

### **GMOD** powering LanzaTech

Asela W. S. Dassanayake Bioinformatics Research Scientist Model Systems Group

2016 GMOD Meeting Indiana University, Bloomington, Indiana, United States June 30 – July 1, 2016 2015 LanzaTech. All rights reserved.



asela.dassanayake@lanzatech.com



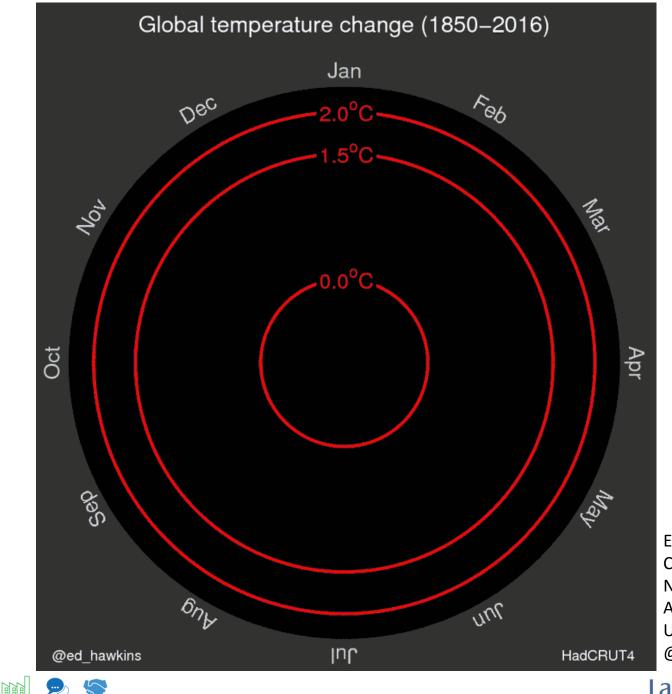


### The outline

- LanzaTech Who we are and what we do
- How GMOD is powering the information flow at LanzaTech
- Proposing a Synthetic Biology platform?







Ed Hawkins, Climate scientist, National Centre for Atmospheric Science, University of Reading. @ed\_hawkins





Must stay in the ground





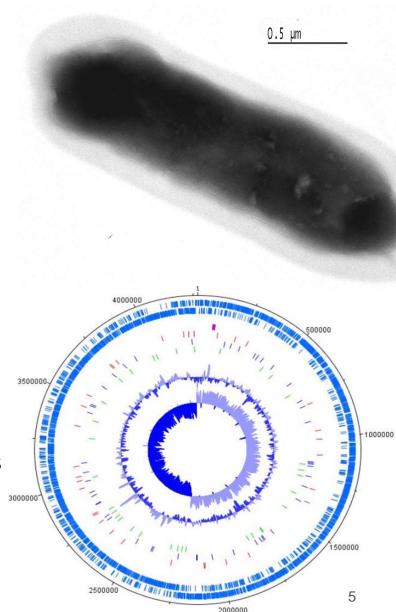


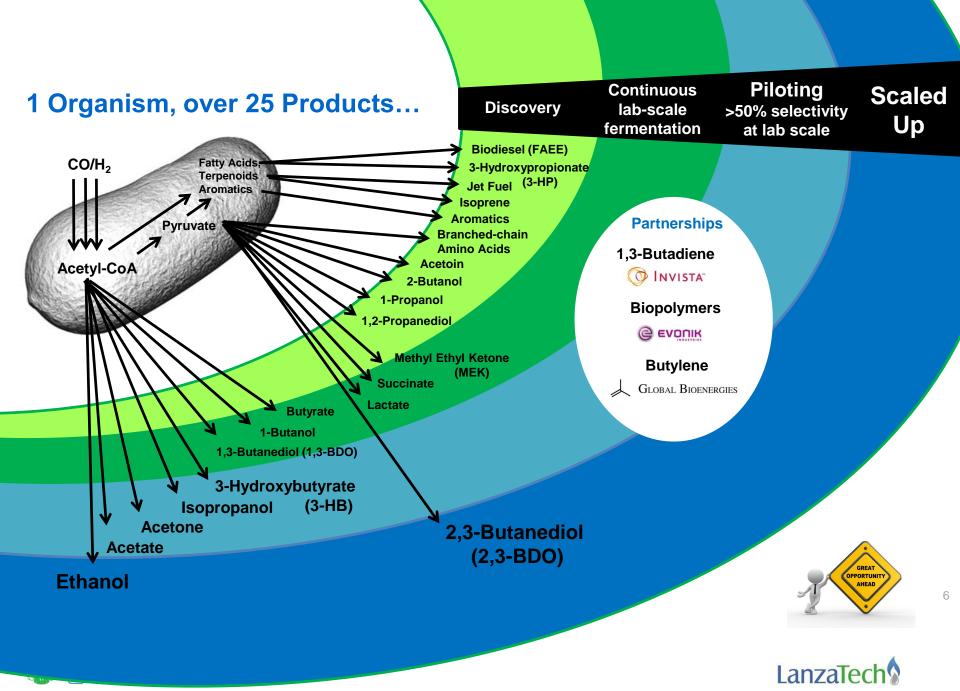
## **Proprietary Acetogenic Biocatalyst**

- Worlds' first autotrophs
- Acetogenic bacterium with ability to utilize <u>sole</u> energy and carbon source
  - CO
  - CO+H<sub>2</sub> or CO+CO<sub>2</sub>+H<sub>2</sub>
  - $CO_2 + H_2$
- LanzaTech has developed a proprietary strain of *Clostridium autoethanogenum*
- Obtained by extensive selection program,

### having improved characteristics

- High gas uptake and ethanol production rates
- Fast growth on defined minimal media
- Non-sporulating and non-motile





### **The LanzaTech Process**



### A sensible path

### We use:



### We do not use:



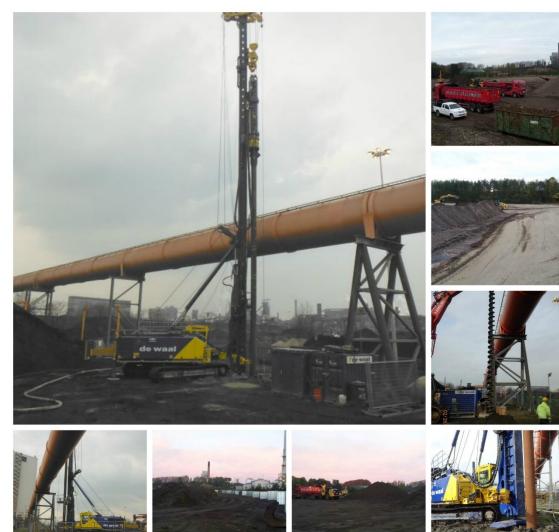




### **3 Commercial projects underway**



### **ArcelorMittal, Gent**



#### Ground Works Started October 2015

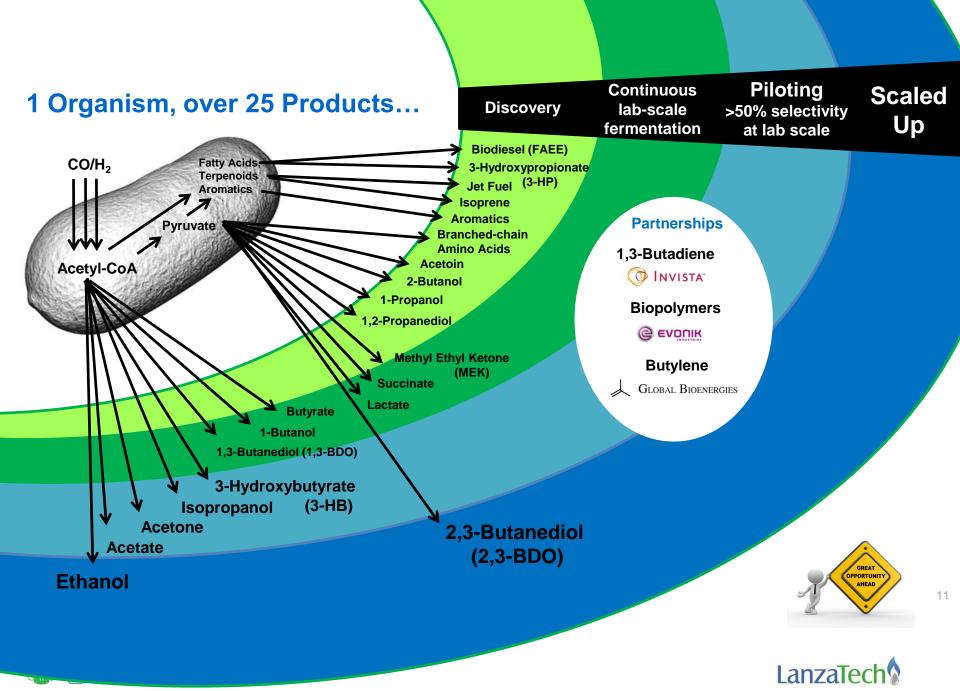
Gas Testing Station Produces Ethanol January 2016



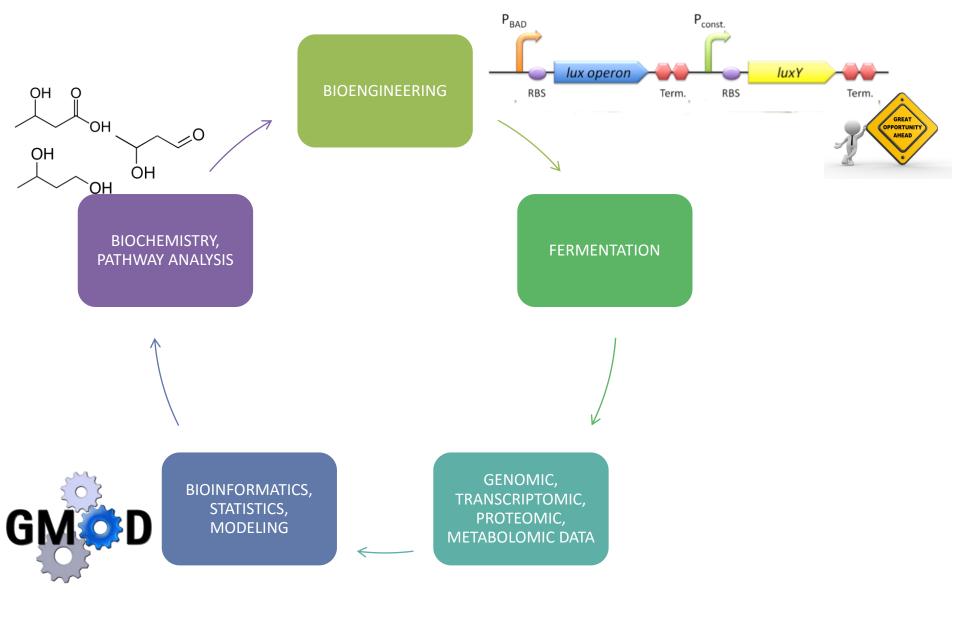
Connection to Steel Mill Gas Lines March 2016







### Information flow at LanzaTech

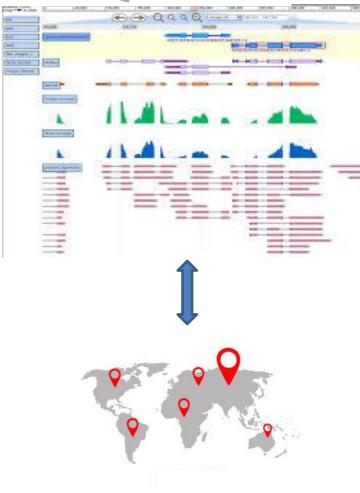






### **GMOD** at LanzaTech





**External Collaborators** 





Chado: Biological database schema







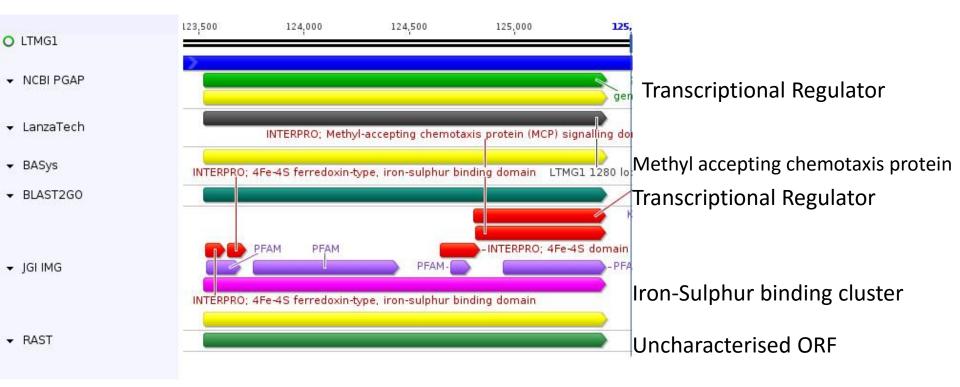


## **Apollo at LanzaTech - Internal**

File Edit View History Tools People Help		ी∎ En ≪ Wed Jun 29 1:17 PM 40
	🖿 Admin_Tricks 🖿 Bioinfor 🖿 Blunt 🖿 Imported 🖿 CompBio 🖿 GMOD 🖿 Literature 🕎 Di	
Clostridium autoethanogenum LZ1561 🝷 File View Tools Help		Full-screen view 🔔 asela.dassanayake@lanzatech.com
0 200,000 400,000 600,000 800,000 1,000,000 1,200,000 1400,000		,200,000 3,400,000 3,600,000 3,800,000 4,000,000 4,200,000
,000 1,325,000 1,330,000	O         O         O         O         O         O         ITMG3 ▼         LTMG3:13198611356320 (36.46 €         Go         Ø           1,335,000         1,340,000         1,340,000         1,345,000	1,350,000 1,355,000
LTMG3 Reference Sequence User-created Annotations	1,340,000 1,340,000 1,340,000	1,30,000
BASys Appotation sysol 264 Hypothetical Protein CLJU_c Uncharacterized hydrolase y4ti	Uncharacterized protein yoaR Spore Coat Protein Lipase 2 Dephospho-CoA kinase	Hypothetical Protein CLJU_c Histidyl-tRNA synthetase Unch
Hypothetical Protein CLJU_c Protein CotJC Hypothetical NADH oxidase	Putative hydrolase NT01CX_1282 Putative Rieske 2Fe-25 iron-sulfur proteinyhfW	Hypothetical Protein CLJU_c Oxygen-independent cc
Hypothetical Protein CLJU_c Putative 2-hydroxyacid dehydrogenase HI_1556 Meti	hyl-accepting chemotaxis protein tlpC UDP-galactopyranose mutase SPBc2 prophage-derived unchai	racterized transglycosylase yomi
pothetical Protein CLJU_c Hypothetical Protein CLJU_c Hypothetical	Putative glycosyltransferase epsH DNA polymerase I	Hypothetical Protein BASYS01292
Hypothetical C	Hypothetical Protein CLJU_c	Hemolysin-3 Aspartyl-tRNA synthetase
Molybdenum cofactor biosynthesis protein A		Hypothetical Protein CLJU_c
RAST Annotation Prized Open Reading Frame     D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)     Uncl	haracterized Open Reading Frame UDP-galactopyranose mutase (EC 5.4.99.9) Soluble lytic murein transglyco:	
	Aracterized Open Reading Frame     UUP-galactopyranose mutase (EC 3.4.99.9)     Soluble lytic murein transgivco     Vancomycin B-type resistance protein VanW     Uncharacterized Open Reading Frame     DNA polymerase I (I	
characterized conserved protein Uncharacterized Open Reading Frame 2		
Uncharacterized Open Reading Frame Uncharacterized Open Reading Frame	Histidinol phosphatase and related hydrolasesof the PHP family	conserved protein FIG00519129: hypothetical protein Hydro
Uncharacterized Open Reading Frame Polypeptide composition of the spore coat protein Cot.JC	Glycosyltransferase (EC 2.4.1) Esterase/lipase	Uncharacterized Open Reading Frame
tein Molybdenum cofactor biosynthesis protein MoaA putative amidohydrolase	related to spore coat protein F Dephospho-CoA kinase (Et	C 2.7.1.24) Aspartyl-tRNA synthetase (EC 6.1.1.12)
Uncharacterized Open Reading Frame	Rieske 2Fe-25 iron-sulfur protein	
membrane protein		
RNAmmer Annotaion		
🔉 Infernal Annotaion		
© CellRecycle Day 9.07 Coverage	10,000	
	annon marchine and the	
S NCBI Annotaion		
Blast2Go Annotaion coat protein f glycerate dehydrogenase 2-enoate reductase	vancomycin resistance protein w spore coat protein f lytic transglycosylase	conserved protein MULTISPECIES: hypothetical protein mbl f
membrane protein spore coat associated protein ja met	hyl-accepting chemotaxis protein udp-galactopyranose mutase esterase dephospho- kinase	MULTISPECIES: hypothetical protein histidyl-trna synthetase
hypothetical protein CLJU_c33360 membrane protein	hydrolase MULTISPECIES: hypothetical protein dna polymerase i	hemolysin d aspartyl-trna synthetase
nc domain protein spore coat peptide assembly protein	glycosyl transferase (2fe-2s)-binding protein	coproporphyrinogen iii 👦
molybdenum cofactor biosynthesis protein a amidohydrolase		
		· · · · ·
🌃 👗 🌐 📷 ج 🤝		LanzaTech <sup>®</sup> 14



### Roshomon





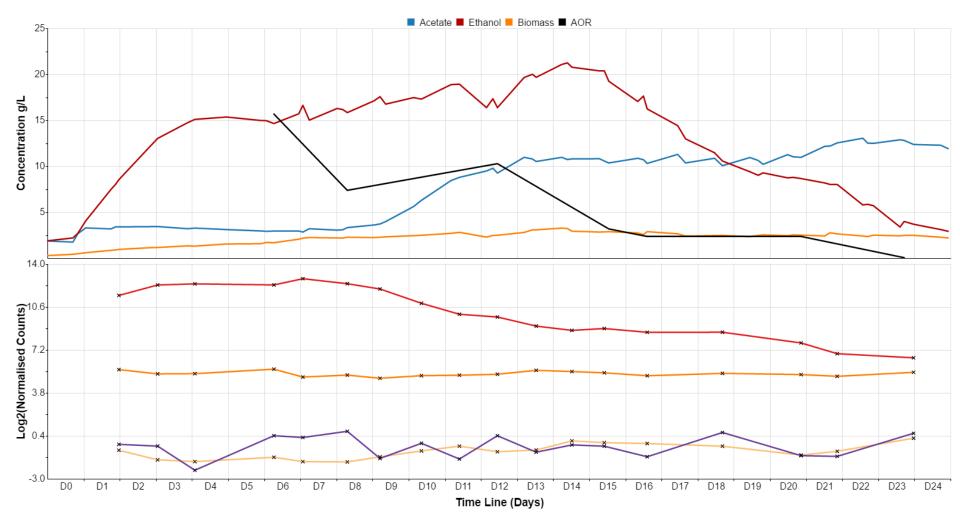


## Tuff-t

i-t				REPo Home Login Bio Control	Help		
				RNASeq Experiment Portal verion 0.01			
				View omics data, beautifully.			
				Provide list of 1-10 Locus IDs to view expression profiles.			
				Experiment Suncor •			
				Gene			
				Gene			
				Gene			
				Gene			
				Submit			
				Generate a list of genes based on Fold Change			
				Experiment Suncor •			
				Select list of genes with Fold Change			
				More than - • All •			
				Less Than - V 1 V			
				Submit			
View co expressed genes for a gene of interest		View co expressed genes for a gene of interest					
				Experiment Suncor •			
				Gene of interest			
				Number of co 10 🔻			
				expressed genes Submit			
				Compare a gene profile between experiments			
				Experiment1 Suncor •			
_		п		Experiment2 Suncor •			
				Gene of			



## Tuff-t



Gene Key

aldehyde:ferredoxin oxidoreductase (LTMG3\_1070)

nitrogenase (LTMG3\_4520)

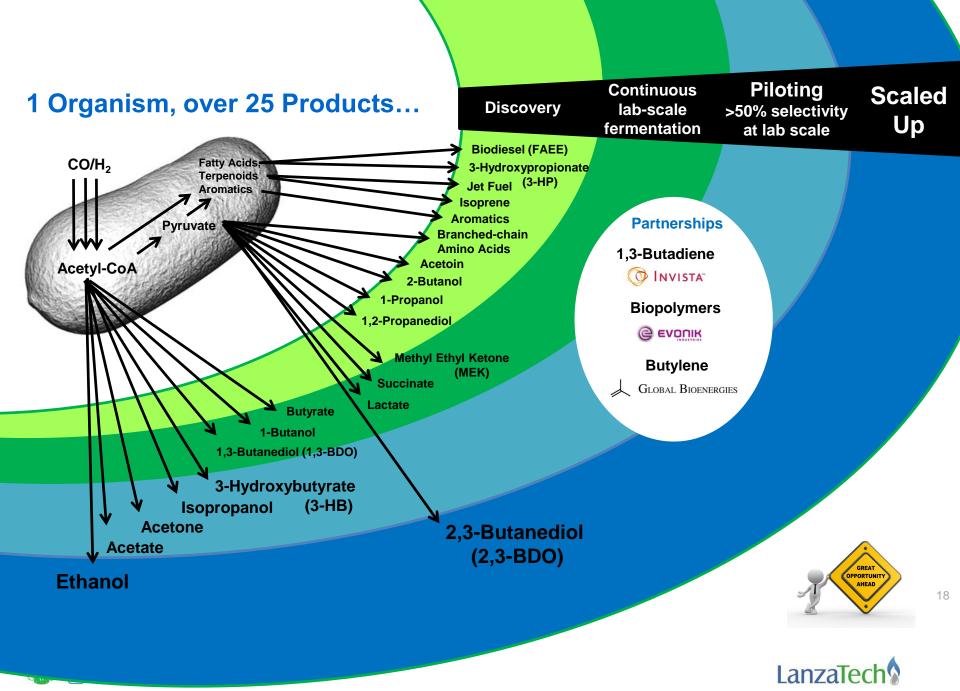
MerR family transcriptional regulator (LTMG3\_7540)

histidine kinase (LTMG3\_9540)

Back to Form







## **Proposing an Integrated Synthetic Biology platform**

- User data organization and management
   DLAST interface
- BLAST Interface
- Database Searching





• Literature searches and bibliography [] Canto

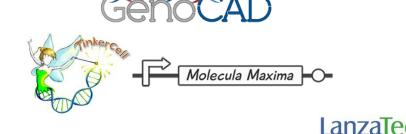
• Genome browser



Data Visualization



• Synthetic Biology CAD with SBML/SBOL





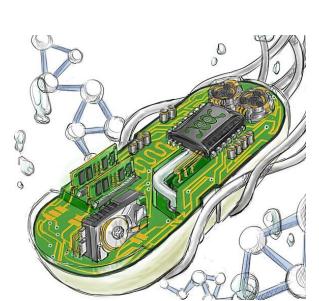
# Integrated Synthetic Biology platform

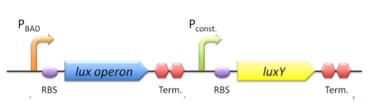
BLAST	Public Data Base search	Genome Browser	Literature and Bibliography	Data Visualisation	SynBio CAD	Sequence Analysis	
▼ Tools and Cont	rols				🔻 Us	er Data	
<ul> <li>blastn</li> <li>blastp</li> <li>blastx</li> <li>tblastn</li> </ul>	blastp   blastx   blastn   Primer-BALST   SmartBLAST   Global Align   CD-search   gBLAST   MA     Exclude   MA     Image: Choose file     From   To   To     From   To     From   To     Or, upload file   Job Title   Enter a descriptive title for your BLAST search @     Choose Search Set   Database   Human genomic + transcript   MA     From   To     Or, upload file   Job Title   Enter a descriptive title for your BLAST search @     Choose Search Set   Database   Human genomic + transcript   Ma     Status     Human genomic + transcript   Ma     Status     Human genomic + transcript   Ma     Choose Search Set   Database   Human genomic + transcript   Ma     Status     Ma     Status     Status     Status     Status     Status     Status     Status     Status     Status     Statu				STN programs search Pro BR Eth DC	▼ User Data       Project     ▼       BRP_crt     Ethanol_test       DGM_tye        MRT_uyp	
	BLAST + Algorithm parar	Show results in a new window	e collection (nr/nt) using Megabi	ast (Optimize for highly similar	sequences)		



### **More Users? Funding?**

→ promoter	-> primer binding site
◯ Cds	restriction site
ribosome entry site	] blunt restriction site
terminator	└── 5' sticky restriction site
operator	3' sticky restriction site
insulator	- 5' overhang
ribonuclease site	— 3' overhang
O rna stability element	assembly scar
★ protease site	× signature
<b>Q</b> protein stability element	user defined
O origin of replication	





GREAT OPPORTUNITY AHEAD







