</i> .	Rosiglitazone	Glucose and/or HbA1c	Yes
Florez <i>et al</i> .	Troglitazone	HOMA–IR tertiles	No
Snitker <i>et al.</i>	Troglitazone	Change in Minimal Model S <sub>I</sub>	No

No reason why the type 2 diabetes susceptibility variant should be underlying the mechanism for TZD response Association between troglitazone response and variants in PPARG (Wolford et al., Diabetes 54:3319–3325, 2005)

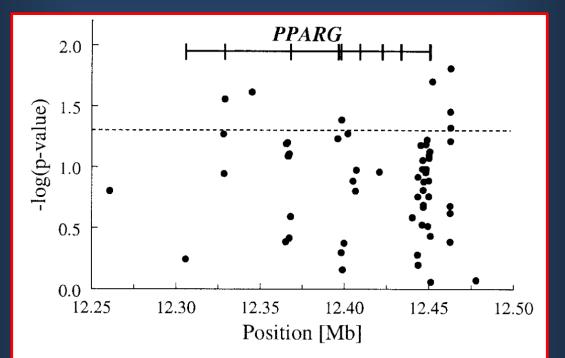
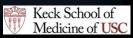


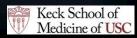
FIG. 1. Single marker association with response to troglitazone. The negative log of the P value for the  $\chi^2$  test of association is plotted according to physical distance. Horizontal dashed line denotes P value of 0.05. Two SNPs in close proximity gave identical P values, so only seven of the eight significant results are visible. The gene structure for *PPARG* is shown at the *top* with the A1 promoter on the *left*.



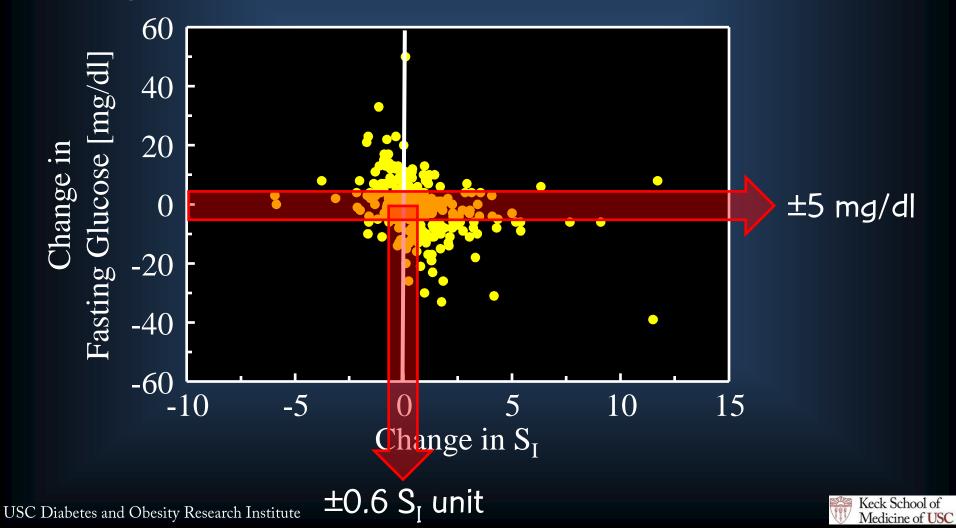
Association between troglitazone response and variants in PPARG (Wolford et al., Diabetes 54:3319–3325, 2005)

	Minor				
SNP	Allele	MAF	OR	C.I.	<i>p</i> -value
rs13073869	A	0.390	2.30	(1.09, 4.87)	0.028
rs880663	С	0.400	2.36	(1.11, 5.04)	0.024
rs4135263	С	0.291	2.19	(1.02, 5.50)	0.041
rs1152003	G	0.410	2.19	(1.13, 4.28)	0.020
rs6806708	Т	0.378	0.46	(0.22, 0.96)	0.035
rs13065455	A	0.391	2.04	(1.00, 4.17)	0.047
rs13088205	G	0.436	2.36	(1.17, 4.76)	0.016
rs13088214	С	0.391	2.04	(1.00, 4.17)	0.047

- An issue with pharmacogenetics studies is the definition of "response"
- Most studies define response as change in fasting glucose or HbA1c
- Makes sense from a clinical care perspective
- But does a change in glucose or HbA1c reflect whether an individual patient "responded" to the drug?



Data from the TRIPOD and PIPOD studies Buchanan *et al.*, Diabetes 51:2796–2803, 2002 Xiang *et al.*, Diabetes 55:517–522, 2006

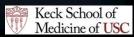


- Many cases where the drug has its intended action, but little to no change in glucose or HbA1c
- Response to medication, but no clinical response
- Suggests alternative mechanisms may be at work
- Need to decide how to leverage such information

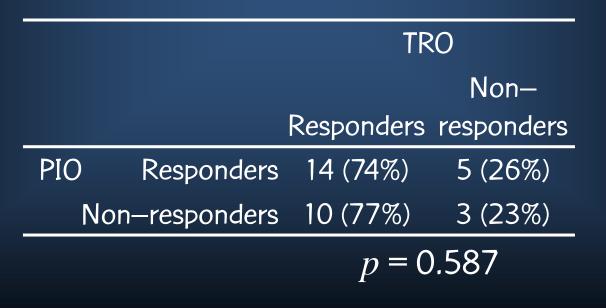
- Members of the same drug class may not react the same to a given genetic variant
- Almost no research in this area
- Example from the TRIPOD and PIPOD studies

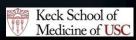
Response to pioglitazone (PIO) Stratified by Previous TRIPOD				
Treatment Group				
		PIO		
		Non-responder	Responder	
TRIPOD Tx Group	Placebo	17 (37%)	29 (63%)	
	Troglitazone	13 (41%)	19 (60%)	
		<i>p</i> = 0.815		

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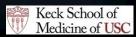
- Participants of PIPOD all came from TRIPOD
- Opportunity to see if response differs between troglitazone and pioglitazone in the same individuals
  - Pitfall: small numbers
- 15 of 32 participants were discordant for response





#### Summary

- Ultimate goal: "Personalized" or "individualized" medicine
- Pharmacogenetics may be just as complex as complex disease
- Ability to identify large subsets of individuals may be possible
- Ability to reach the "individual" level will be more challenging
- Therapeutics will change over time
- Need to consider whether should focus on individual drugs or potential mechanisms



## Donald E. and Delia B. Baxter Family Foundation

# The FUSION Study

# The DIAGRAM (+) Consortium

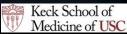


Genetic Investigation of ANthropometric Traits









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#### Acknowledgements





Dr. Mary Helen I Black

Dr. Zhanghua Chen



Dr. Jie Ren



Dr. Yu–Hsiang Shu



Cpt. Alyson Kil, M.D.



Dr. Nan Wang



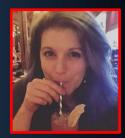
Michael Arias



David Phan



Therlinder Lo



Tara Kerin



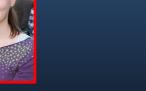
Zhu Chen

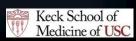


Enrique Trigo



Adrienne McKay





# **Conflict of interest disclosure**

# None

**Committee of Scientific Affairs** 

