Wheat Proteogenomics Research

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Wheat Proteogenomics Research

- Background
- Analysis strategy
- Results
- Value of wheat proteome atlas research

Background

- The process of annotating all the genes is a challenging and ongoing process, even for model plants, such as rice, maize.
- The version 1.1 wheat genome annotation (including HC and LC genes) needs further confirmation, refinement and new discovery
- The proteogenomics method can provide a new refinement dimension different from traditional genome annotation
- Wheat A, B, D-homology proteins expression
- Wheat tissue and period-specific proteins difference comparison

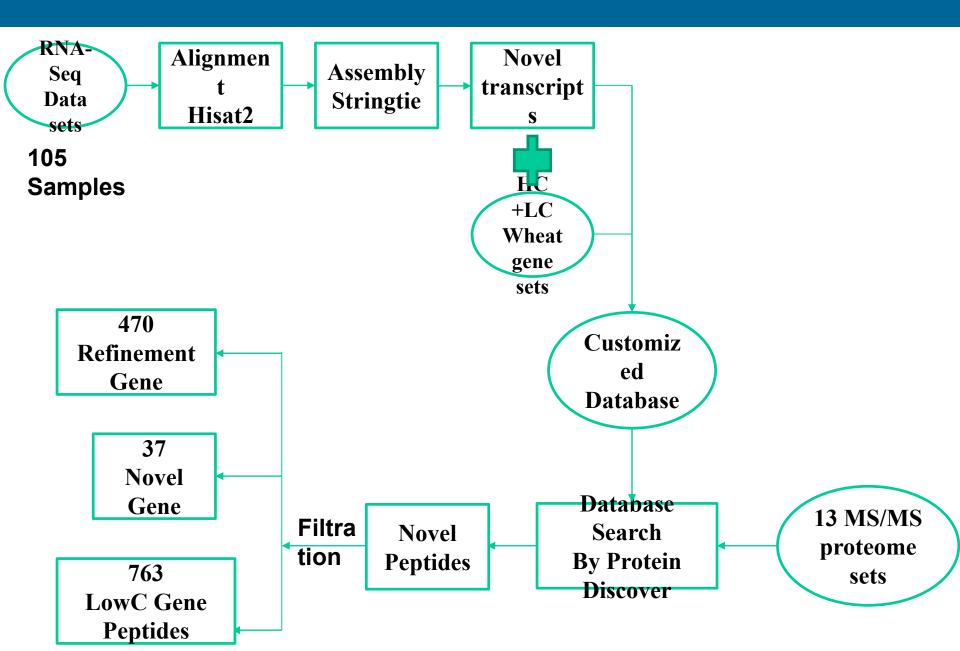
Description of wheat proteome data (public and ourselves)

	vegetative growth							reproductive growth											
	0day	10days	14 days			17days	ys 24 days ea		ear period	anthesis	10dpa	15dpa	20dpa		25dpa	30d			
grain												ERR392072 ERR392061 ERR392057 ERR392055		ERR392083	ERR392073 ERR392070 ERR392068			ERR392079 ERR392071 ERR392069 ERR392067 ERR392066 ERR392065 ERR392062	ERR392060
leaf				ERR2174402 ERR2174403 ERR2174404 ERR2174405 ERR2174406 ERR2174407 ERR2174408	ERR2174410 ERR2174411	SRR6799259 SRR6799258 SRR6799257 SRR6799256	ERR2403087 ERR2403088 ERR2403089 ERR2403090 ERR2403091			SRR3068387 SRR6802615 SRR6802608	SRR3068439		SRR3068477				SRR3068481	SRR3068482	
root	DRR003150 DRR003149 DRR003148		ERR1598029			SRR6799265 SRR6799264 SRR6799263 SRR6799262 SRR6799261	ERR2403094	SRR946457 SRR946458 SRR946459 SRR946460 SRR947016	SRR947017										
spike										SRR6802614 SRR6802611 SRR6802610 SRR6802609 ERR1598032	SRR6799268 SRR6799267								
shoots	DRR003154 DRR003155 DRR003156	DRR003157						SRR947006 SRR947014	SRR946453 SRR946454 SRR946455 SRR946456										

Wheat Proteome Atlas Research

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Analysis strategy



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- Summary of wheat genome annotation refinement
- Novel gene (new gene loci) detection
- Known gene (high confidence gene) refinement
- Low confidence gene confirmation
- Wheat proteome detection in leaf and root

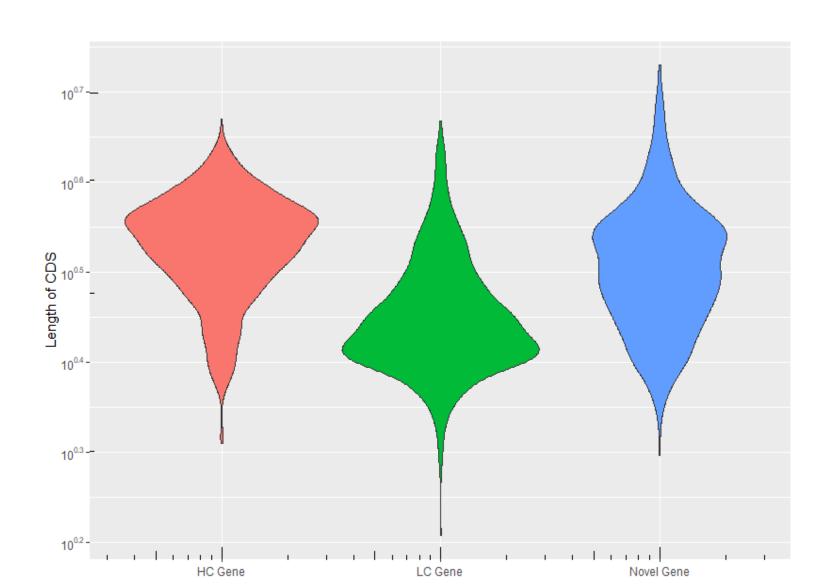
Summary of wheat genome annotation refinement

Refinement type	Gene number
Novel gene (new gene loci) detection	37
Known gene (high confidence gene) refinement	470
Low confidence gene confirmation	763

The pI and MW distribution between new and known (HC) genes are similar

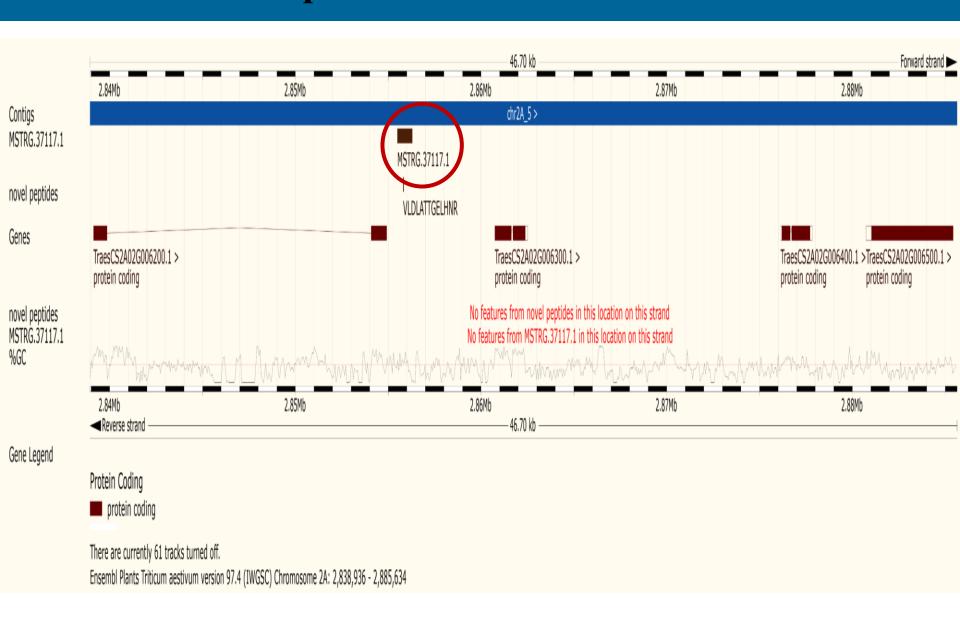


The CDS length distribution among new, known (HC) and LC genes are different

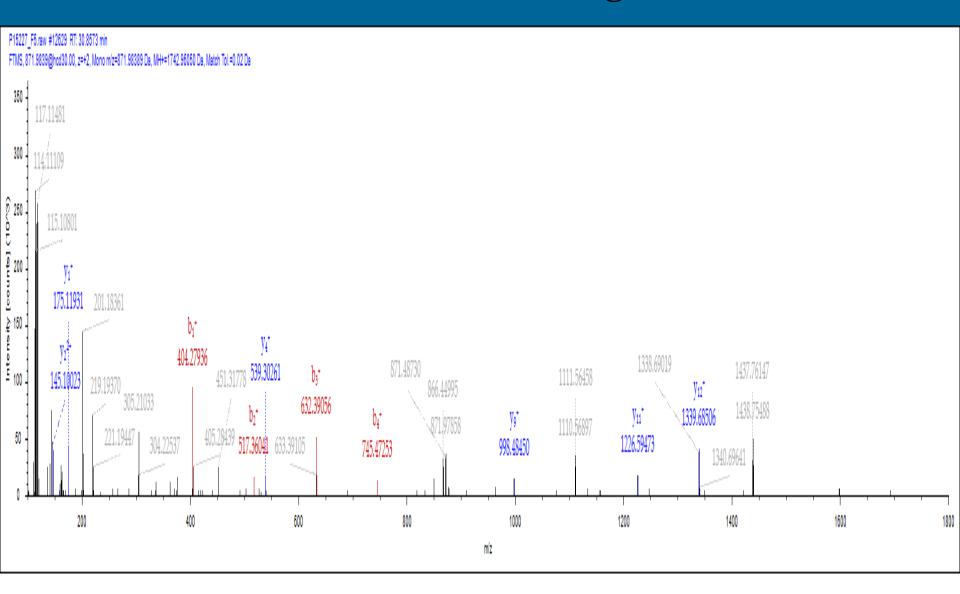


- Summary of wheat genome annotation refinement
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Example of Novel Gene Loci detection

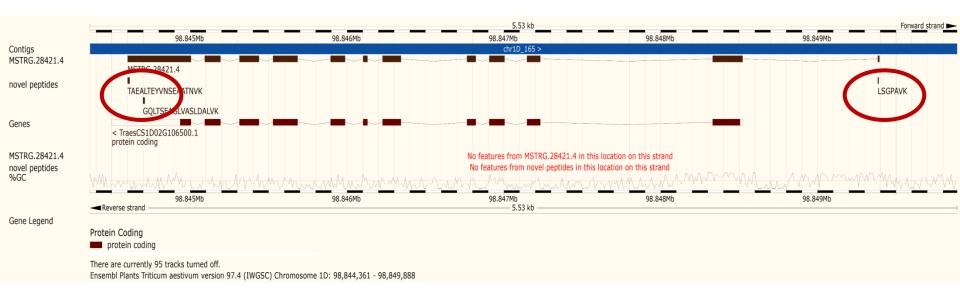


MS/MS data of novel gene loci

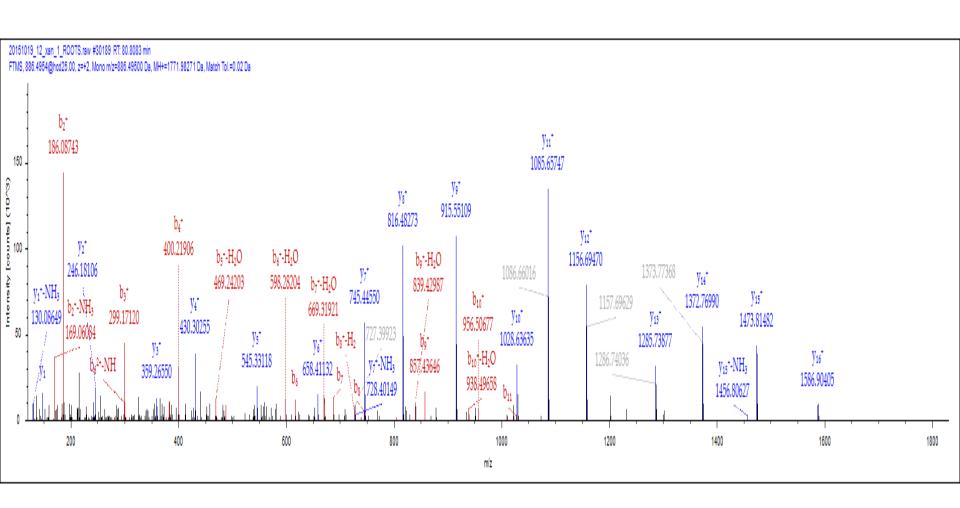


- Summary of wheat genome annotation refinement
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Example of known gene refinement

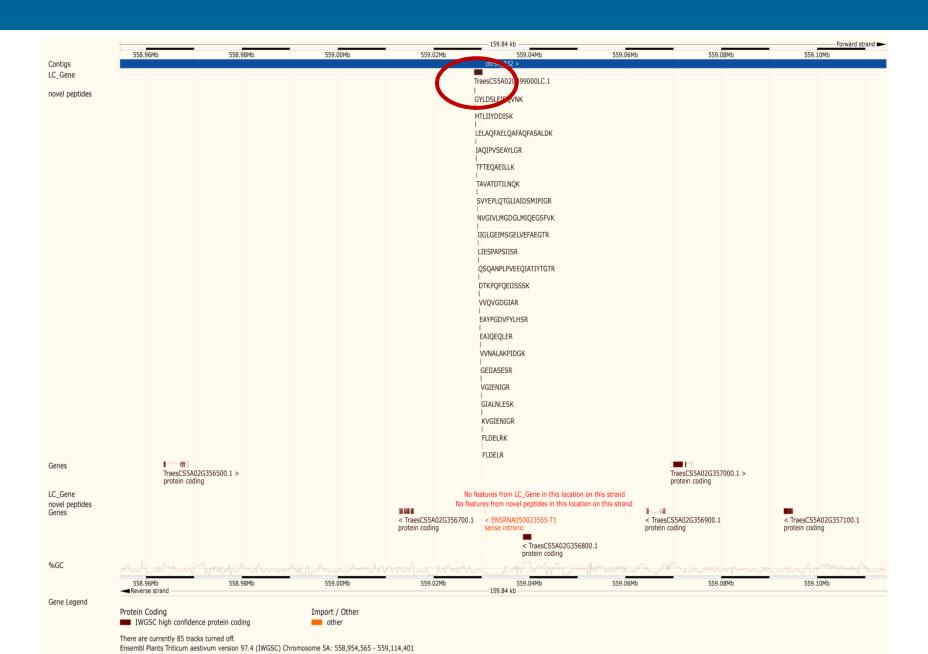


MS/MS data of known gene refinement

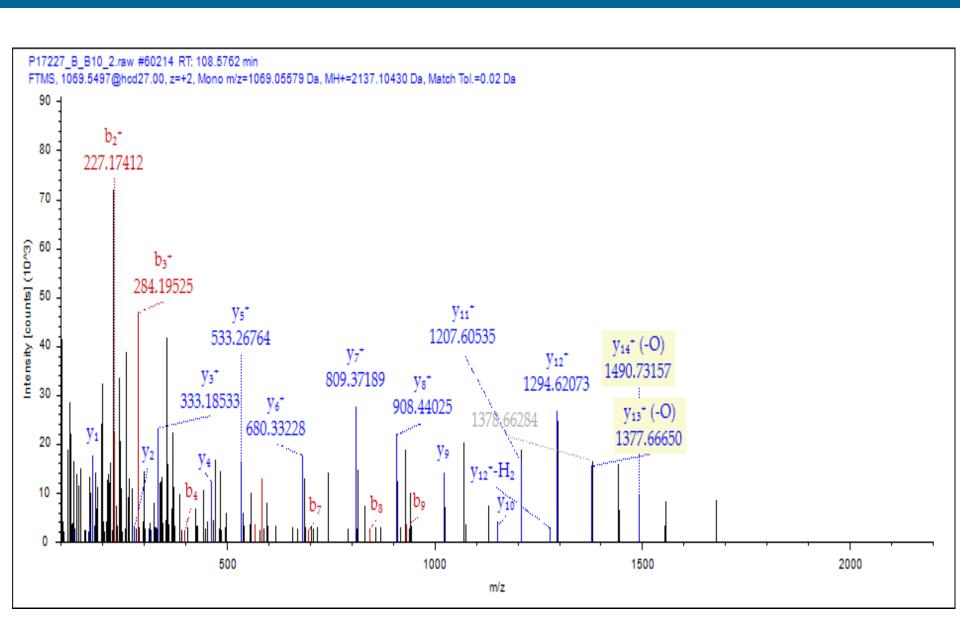


- Summary of wheat genome annotation refinement
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Exampel of wheat LC gene confirmation



MS/MS data of wheat LC gene example



- Summary of wheat genome annotation refinement
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Wheat proteome identification in leaf and root

	Leaf	root
Identified protein group (1% FDR)	6,579	7,466
Identified peptides	28,829	32,959

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Value of wheat proteome atlas research

- Wheat genome annotation refinement from proteome dimension: including novel gene detection, known gene refinement, low confidence gene confirmation
- Wheat alterative splicing gene confirmation
- A comprehensive wheat proteome atlas, especially for A, B, D-homology proteins expression
- Wheat tissue and period-specific proteins difference comparison
- Wheat proteins function analysis based on proteome expression clustering analysis

- We propose to carry out proteogenomics analysis with v.2 assembly and annotation for further confirmation and improvement.
- In addition, we propose to carry out wheat (Chinese Spring) proteome atlas research. We would like to see this as a collaborative effort of the consortium.

