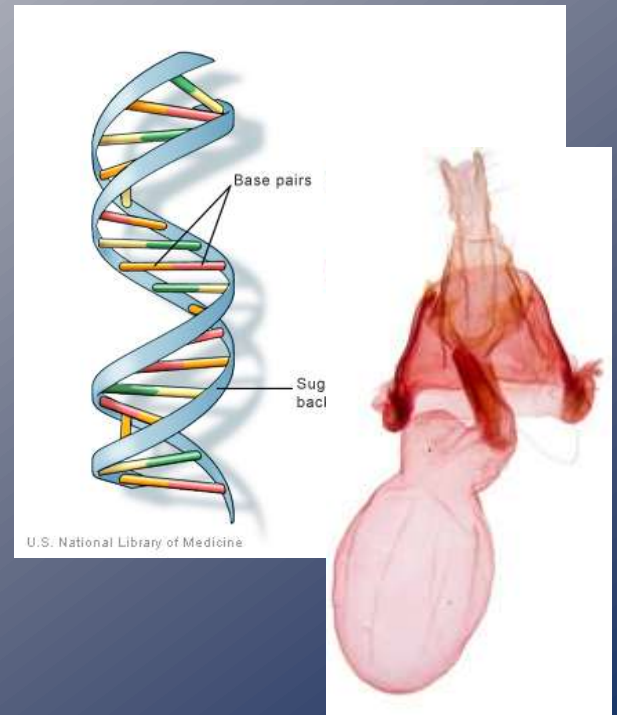


# Lepidoptera taxonomy: morphology and molecules

SWRS Lepidoptera Course, Aug. 2011  
Chris Schmidt  
Canadian National Collection of Insects  
Ottawa, CAN



# Overview

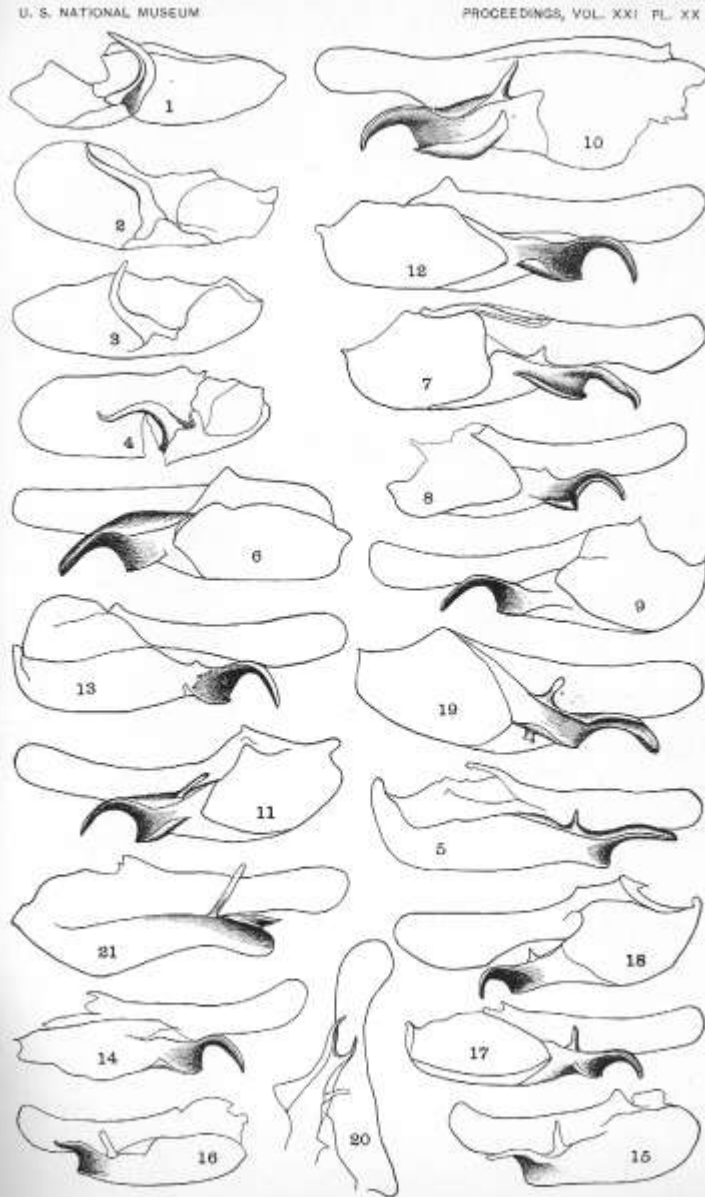
- morphology
- morphometrics
- DNA
- immature stages

# Genitalic morphology

**Genitalic morphology:** very important character set in Lepidoptera taxonomy.

- genitalia structurally complex (so lots of characters)
- little within-species variation
- high between-species variation

# History of genitalic morphology

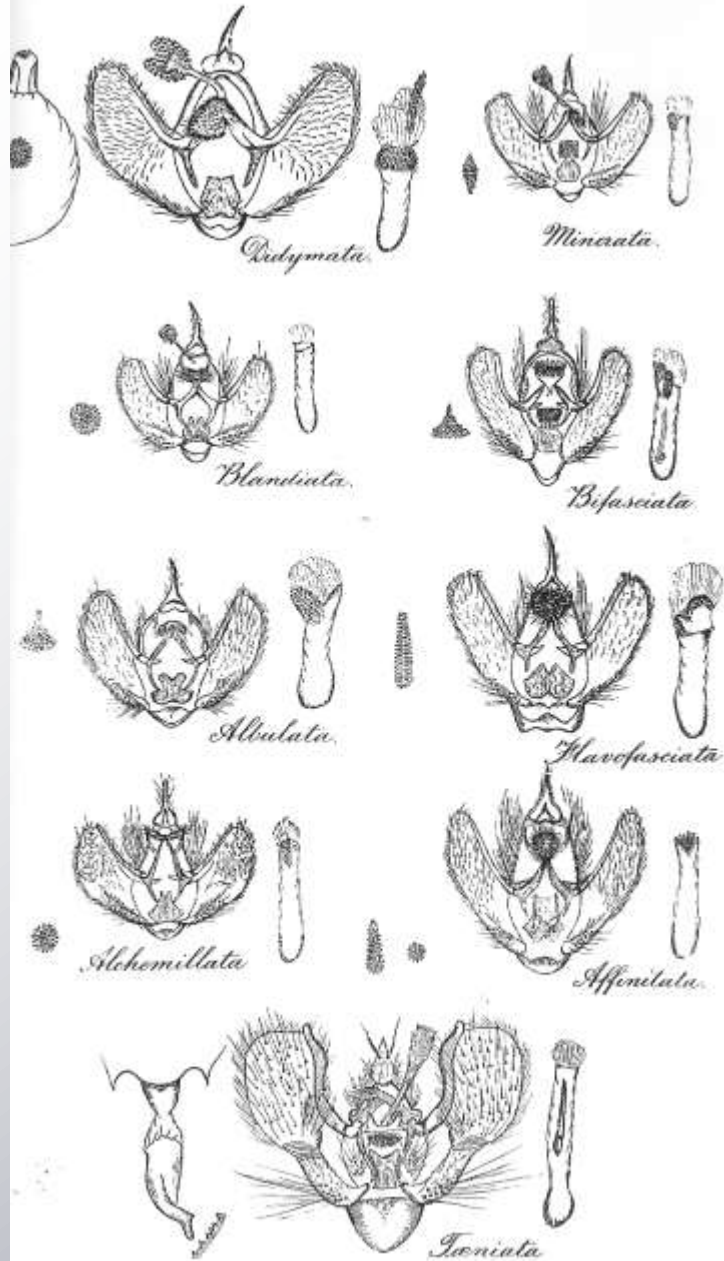


GENITAL STRUCTURES IN *ACRONYCTA*.  
FOR EXPLANATION OF PLATE SEE PAGES 192, 193.

late 1800's: **JB Smith** - snapped off the valves of noctuids

eg. Smith & Dyar 1899: *Acronycta* revision

early 1900s: Hampson - "Catalogue of the Lepidoptera Phalaenae" remains one of the most important works in "noctuidology" – but did not use genitalia (retired about 1912)



Pierce 1914

~1910: **Pierce** – “Genitalia of the British Lepidoptera”

- also included female genitalia

1900-1920s: **Barnes & McDunnough** (“Contributions...”)

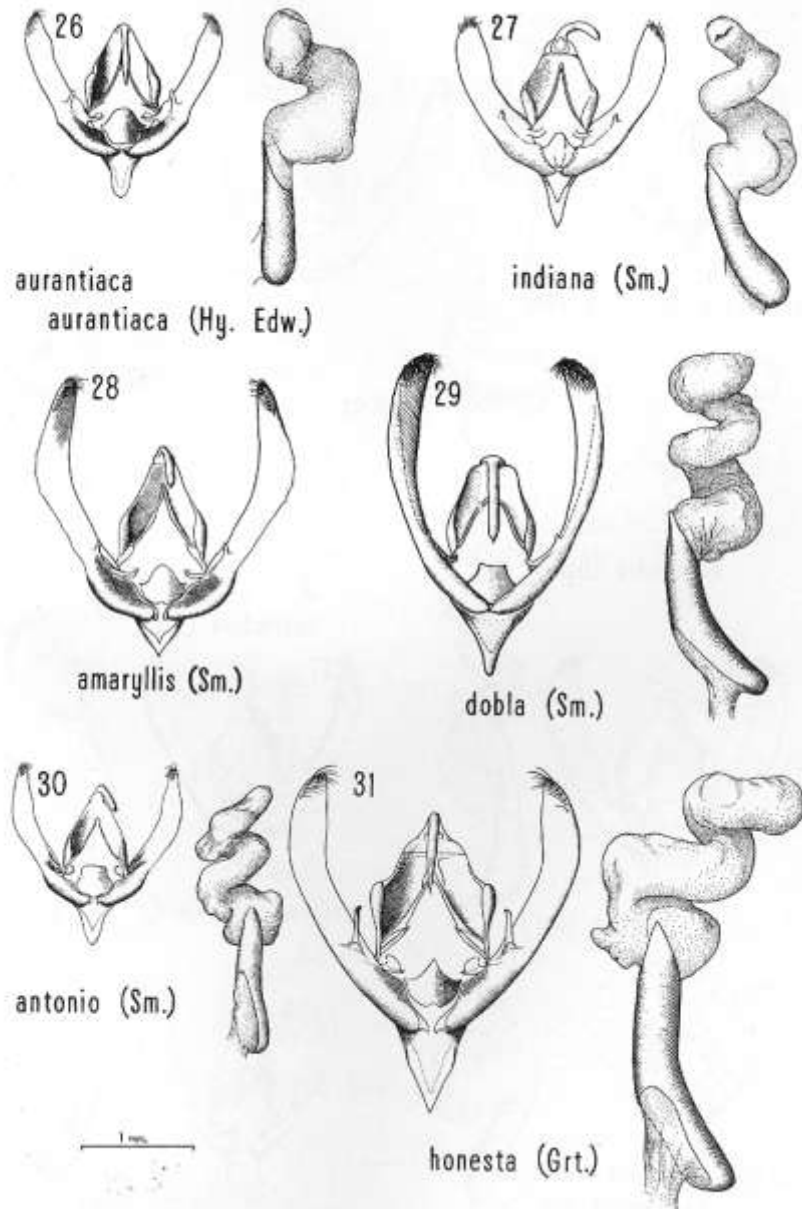
- looked at and used genitalia, although often not illus. (later volumes); McD started at CNC in 1921, extensive dissections thereafter

## Vesica inflation – major innovation in Lep. morphology

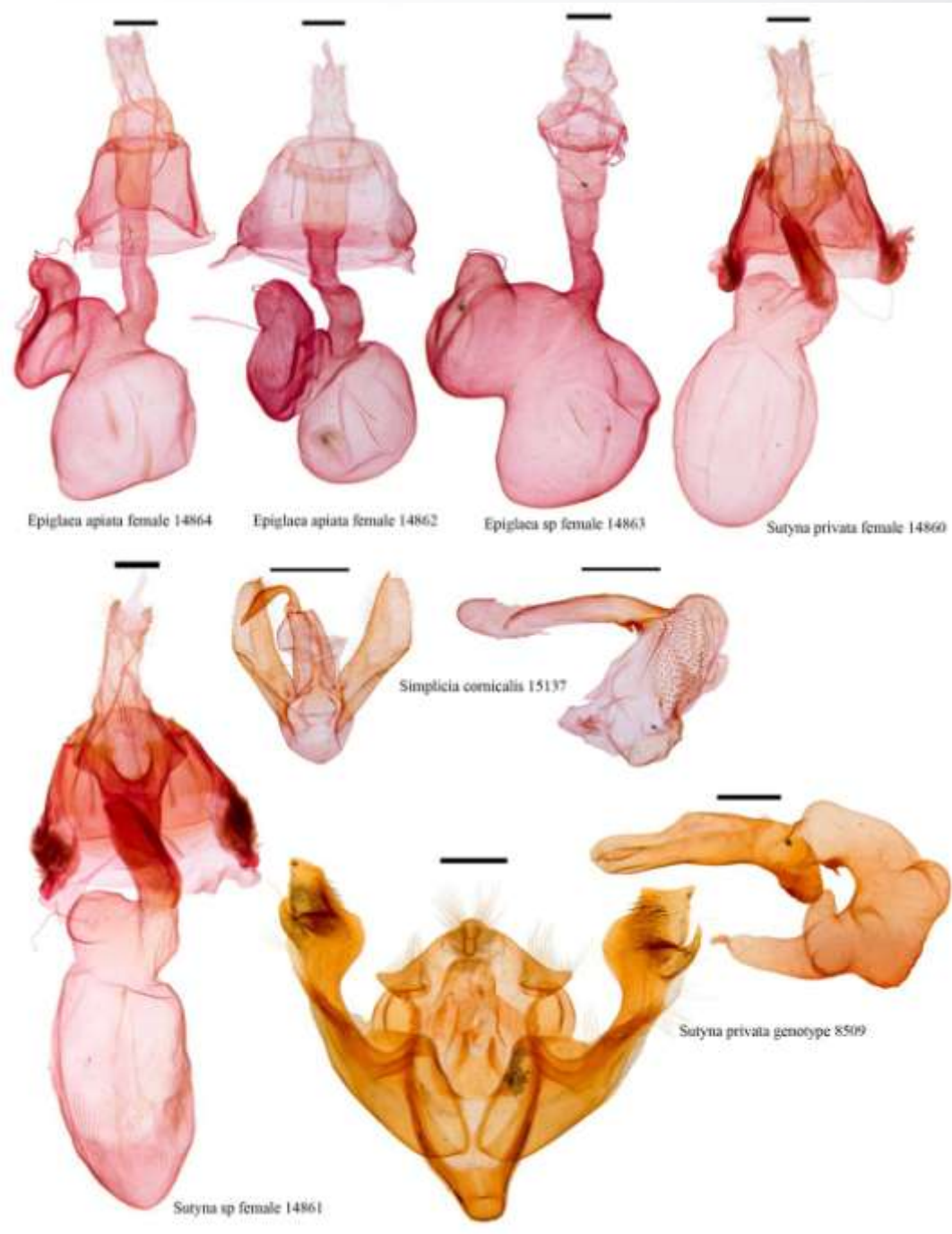
1950: **DF Hardwick** -  
techniques paper the first to  
describe genitalic dissection  
and inflating vesicae:

“Preparation of slide  
mounts of **Lepidopterous  
genitalia**” (Canadian  
Entomologist 82:231-235)

1958: first illustrations of  
inflated vesicae (*Schinia*)



Figs. 26-31. *Schinia* spp. Male genitalia.



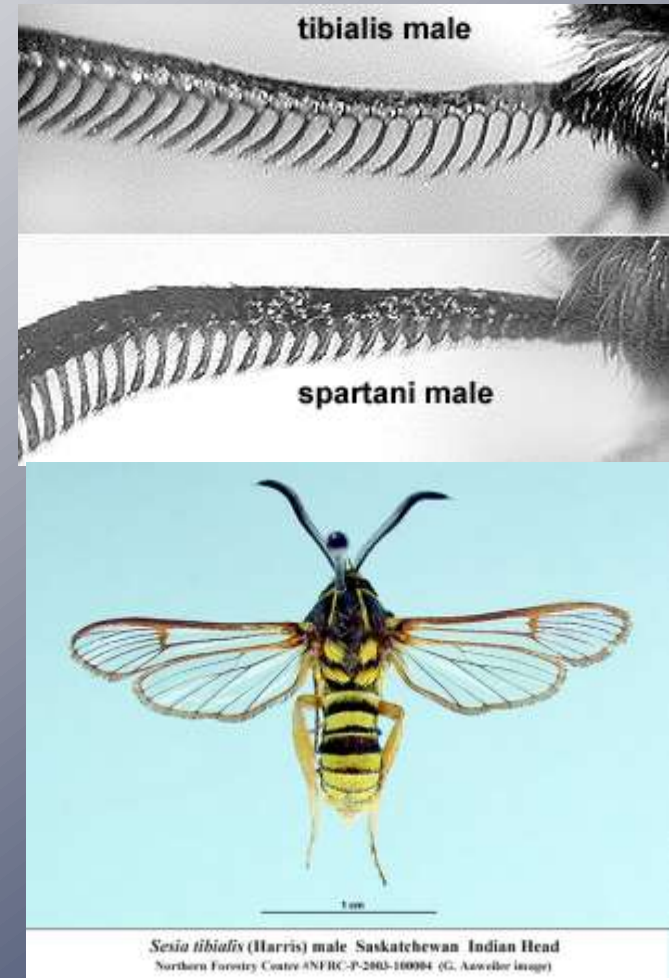
Study of genitalic morphology now essential standard for species-level taxonomy and inferring phylogentic relationships

# Morphology

Genitalia usually most important structural character, but others:

- Antennal morphology
- Immature stages
- Secondary sex structures

Biological (eg. flight time, behaviour, host plant use, etc.)





# Morphometrics

Morphology cannot always discriminate sibling species (i.e. overlap of characters between species, highly simplified genitalia, etc):

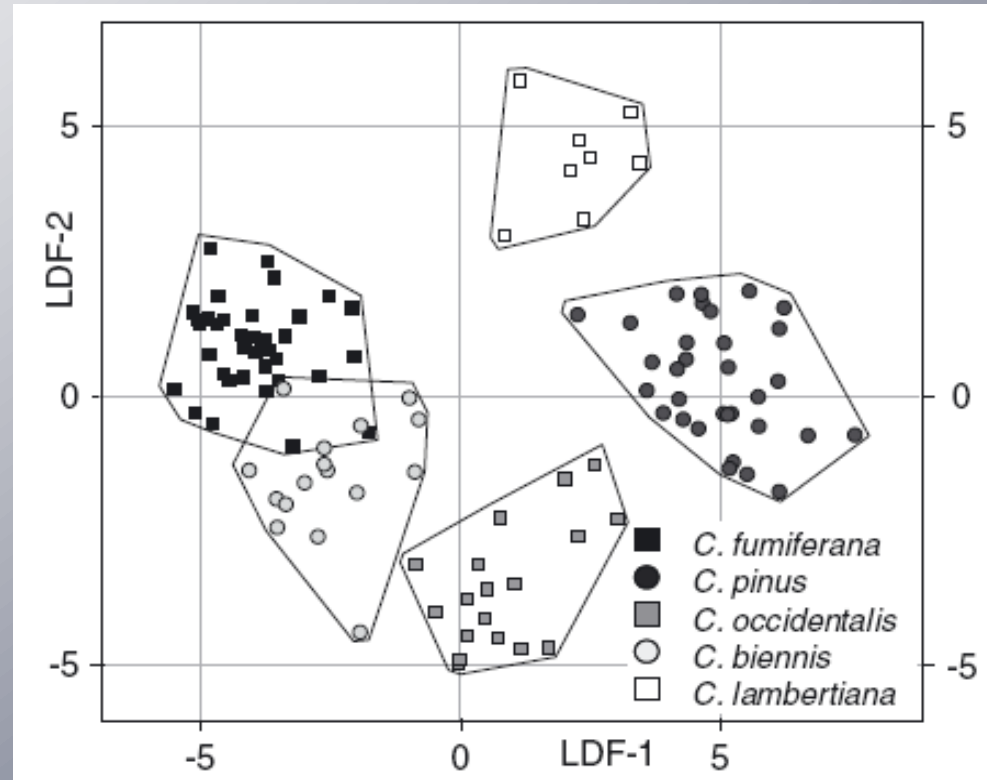
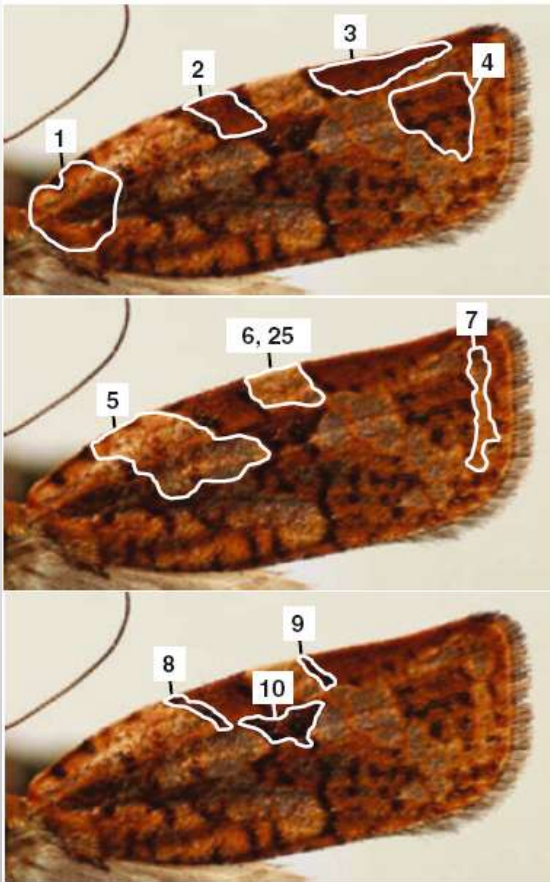
How to deal with species complexes?

- Quantify multiple character sets and do statistical comparison – **morphometrics**

# Morphometrics

eg. spruce budworm complex: digital analysis of colour components of wing patterns

Lumley & Sperling 2010 Syst. Ent.



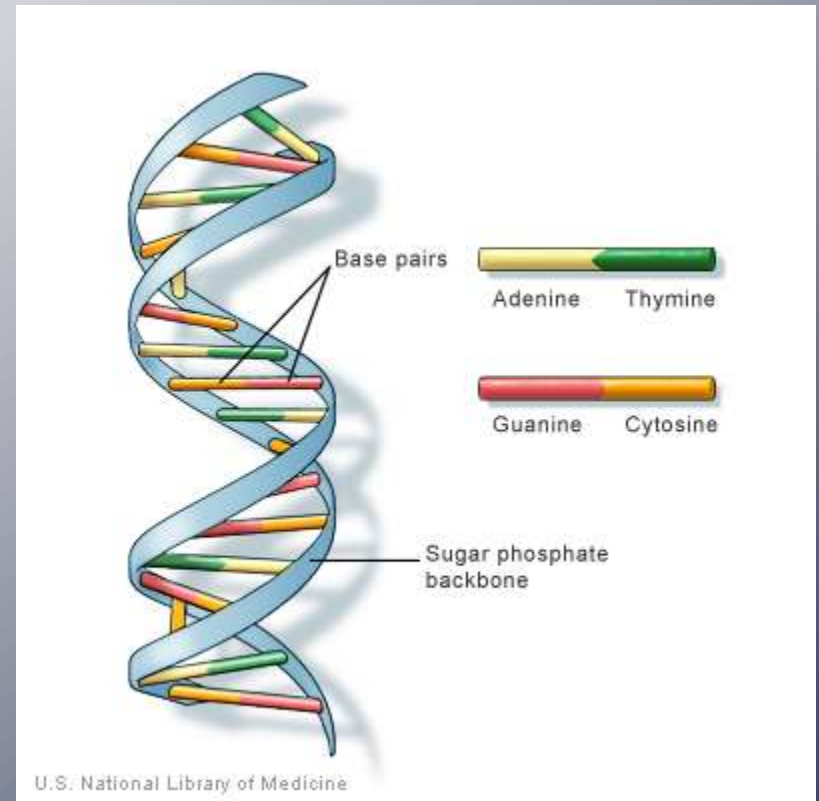
- in this case, greater discriminant ability than DNA barcode

# What else is in the taxonomist's tool kit?

- morphology (adult & immatures)
- biology
- morphometrics
- **molecular analysis: DNA sequence variation**

# Why DNA?

- character set independent of other character sets – more types of data give a better picture of evolutionary history
- DNA reflects molecular evolution (genes) of organism, and if gene tree approximates species tree, very powerful tool
- DNA ‘barcode’: ~650 base-pairs from the *cytochrome oxidase i* gene of mitochondrial DNA – so far the ‘ultimate’ identifier of species



DNA sequence data summarized and visualized using branching diagrams (trees), where **horizontal** lines reflect sum of differences in base-pairs between any two taxa:



Differences between:

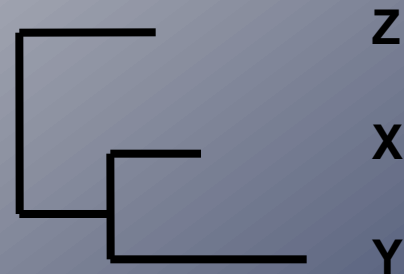
X vs Y: 1



X vs Z: 3



Y vs Z: 4

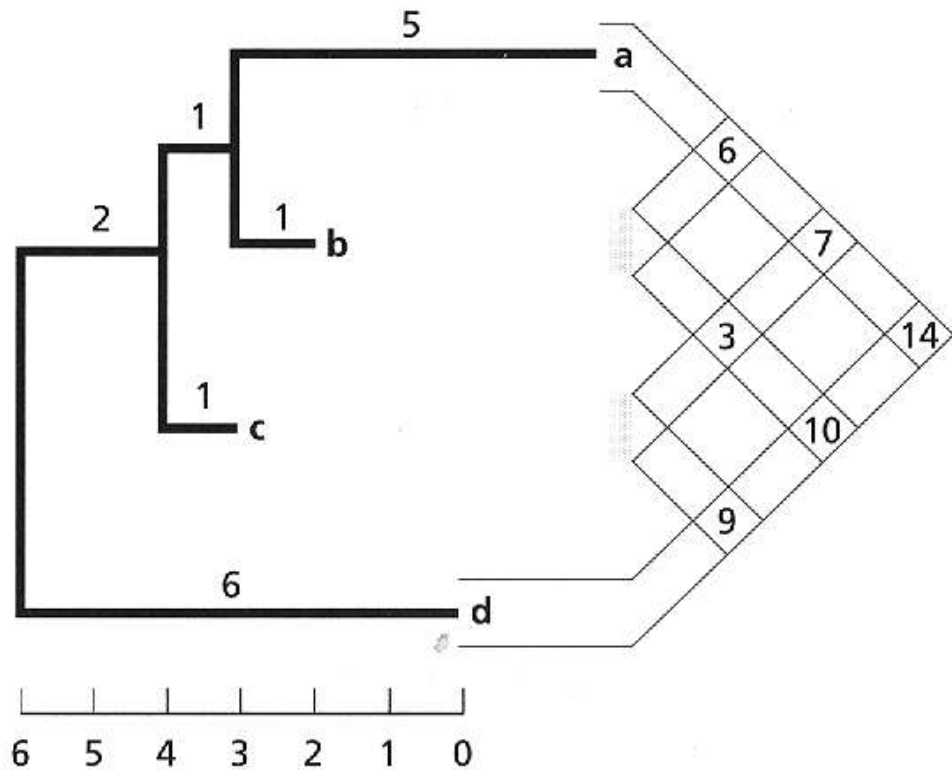


\* vertical lines do **not** reflect distance, only horizontal

Distance matrix

a				
b	6			
c	7	3		
d	14	10	9	
	a	b	c	d

Tree

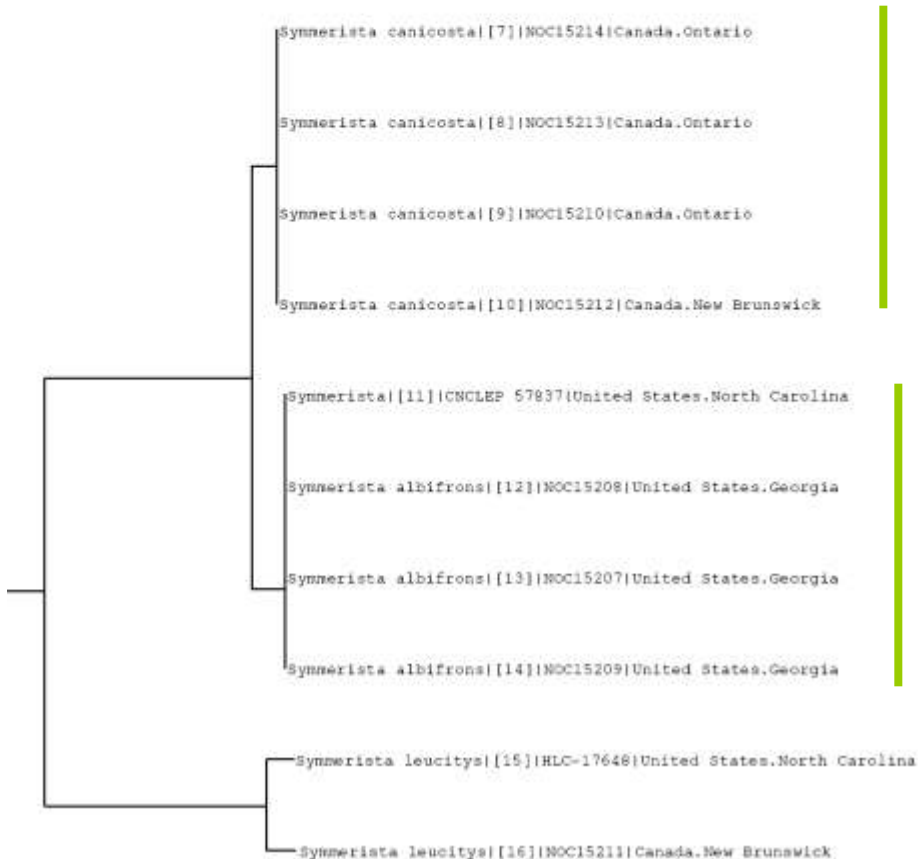


horizontal lines are sum of differences between taxon pairs  
(vertical line length is non-metric!)

# *Symmerista* barcodes (Notodontidae)



—  
scale bar = 1% difference



*S. canicosta*

-straight vertical line  
shared among  
terminal nodes  
indicates terminals  
are exactly the same  
(same DNA seq. =  
same haplotype)

*S. albifrons*

*S. leucitys*

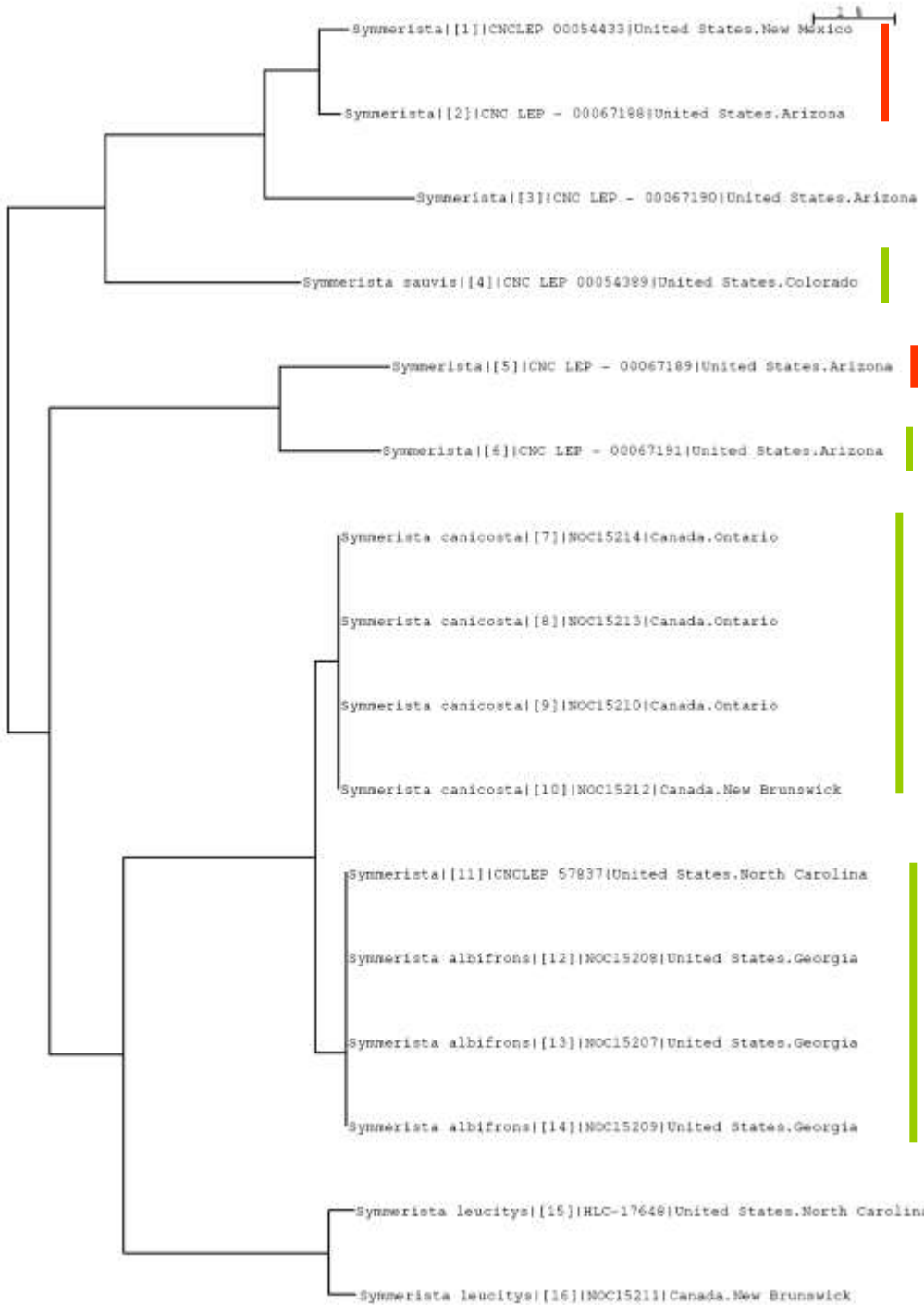
# Interpreting distance phylograms (Neighbour-Joining trees)

## How much mtDNA divergence (difference) is significant?

- initial 'rule' that greater than 2% indicates separate species; should be considered an average (many exceptions!)
- separate species should have non-overlapping haplotype clusters (**haplotype** = any unique nucleotide sequence)
- broad geographic coverage important to assess DNA variation



# Barcodes in taxonomy: *e.g. Symmerista*



*S. suavis*

*S. zacualpana*

*S. canicosta*

*S. albifrons*

*S. leucitys*



# Barcodes

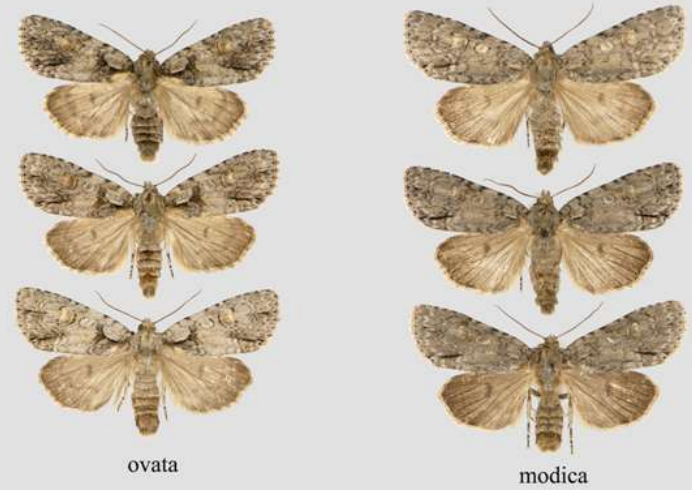
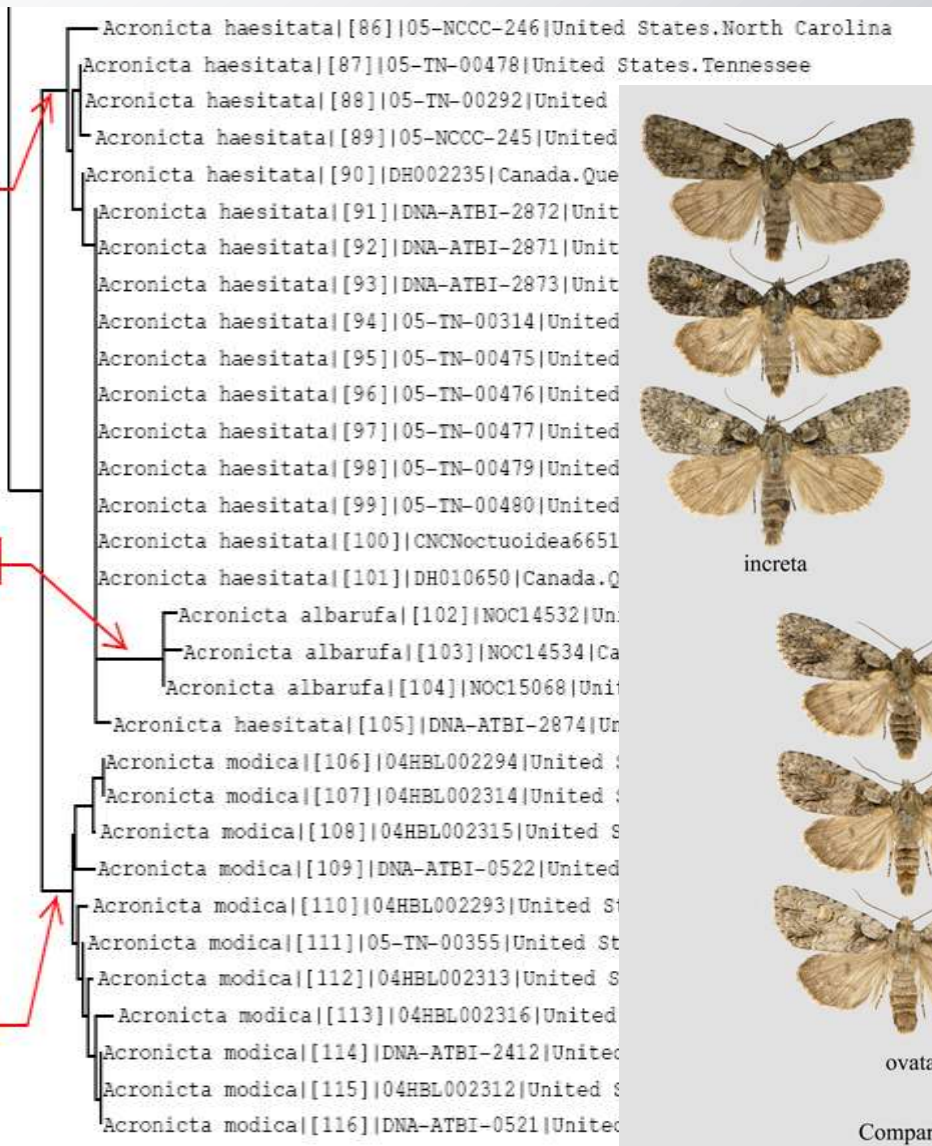
– greatest utility in taxonomically difficult (morphologically similar) groups

eg. *Acronicta increta* group

E (haesitata)

F (albarufa)

G (modica)



Comparison of *Acronicta increta* grp, southeastern Ontario

# Integrative taxonomy

synthesis of all taxonomically relevant data:

wing pattern variation, larval biology, host plants, phenology, distribution, molecular variation



## *Acronicta ovata*

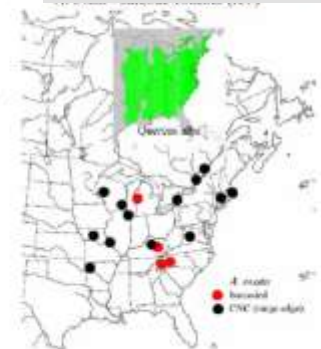
Consistent Franclemont's concept of *ovata* (fig's in Rings et al. 1992); barcodes from TN, NC, MI, KY, ON.

Most similar to some forms of *inereata*, and particularly *exilis*, which looks like a diminutive version of *ovata*.

Distinguishable by contrasting pale FW basal patch, brown scales in reniform, and overall less blotchy, smoother FW pattern compared to *inereata*. Relatively little geographic and local variation.

Foodplants: Wagner (2005) has it from beech, chestnut and oak; northern range limits are S of the northern extent of red oak and beech, and in southern ON *ovata* occurs in association with white oak, but not red oak, bur oak, or beech.

Examined specimens from southern ON and QC to MO, NC and NJ. Forbes also indicates TX, CO, NS (but Ferguson does not list it from NS) and MB.



# Resurgence in taxonomy?

Species descriptions by decade

