Evolutionarily Significant Units: Crandall et al. 2001 TREE 15:290-295.

ESU's are closely related (sometime synonymous) to subspecies and distinct population segments (DPS, as defined under the endangered species act).

Many suggest that all three of these are "population units that merit separate management and have a high priority for conservation".

The fundamental idea here is that conservation should aim to preserve:
* evolutionary processes
* adaptive potential
* not just current species (without regard to losing significant variation *within* species)

Decisions about priority for conservation action are perhaps debatable.
First, focus on one simple question:

What defines an ESU?

Original definitions (Ryder 1986, Waples 1991) had *two* components.
ESU's show:
* reproductive isolation (and consequently, genetic distinctness)
* ecological distinctness (unique adaptations)

But recent definitions have shifted to emphasize *one* crtierion, genetic distinctiveness.
E.g. Moritz (1994).
ESU's show:
* reciprocal monophyly for mtDNA alleles
* significant divergence of allele frequencies at nuclear loci

The changes in definition serve as a starting point for good discussion by Crandall et al of the critical aspects of an ESU.

(1) Moritz's definition requires an examination of both ***historical*** and ***recent*** restriction of gene flow. This is good, because it makes criteria for genetic distinctiveness more concrete. Moritz definition requires evidence for ***long term*** divergence, ***continuing*** in the present.

   mtDNA - evolves slowly (in animals). Therefore, distinctiveness in mtDNA reflects ***long term*** restriction of gene flow.

   reciprocal monophyly:

ESU 1
ESU 2
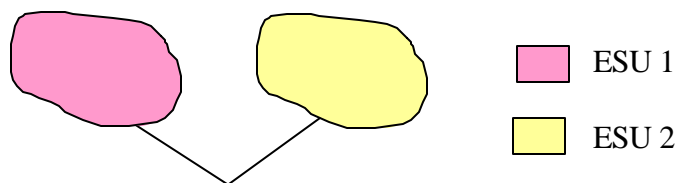
each ESU is a monphyletic group (ancestral population and all descendant populations) that does not include any portion of the other.

(Ohead- AWD mtDNA patterns)

nuclear loci - implicitly, they are speaking of selectively neutral or unexpressed nuclear variation. Most commonly ***microsatellites***.

(explain microsats).

Free from selection, mutations at these loci accumulate very rapidly, thus reflect short term restrictions of gene flow, and are even *capable of detecting genetic distinctiveness that is trivial with resect to differences among population segments in adaptive potential.*

Crandall et al.: "with the increasing resolution of molecular techniques, significant variation can be found at very small scales, even down to the individual".

So care needed in what genetic markers are used.

But congruence of 'slow' and 'fast' markers is evidence for historical isolation that persists today.

(2) Crandall et al point out a problem with the requirement for reciprocal monophyly in mtDNA alleles.

Reciprocal monophyly is a pattern that *guarantees* historical restriction of gene flow occurred.

But ecologically important genetic differences may have accumulated *without* this pattern - so the *reciprocal monophyly criterion is overly strict*.

(Ohead: *Nesticus* spiders in N. Carolina)

(3) Moritz's definition no longer mention ecological distinctness. Implicitly assumes that genetic divergence will be associated with ecological divergence. As Crandall et al point out, this is not necessarily a safe assumption.

Can get rapid ecological divergence with little evidence of historical isolation Conversely, can have long accumulation of neutral genetic differences with little ecological divergence.

If the goal is to maintain *adaptive potential*, need to consider these possibilities. Need to restore focus on *adaptations, not just neutral genetic variation*.

Crandall et al propose solution: "cross-hair analysis"

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         +/-    |    +/-          ┌──────────┐
       ─────────┼─────────        │  Recent  │
         +/-    |    +/-          └──────────┘
                |
                |                  ┌──────────┐
                                   │  Ancient │
                                   └──────────┘

   ┌────────────┐   ┌────────────┐
   │  Genetic   │   │ Ecological │
   │ divergence │   │ divergence │
   └────────────┘   └────────────┘
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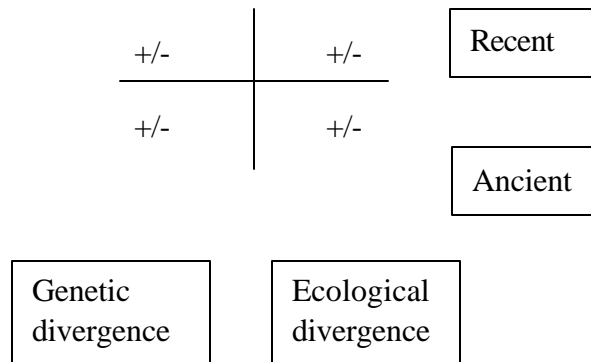
+ reject Ho of exchangeability, evidence exists for divergence
-    accept Ho of exchangeability, failure to detect divergence

1) Strong emphasis on top right quadrant. (see their Fig 1).

2) Underemphasize problems of assessing right side, especially bottom right.

3) Assessing genetic distinctiveness: see lecture notes on F-statistics.

Recommendations:

1. Require cross hair type analysis before deciding whether ESU or not (ecology &
    genetics, historical and recent)

(See their Fig. 2)

2. If ESU manage as distinct populations.
3. If not ESU, maintain natural patterns of gene flow (keep evolutionary processes
    intact).