May 22nd, 3:00 PM - 4:30 PM

Empower research through comparative genomics & next-gen sequencing

Li-Jun Ma
University of Massachusetts - Amherst

Follow this and additional works at: https://escholarship.umassmed.edu/cts_retreat

Part of the Genetics and Genomics Commons, and the Pathogenic Microbiology Commons

Creative Commons Attribution-Noncommercial-Share Alike 3.0 License

This work is licensed under a Creative Commons Attribution-Noncommercial-Share Alike 3.0 License.

Ma, Li-Jun, 'Empower research through comparative genomics & next-gen sequencing' (2012). UMass Center for Clinical and Translational Science Research Retreat. 5.
https://escholarship.umassmed.edu/cts_retreat/2012/presentations/5

This material is brought to you by eScholarship@UMMS. It has been accepted for inclusion in UMass Center for Clinical and Translational Science Research Retreat by an authorized administrator of eScholarship@UMMS. For more information, please contact Lisa.Palmer@umassmed.edu.
Empower research through comparative genomics & next-gen sequencing

Li-Jun Ma

UMass Center for Clinical and Translational Science
3rd Annual Research Retreat
May 22 2012
Hoagland-Pincus Conference Center, Shrewsbury MA
Disclosure

for Presentations at ACCME
- Accredited Conferences
DISCLOSURE

• I have no actual or potential conflict of interest in relation to this program or presentation.
Fusarium keratitis outbreak associated with contact lenses
Fusarium oxysporum – a fungus

- Macroconidia
- Microconidia
- Chlamydospore

Fourie G. et al. 2011. Infection, Genetics and Evolution
An emerging human pathogen

- Localized skin or corneal infections
- Cause disseminated infections in immunocompromised patients
- Difficult to control (resistant to antifungals), often lethal outcome
Understand pathogenicity using genomics???
Wilt diseases caused by *F. oxysporum*
formae specialis – host specificity

- Each *forma specialis* consists of strains with ability to cause wilt on a unique host or a set of plant host species.

- More than 120 *formae speciales*. 
Comparative genomics

- F. verticillioides
  - F. oxysporum
  - F. graminearum
    - F. solani
      - Verticillium dahliae
        - Magnaporthe grisea
          - Neurospora crassa
            - Aspergillus nidulans

0.1 substitution per site
Genomic Structural Difference

<table>
<thead>
<tr>
<th>Species</th>
<th>Genome Size (Mb)</th>
<th>Number of Chromosomes</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>F. verticillioides</em></td>
<td>42</td>
<td>11</td>
</tr>
<tr>
<td><em>F. oxysporum</em> f. sp. lycopersici</td>
<td>36</td>
<td>4</td>
</tr>
<tr>
<td><em>F. graminearum</em></td>
<td>42</td>
<td>11</td>
</tr>
<tr>
<td><em>Nectria haematococca</em> (F. solani)</td>
<td>52</td>
<td>17</td>
</tr>
</tbody>
</table>
Pairwise comparison revealed highly conservation genome structure
Pairwise comparison defines lineage-specific chromosomes in *F. oxysporum* f. sp. *lycopersici*
Linage specific chromosomes in *F. oxysporum* f. sp. *lycopersici* (Fol)

Uniquely present in Fol genome

Enriched for TE and repeats

Lack house keeping genes

Encode virulence factors

Horizontal transmission introduce disease

Ma et al 2010 Nature
Optical maps reveal unique sets of LS chromosomes in plant and human isolates.
Horizontal transfer of lineage-specific chromosomes determines pathogenicity
Tip of the iceberg

• Origin(s) of the LS chromosomes?

• Mechanisms of the transfer?

Many asexual fungal pathogens have variable karyotypes (Kistler 1992)
Acknowledgement

H. Corby Kistler
U. Minnesota

Martijn Rep
U. Amsterdam

Manfred Grabherr
U. Uppsala

Andy Berg
Umass Amherst