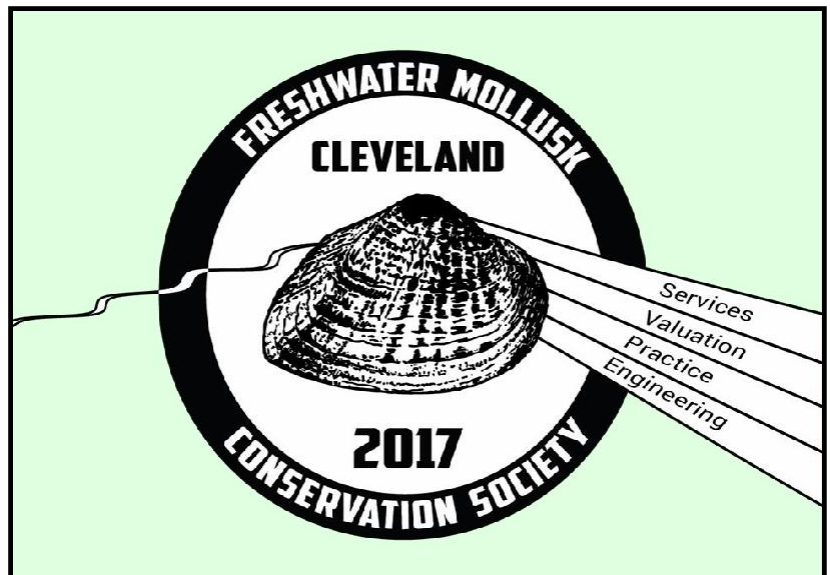




Newsletter of the Freshwater Mollusk Conservation Society
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**Planning Well Underway for Our 2017
 Symposium in Cleveland, Ohio**

The 10th Biennial FMCS Symposium will be held on March 26 -30, 2017, at the Cleveland Downtown Marriott at Key Center, in Cleveland, Ohio. The Planning Committee is pleased to announce that our conference theme will be: *Ecosystems, Engineering, Valuation, and Practice - The Roles of Freshwater Mollusks in a Changing Environment*. The goal for this Symposium is to focus on how freshwater mollusks affect nature and society by: (1) providing ecosystem services, (2) being ecosystem engineers, (3) understanding their value relative to other biota and us, and (4) guiding the regulations and actions we use in

Contributed Articles

The following articles have been contributed by FMCS members and others interested in freshwater mollusks. These contributions are incorporated into Ellipsaria without peer review and with minimal editing. The opinions expressed are those of the authors.

The Identity of the “Fat *simplex*” Population Inhabiting Pistol Creek in Maryville, Tennessee

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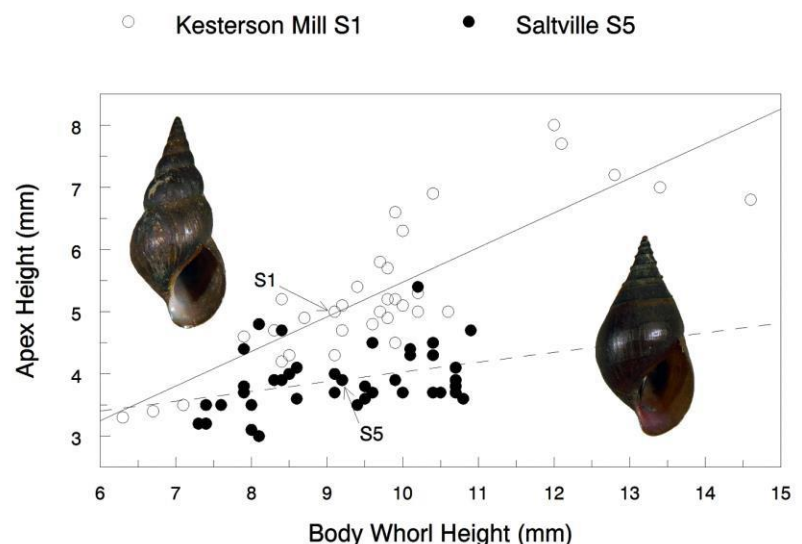
In an accompanying article, Dillon (2016) reported allozyme and shell morphometric evidence suggesting the presence of two reproductively-isolated populations cryptic under the nomen *Pleurocera simplex* at Pistol Creek site S6 in Maryville, Tennessee (35.7535°N; 83.9711°W). These observations prompted us to re-examine data previously published by Dillon and Robinson (2007) on gene frequencies at ten allozyme-encoding loci in five populations of nominal *P. simplex* inhabiting southwest Virginia. That 2007 study included a sample from Thomas Say’s type locality S5, the mouth of Cedar Branch as it enters the North Fork Holston River at Saltville, Smyth County, Virginia (36.8907°N; 81.7491°W). Among the four other nominal *P. simplex* populations sampled by Dillon and Robinson, the most genetically divergent from S5 was population S1, sampled in Indian Creek at Kesterson Mill, Lee County, Virginia (36.6283°N; 83.5019°W). Our (2007) Table 1 reminded us that the Indian Creek population S1 was nearly fixed for the S6s “skinny” Pistol Creek marker allele, Oldh¹⁰⁴, while the Saltville type population S5 was fixed for the S6f “fat” marker allele Oldh¹⁰⁰.

So, in August of 2008, we returned to *simplex* type locality S5 at Saltville for additional samples, collecting 54 individuals, and to site S1 at Kesterson Mill, collecting 77 individuals. Each of these samples was divided into two subsamples. Subsamples of 14 individuals from the Saltville type population S5 and 41 from the Indian Creek population S1 were analyzed electrophoretically together with the 71 individuals from Pistol Creek as outlined by Dillon (2016) to confirm allelic matches across the two-state region. These data were combined with the larger data sets previously published by Dillon & Robinson (2007). Then BIOSYS version 1.7 (Swofford & Selander, 1981) was used to calculate matrices of Nei's (1978) unbiased genetic identity and Cavalli-Sforza and Edwards (1967) chord distances between all pairs of control populations S1 and S5 and the two cryptic populations co-occurring in Pistol Creek S6. Chord distances were used as the basis for a neighbor-joining tree calculated using PHYLIP v3.65 program NEIGHBOR (Felsenstein, 2004).

The shells of the remaining 40 individuals from Saltville S5 and 37 individuals from Kesterson Mill S1 were measured and analyzed by analysis of covariance, following the morphometric procedures described by Dillon (2016) for the 71 individuals sampled from Pistol Creek. These shells have been deposited in the Academy of Natural Sciences of Philadelphia under catalog number 426375 for Saltville S5 and number 426377 for Kesterson Mill S1.

The snails sampled from the Saltville type locality S5 tended to demonstrate "fatter" shell morphology than the snails sampled from Kesterson Mill S1. Figure 1 shows that the simple regression of apex height (A) on body whorl height (B) for the Saltville type population S5 was $A = 0.157B + 2.46$ ($r = 0.36$), very significantly different (ANCOVA $t = -9.52$, $p < 0.0001$) from the regression for the Kesterson Mill population S1, $A = 0.556B - 0.09$ ($r = 0.84$).

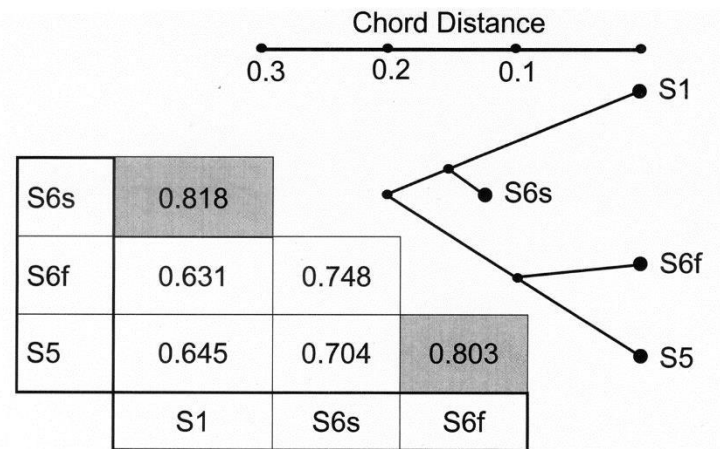
Figure 1. Shell apex height (A) as a function of body whorl height (B) in *Pleurocera* population S1 sampled from Indian Creek at Kesterson Mill, and in topotypic *P. simplex* population S5 sampled from the mouth of Cedar Branch in Saltville. Data corresponding to the two exemplar shells are marked with arrows.



Negligible genetic variation was uncovered at five of the 10 allozyme loci analyzed across the four combined samples: the 20 + 17 = 37 Pistol Creek S6f, the 51 + 13 = 64 Pistol Creek S6s, the 14 + 34 = 48 topotypic *P. simplex* from Saltville S5, and the 41 + 37 = 78 individuals from Kesterson Mill S1. All four of the populations were fixed (or nearly fixed) for different alleles at the *Opdh* locus. Population S1 was distinguished from the other three populations by higher frequencies of *Xdh*⁹⁵ and *Idhf*¹⁰⁴, consistent with the results of Dillon and Robinson (2007), and both S5 and S6f had unique alleles at the *Pgm* locus in high frequencies. But overall, the matrix of Cavalli-Sforza and Edwards chord distances and the neighbor-joining tree (Figure 2) confirms that the fat population S6f of Pistol Creek was more genetically similar to the *simplex* type population inhabiting Cedar Branch at Saltville (S5), and the skinny population S6s from Pistol Creek was more genetically similar to population S1 inhabiting Indian Creek at Kesterson Mill.

Since the fat Pistol Creek population S6f matched topotypic *P. simplex* S5 both genetically and morphologically, only the allozyme data from that subsample of 37 here designated S6f were (ultimately) reported among the *P. simplex* controls in the study of Dillon (2011). The specific identity of the skinny *simplex* population S6s inhabiting Pistol Creek, as well as that of the S1 *Pleurocera* population inhabiting Indian Creek at Kesterson Mill, will be addressed in a subsequent article.

Figure 2. Data below the diagonal are Nei's unbiased genetic identities between four pleurocerid populations of east Tennessee and southwest Virginia, with conspecific values shaded. A neighbor-joining tree based on Cavalli-Sforza and Edwards chord distances is shown above the diagonal. S1 was sampled from Kesterson Mill, S5 was sampled from the *P. simplex* type locality at Saltville, S6f is the fat *simplex* population from Pistol Creek, and S6s is the skinny *simplex* from Pistol Creek.



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