Repeat expansions in HTT and ATXN2 and the risk of ALS in a Norwegian cohort

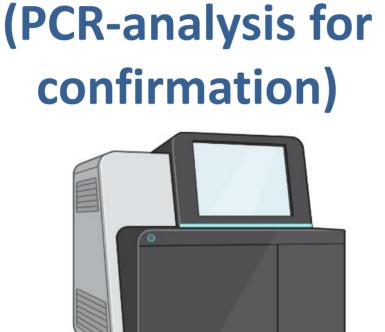
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- ✓ Genetic repeat expansions may cause multiple clinical phenotypes and play a role in several neurodegenerative diseases.
- ✓ HTT repeat expansions have been reported in individuals with ALS.
- ✓ *ATXN1* and *ATXN2* repeat expansions (≥ 33 repeats and ≥ 29 repeats) are known genetic risk factors of ALS.
- ✓ AR repeat expansions cause Kennedy's disease; a differential diagnosis of ALS.
- ✓ ExpansionHunter software detects repeat expansions on exome sequencing data.

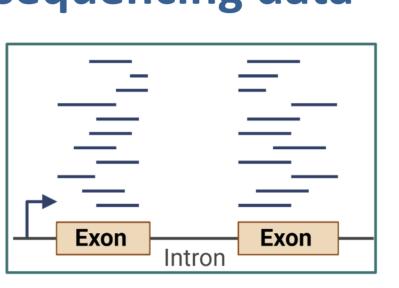
Methods

ALS patients (n = 414) and neurologically-healthy controls (n = 713)

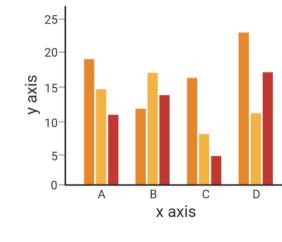


Exome sequencing

ExpansionHunter software on exome sequencing data



Statistical analyses of repeat expansions in **ALS** patient compared to controls



Results: Repeat expansions

HTT (36-40 repeats)

- ✓ Six ALS patients (1.5%)
- ✓ Two controls (0.3%)
- Odds ratio 10.4* (95% CI: 1.9-58.6)

ATXN2 (29-34 repeats)

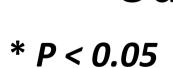
- ✓ Seven ALS patients (1.7%)
- ✓ Three controls (0.4%)
- Odds ratio 4.8* (95% CI: 1.1-21.2)

- AR ✓ One ALS patients
- ✓ None controls



ATXN1 (34-45 repeats)

- √ 32 ALS patients (7.7%)
- ✓ 56 controls (7.9%)
- Odds ratio 1.1 (95% CI: 0.7-1.9)





Results: HTT

Table 1 Clinical characteristics <i>HTT</i> gene (≥36 repeats).	for ALS patients car	rying intermediate expans	ion in
. ,	HTT+ (n=6) (1.45%)	HTT- (n=408) (98.55%)	P-value
Mean age at onset, years (SD)	49.00 (18.95)	63.26 (12.12)	0.005*
Motor neuron loss, n (%)			
UMN	0 (0)	26 (6.37)	0.696
LMN	I (16.67)	29 (7.11)	
Both	5 (83.33)	335 (82.11)	
Uncertain ^a	0 (0)	18 (4.41)	
Site of onset, n (%)			
Spinal	6 (100)	251 (61.52)	0.324
Bulbar	0 (0)	106 (25.98)	
Both	0 (0)	48 (11.76)	
Uncertain ^a	0 (0)	3 (0.74)	
Cognitive impairment, п (%)			
Yes	I (16.67)	30 (7.35)	0.540
No	5 (83.33)	359 (87.99)	
Uncertain ^a	0(0)	19 (4.66)	
El Escorial, n (%)			
Yes	5 (83.33)	307 (75.25)	0.621
No	0 (0)	56 (13.73)	
Uncertain ^a	I (16.67)	45 (11.03)	
alncludes uncertain and missing data $*P < 0.05$.			

Results: Allele size

Case ID	Gene expansion	Repeat size	Other genetic variants	Sex	Age at onset	Family with ALS	Site of onset	Cognitive involvement	Motor neuron loss	Neurophysiology compatible with ALS	El Escorial criteria fulfilled	Disease duration ^a (months)
I	HTT	40		М	58	No	Spinal	Yes		Yes	Yes	120
2 ^b	HTT	39		М	32	No	Spinal	No		Yes	Yes	76*
3	HTT	39	C9orf72 expansion	F	69	No	Spinal	No		Yes	Yes	10
4	HTT	39		М	70	No	Spinal	No		Yes	Yes	49
5	HTT	36	SOD1°	М	28	Yes	Spinal	No		Yes	Uncertain	116*
6	HTT ATXN2	37 31	C9orf72 ^d	М	37	No	Spinal	No		Yes	Yes	157*
7	ATXN2	34		М	55	No	Spinal	No		Yes	Yes	85
8 ^e	ATXN2	33		F	64	No	Spinal	No		No	No	145*
9	ATXN2	30		М	71	No	Spinal	No		Yes	Yes	11*
10	ATXN2	30		М	77	No	Spinal	No		Yes	Yes	19
П	ATXN2	29		F	67	No	Spinal	No		Yes	Yes	34
12	ATXN2	29		F	61	No	Bulbar	No		Yes	Yes	32
13	AR	45		М	67	No	Both	Yes		Yes	Yes	32*
amily his (His47A termedi	y months from s tory of Huntingt .rg) ate repeat expar d with primary la	on's disease nsion (27 rep	eats)							records were re-eval dent neurologists.	uated by two	

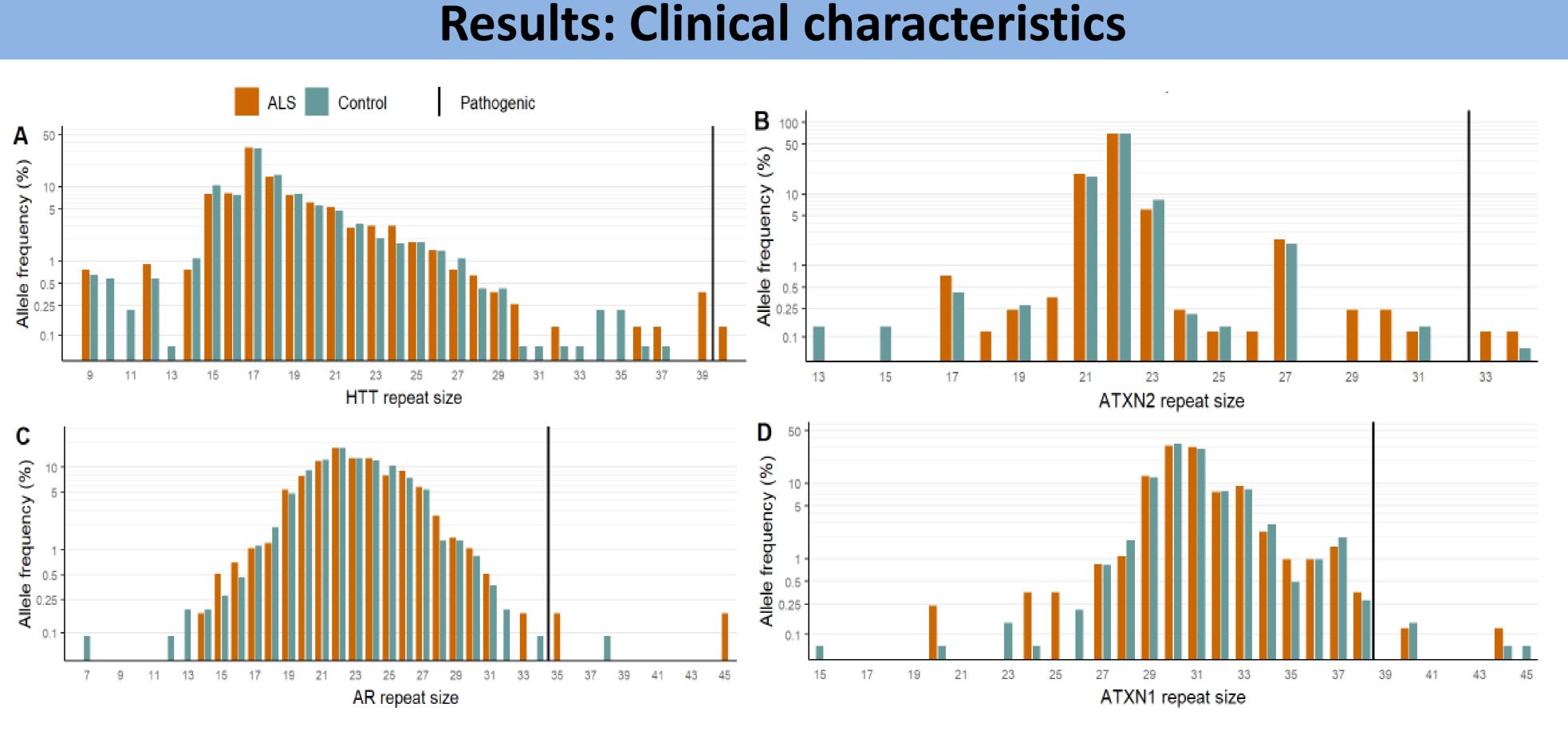


Figure 1 Distribution of total alleles and sizes in ALS patients compared to controls. (A) HTT repeat expansions in 391 ALS patients and 695 controls. (B) ATXN2 repeat expansions in 414 ALS patients and 712 controls. (C) AR repeat expansions in 414 ALS patients and 712 controls and (D) ATXN1 repeat expansions in 414 ALS patients and 713 controls. The number of ALS patients and controls differs since samples with low coverage for a specific repeat were removed from the analysis

Conclusion

- HTT and ATXN2 repeat expansions is associated with increased risk of ALS in our cohort
- HTT repeat expansions is associated with earlier onset of ALS in our cohort



UMN = Upper motor neuron LMN = Lower motor neuron





Presenting author: