# Nest site selection by red-naped sapsuckers: Influence of willow availability, aspen heartwood rot fungus, and other ecological factors

## aspen hear

CHRIS FLOYD\*1, MATT TROIA, MATT FAUST, LEAH ULLOM, TIM MILLER, ABE MILLER-RUSHING, RACHEL SCHWARTZ, and EVAN WEIHER

1 Department of Biology, University of Wisconsin-Eau Claire; Rocky Mountain Biological Laboratory, Crested Butte, CO; Department of Biology, University of Texas at Tyler, TX, Department of Biology, Colorado State University, Ft Collins, CO



#### **Abstract**

Woodpeckers are considered keystone species because they excavate tree cavities that provide habitat for other cavity nesting species. In aspen (Populus tremuloides) woodlands of the southern Rocky Mountains, red-naped sapsuckers (Sphyrapicus nuchalis) are the predominant woodpecker, providing essential nest cavities for multiple bird species. Sapsuckers also create sap wells in willows (Salix sp.) and aspen, providing food for many species. Previous work indicated that sapsucker nest densities decreased strongly with distance from willows. However, previous work did not account for potentially confounding effects of other variables such as the prevalence of the heartwood rot fungus, Phellinus tremulae. The sapsuckers nest almost exclusively in Phellinus-infected aspens. In the summers of 2007-08, we sampled willow proximity (distance to nearest willow), willow cover, fungal prevalence, and other variables in 0.25 ha plots centered on aspens with sapsucker nests ("nest sites") and otherwise suitable aspens without ("null sites"); our objective was to determine how these variables influence nest tree selection by sapsuckers. We found no difference between nest sites and null sites in terms of willow proximity. However, nest sites had significantly more surrounding willow cover (within 300m and 900m radii) and significantly higher prevalence of heartwood rot fungus. Nest sites and null sites differed weakly with respect to other variables, such as size of the center tree and elevation. Our results suggest that the availability of willows and prevalence of large (≥ 17 cm DBH), Phellinus-infected aspens may be the most important factors influencing sapsucker nest site selection. To properly conserve the sapsucker associated community we need to better understand the ecology of Phellinus and relationships among multiple factors in the aspen-willow-Phellinus system.

#### **Background**

### Red-naped sapsucker as a keystone species and ecosystem engineer



Figure 1. Red-naped sapsucker (S. nuchalis) about to feed its nestlings

The red-naped sapsucker (Sphyrapicus nuchalis; Fig. 1) is the predominant woodpecker species in the southern Rocky Mountains. Sapsuckers function as a keystone species and ecosystem engineers by:

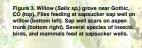
□ excavating new nest cavities every year, providing essential nest sites for secondary cavity nesting animals (Fig. 2), and □ drilling and maintaining sap wells in willows (Salix sp.) and aspen, providing food for many species of birds, mammals, and insects (Fig. 3)

Daily et al. 1993 found that the prevalence of sapsucker sign (aspen sap well scars; Fig 3) decreased strongly with distance from willows. However, this previous work did not consider the effect of other variables, such as the prevalence of the aspen heartwood rot fungus; Phellinus termulae: Fig 4).



Figure 2. Violet-green swallow (left) and tree swallow (right) are among several species that nest in aspen cavities excavated by red-naped sapsuckers.

## Aspens and heartwood rot fungus



Red-naped sapsuckers nest almost exclusively in large (DBH [diameter breast height] ≥ 17 cm) aspens infected with heartwood rot fungus (Phellinus tremulae), which

promotes cavity excavation by softening the heartwood







Figure 4. Left: Aspen tree infected with the heartwood rot fungus, Phellinus tremulae, Middle: reproductive conk of Phellinus. Right: Phellinus-infected aspen tree that snapped at sapsucker cavity.

#### Question

Which factors are most important to sapsuckers in their choice of nest sites?

To address this question we compared sites with sapsucker nests to sites without with respect to the following factors:

- proximity to willows
- area of willow cover within 100, 300, and 900 m
- ☐ prevalence of aspen heartwood rot fungus☐ proximity to riparian zones and meadows
- ☐ tree size, elevation, woodland density, etc.

#### Methods Study sites

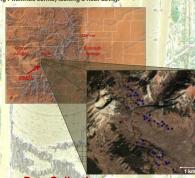
☐ Study site: upper East River valley near the Rocky Mountain Biological Laboratory in Gothic, CO (Fig. 5).

Somin, Co (1):3.3/.

Sapsucker nests were found during June-July, 2005-2007, by traversing aspen groves on foot, looking for sapsuckers/cavities, and listening for sapsucker calls.

Sites with asspucker nests were compared to null sites, which were randomly chosen sites with no recent (2005-2007) sapsucker nest or other null site within 100 m. Each sapsucker site (n = 44) was centered on an aspen tree containing a recent sapsucker nest. Each null site (n = 44) was centered on a randomly chosen suitable aspen (> 17 DBH, containing Phellinus conks) lacking a nest cavity.

Figure 5. The Rocky Mountain Biological Laboratory (RMBL) is located in west-central Colorado (aboye). Data were collected from 88 sites in aspen woodlandnear RMBL. Yellow markers (right) represent sapsucker nesting sites from 2005-2007. Blue markers represent null sites (randomly chosen sites lacking recent sapsucker nests or other sapsucker nests or other



#### **Data Collection**

The following variables were measured within 0.25 ha circular plots (Fig. 6) each centered on a sapsucker nest tree or null-site tree:

- □ Number of large (≥ 17 cm DBH) and small (≥ 5 and < 17 cm DBH) aspen trees; number of large and small aspens with *Phellinus* conks, sapsucker well scars, and/or cavities; number of large snags and conifers
- Distance between center tree and
- nearest stand of suitable willows
- nearest willow bearing sapsucker damage
- nearest water
- □ edge of nearest meadow (defined as area ≥ 100 m² lacking trees ≥ 5 cm DBH)

# Nearest meadow edge 0.25 ha plot 28.2 m radius Focal Tree Nearest willow

Figure 6. Example of 0.25 ha study plot centered on a sapsucker nest tre

#### Results

- □ Prevalence of heartwood rot fungus was significantly higher in sapsucker nest sites relative to null sites (Fig. 7). □ Compared to null sites, nest sites had significantly more
- willow cover within 300 m and within 900 m (Fig. 8)
- Mean willow proximity did not significantly differ (P = 0.63) between site types (nest: 119.1 ± 16.7 [SE] m; null: 130.8 ± 17.0 m).
- □ Nest trees were slightly larger and located at slightly higher elevations than null site (center) trees:
- ☐ nest tree mean DBH = 28.1 cm (SD = 3.5); null tree mean DHB = 26.3 cm (SD = 6.1); P < 0.1
- nest tree mean elevation = 2935 m (SD = 64.2); null tree mean elevation = 2966 m (SD = 56.7); P < 0.02

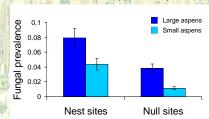


Figure 7. Proportion of aspen trees infected with heartwood rot fungus (*P. tremulae*) within 0.25 ha circular plots centered on a sapsucker nest tree (Nest sites) or suitable aspen with no sapsucker nest (Null sites) ≤ 100 m of the tree. Shown are means  $\pm$  SE at 44 sapsucker nests sites and 44 null sites for large (≥ 17 cm DBH) and small (≥ 5 and < 17cm DBH) aspens. Fungal prevalence was significantly higher at nest sites (proportions were arcsine transformed for t-tests; p < 0.004).

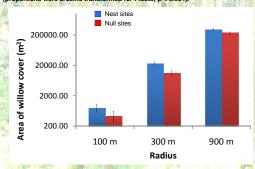


Figure 8. Mean  $\pm$  SE area (m<sup>3</sup>) of willow (Salix sp.) cover within concentric circles of 100, 300, and 900 m radii centered on each of 44 sapsucker nests and 44 null sites (t = 1.25, P = 0.22; t = 2.87, P = 0.01; t = 2.26, P = 0.03). Area was estimated using

#### Conclusions

- □ Nest-site selection by sapsuckers is explained best by willow availability and prevalence of *Phellinus*-infected aspens.
- ☐ To properly conserve the sapsucker-associated community we need to better understand the ecology of *Phellinus* and the multivariate relationships in the aspen-willow-*Phellinus* system.

#### **Acknowledgements**

We thank the University of Wisconsin-Eau Claire Office of Research and Sponsored Programs, and Blology Dept for funding this research. The Rocky Mountain Biological Laboratory provided housing and other assistance. We are also grateful to lan Billick, Jennie Reithel, Gretchen Dally, and Paul Ehrlich for their helpful comments, and Tom Anderson, Mitchell Banach, and Ashley Nichols for programs to the field.