Table 8.2. Individual sage-grouse sampled in Benedict et al. (2003) by population and haplotype. Alpha represents the proportion of haplotypes from clade I. N* represents the number of individuals sequenced. The bottom two rows show the Lyon/Mono population vs. all others.

			Haplotype (clade I underlined and in italics, clade II in bold)																																			
Location	N*	α	*A*	**B**	*F*	**O**	**Q**	**T**	**U**	**X**	*AG*	*AU*	**AV**	*AZ*	*BB*	**BD**	**BF**	**BO**	*BX*	*CH*	**CJ**	**CK**	**CN**	**CR**	*DA*	*DB*	*DC*	*DD*	**DH**	**DL**	**DM**	**DS**	*DT*	**BJ**	**BK**	*BL*	*BM*	**BQ**	**DP**	*DQ*
Yakima WA	18	0.00								18																														
Douglass/Grant WA	18	0.11								13																						3	2							
Whitehorse OR	33	0.42	14	1			1	10	4	2											1																			
Steens OR	21	0.29	5	1	1		1	8		4																					1									
Warner OR	19	0.37	4		1		2	2		5													1	2				1					1							
Wagontire OR	19	0.42	6		1		4	2	1	1										1			3																	
Beatty's OR	21	0.29	4				1			6			4							2	2	1		1																
Churchill NV	18	0.06		2				5		8				1		1	1																							
Washoe NV	20	0.40	6				3		1	6				1				1	1		1																			
Elko NV	20	0.50	3	3						5	1	4	2												1		1													
Humboldt NV	21	0.67	10	2			1	1		3																4														
Sheldon NWR NV	19	0.16	2			1	2	6	1	6					1																									
Nye NV	20	0.30		4				1		9	1			4	1																									
Lyon NV	20	0.20					1																											5	9	3	1	1		
Mono CA	23	0.65																																7		4	8		1	3
Lassen CA	22	0.23	5				4			8			1																1	1	2									
Others	289	0.31	59	13	3	1	19	35	7	94	2	4	7	6	2	1	1	1	1	3	4	1	4	3	1	4	1	1	1	1	3	3	3							
Lyon/Mono	43	0.44					1																											12	9	7	9	1	1	3