

# Using Genetics to Understand and Conserve the Red Siskin (*Carduelis cucullata*)

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*The following article is an update on a project that was first reported on in "2001 Discovery in Guyana," written by Mark Robbins, Mike Braun, and Davis Finch. For the past few years since that article, I've been sending Mike Braun Red Siskin specimens whenever a bird in my flock dies. The initial results you are about to read compare DNA from the birds discovered in Guyana, with captive birds (my flock, which we assume descend from past importations of Venezuelan stock).*

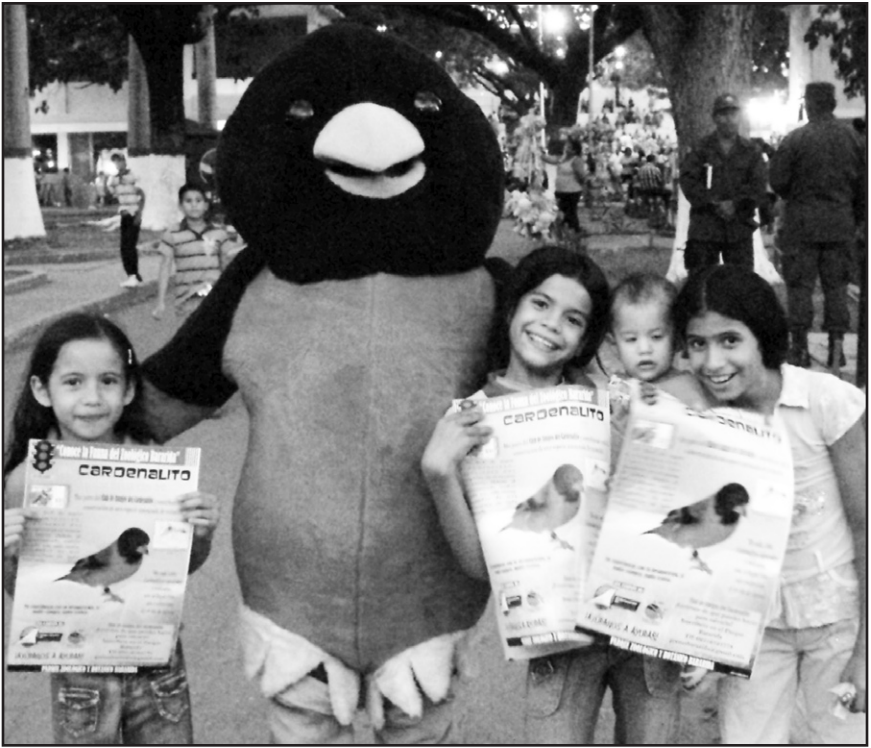
*What does this mean for Red Siskins? It means so far that at least some genetic variation is present, which is great because it can continue to be detected and analyzed, and compared against other isolated flocks in the wild and your flock in your bird room. But it also means that they don't know yet how much genetic variation is really present. As you will read, the DNA comparisons are still only preliminary, because they had only 8 captive birds to work with, which is not enough to represent all US captive birds. What they really need is at least a few birds from each captive flock.*

*What does this mean for Red Siskin breeders? It means these scientists need your help! We need other Red Siskin breeders to join us in order to expand this study, to learn about genetic variation in US captive birds, and to help conserve wild ones. You just have to be willing to invest a bit of time and energy to participate, by sending them samples. It is not hard to do, and you will get a peek at what the genetic variation is in your flock. If they can expand this study, they may one day be able to tell you how pure your flock is too!*

## INTRODUCTION

The Red Siskin is one of Venezuela's most endangered birds because of illegal trapping for the pet trade. Ex situ conservation of this species is an important safeguard against extinction while this threat is brought under control. However, for captive birds to be useful to a formal conservation breeding

program, they need to: 1) represent the natural variation of the species; 2) not be highly inbred; and 3) not be hybrids or have ancestors who were hybrids with Canaries or other *Serinus* or *Carduelis* species. This project aims to develop and use molecular genetic tools to address these concerns.



A zoo in Barquisimeto, Venezuela, has already begun a captive breeding and education program and needs our help.





*Captive Red Siskins may have ancestry from other species due to past hybridization.*



## OBJECTIVES

1. Understand the distribution of genetic variation in wild Red Siskins to compare with captives, using existing molecular markers (mitochondrial genes and AFLP, or Amplified Fragment Length Polymorphisms).
2. Develop new, highly variable molecular markers (microsatellites and SINEs, or Short INterspersed repeated Elements).
3. Characterize the captive bird population using all markers, to assess inbreeding and hybridization.

## RESULTS TO DATE AND IMPLICATIONS

- A small survey of 5 wild Red Siskins from Guyana and 8 captive birds of presumably “Venezuelan” origin, at 2 mitochondrial genes and 228 AFLP loci, revealed moderate divergence between the two countries, and variation within each (see Figure 1, Table 1). The presence of differences between “countries” and of variation within them, in a very small sample size, is encouraging. It suggests that real patterns may become clearer when more birds are analyzed.
- Five additional captive birds of “Venezuelan” origin are presently being analyzed.
- All major US natural history collections with Red Siskin museum specimens have granted us genetic samples of wild individuals, which will greatly increase our ability to characterize wild populations.

## HOW YOU CAN HELP

We need genetic samples of birds from each US captive flock. Acceptable samples can include anything from eggshells to blood feathers to whole frozen birds – we will pay for shipping. We can’t develop genetic screening tests for captive birds without these samples! For more details, please contact us at [kmrodriguezclark@gmail.com](mailto:kmrodriguezclark@gmail.com) or [braunm@si.edu](mailto:braunm@si.edu), call us at 301-238-1113, or contact Paula Hansen of the National Finch & Softbill Society – [FinchSave at pphansen@earthlink.net](mailto:FinchSave@earthlink.net).

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Figure 1: Phylogenetic tree generated using DNA sequence data from 2,541 base pairs of two mitochondrial genes [cytochrome B and the control region] showing that birds caught in the wild in Guyana group apart from captive birds (of presumably Venezuelan origin), and that there is variation within the “Venezuelan” birds. Numbers on branches are bootstrap support values.

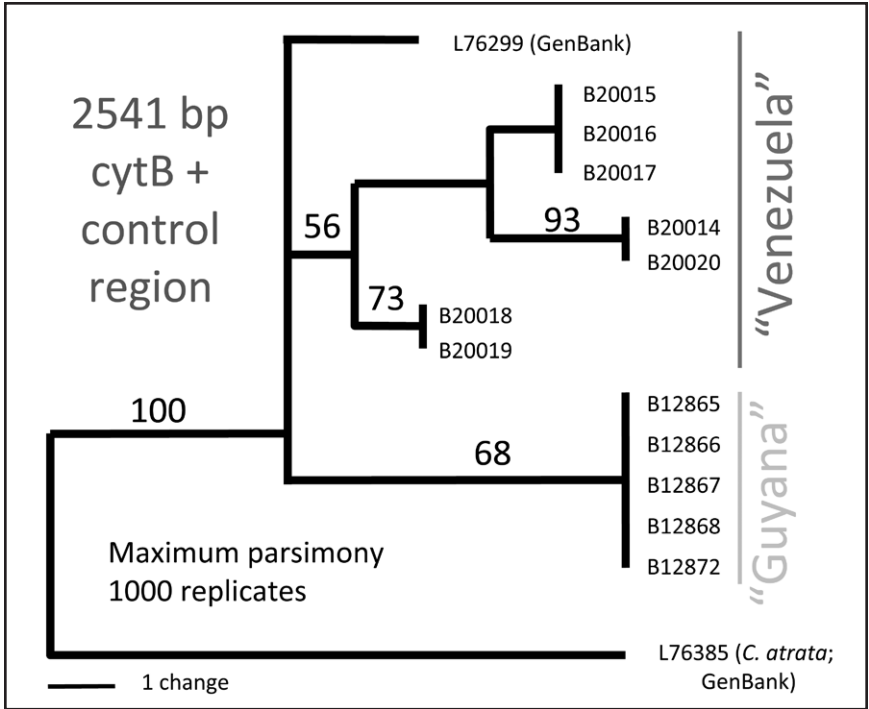


Table 1: Band presence (1) or absence (0) for 14 AFLP loci selected at random from a total set of 228 AFLP loci scored in 13 Red Siskin individuals. One locus varies in frequency (13\_248, circled in blue) and one has a fixed difference (13\_322, circled in red). Of the 228 AFLP loci evaluated (data not shown), 21 diverged in frequency and two had fixed differences between “Venezuela” and Guyana, with 62 and 36 polymorphic loci in each, respectively.

	A	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
17	Sample Name	13_94	13_128	13_133	13_145	13_161	13_170	13_216	13_235	13_242	13_248	13_250	13_254	13_268	13_322
18	B20014_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	0
19	B20015_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	0
20	B20016_05_13	1	0	0	1	1	0	1	0	1	0	0	1	0	0
21	B20017_05_13	1	0	1	1	1	1	1	1	1	1	0	1	1	1
22	B20018_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	0
23	B20019_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	0
24	B20020_05_13	1	0	1	1	1	1	1	1	1	0	1	1	1	0
25	B20021_05_13	1	0	0	1	1	1	1	1	1	0	1	1	1	0
26	B12865_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	1
27	B12866_05_13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
28	B12867_05_13	1	1	1	1	1	1	1	1	1	1	1	1	1	1
29	B12868_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	1
30	B12872_05_13	1	0	1	1	1	1	1	1	1	1	1	1	1	1
31	negative_05_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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