Genetic dissection of barley morphology and development

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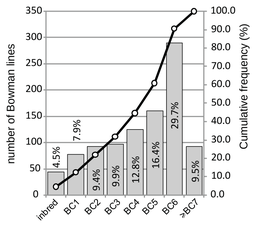
physical mapping · gene cloning · BARCODE · genome sequencing · genetic mapping

genomics assisted dissection of barley morphology and development

Bowman NILs



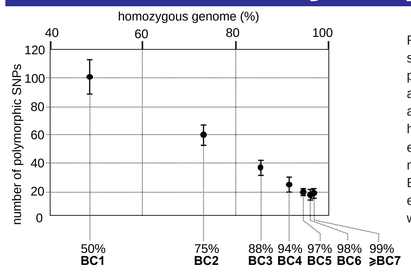
	Total	BC1	BC2	BC3	BC4	BC5	BC6	≥BC7
Male sterile	105	11	20	5	5	18	40	5
Reaction to Puccinia hordei	95	2	3	9	16	40	13	12
Eceriferum	92	2	8	11	17	6	40	8
Semidwarf	53	6	7	11	13	8	6	1
Laxatum	38	6	9	8	5	3	6	
Chlorina	36	4	2	4	4	3	9	4
Brachytic	32	2		1	1	10	16	2
Erectoides	30		2	2	2	5	13	5
Breviaristatum	29	1	3	1	5	7	8	3
Necrotic	28	6	1	5	4	3	7	1
Dense spike	27		4	3	8	4	7	1
Desynapsis	24	3	2	2	6	10		

	Total	BC1	BC2	BC3	BC4	BC5	BC6	≥BC7
Bonus	183	11	18	27	28	24	58	11
Foma	58	4	14	11	8	6	14	1
Betzes	39	1	1	3	5	15	11	2
Akashinriki	34			3	4	4	15	8
Morex	34	6	4	5	7	1	3	2
Steptoe	30	7	5	7	3	2	1	
Birgitta	21	1	1	2	2	4	8	3
Volla	20	1	2	4	4	4	5	

	Total	BC1	BC2	BC3	BC4	BC5	BC6	≥BC7
spontaneous	398	37	31	34	49	74	101	35
X-ray	126	2	11	11	15	14	56	11
ethyl methanesulfonate	86	6	11	8	11	18	25	5
neutron	83	5	7	14	12	12	24	6
γ-ray	74	7	11	7	14	9	23	2
ethylene imine	52	8	4	8	7	7	14	3
sodium azide	44	4	4	4	3	8	13	8

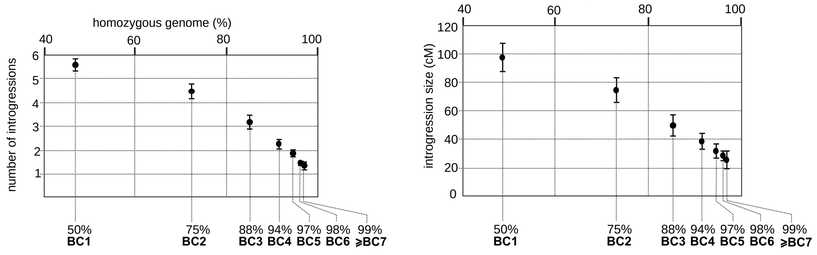
Basic features of the Bowman NIL population. Combined bar and line graph shows population-wide distribution of backcrossing levels of 978 lines. Absolute (histogram, left y axis) and cumulative (line graph, right y axis) frequencies are plotted. Relative frequencies of the individual lines are shown above or within the histograms as percentages. Heat maps show number of NILs at different backcross generations according to the original parent, the mutagen used and the phenotypic classification. Only groups, represented by a total of >20 NILs are shown. Cell shading (white to black) is based on the number of NILs (shown within the cells) within each individual group. Groups are ordered according to the total number of lines per class (highest on the top).

genotyping



Reduction in genome complexity by backcrossing. Scatterplot shows the observed increase in % of the homozygous recurrent parent genome during backcrossing (x-axes) plotted against the average values of the polymorphic SNP frequencies. Bottom x-axis shows predicted or theoretical fraction (r) of the homozygous recurrent parent genome after each backcrossing event, calculated using the following formula $r=(2^m-1)/2^m$ (where m is the number of backcrosses). Vertical error bars show 95% Bonferroni corrected confidence intervals for the mean with errors pooled across the groups. In total, up to 3072 gene SNPs were used for genotyping 978 Bowman lines.

mapping



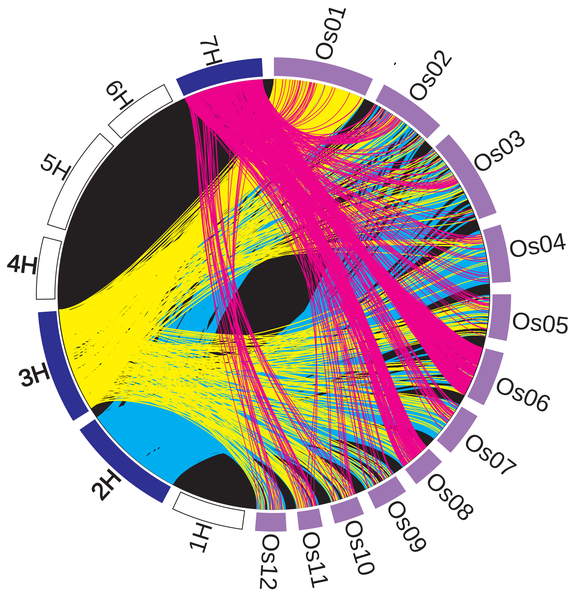
Reduction in genome complexity by backcrossing. Scatterplots show the observed increase in % of the homozygous recurrent parent genome during backcrossing (x-axes) plotted against number of introgressions and the interval size. Bottom x-axes show predicted or theoretical fraction (r) of the homozygous recurrent parent genome after each backcrossing event, calculated using the following formula $r=(2^m-1)/2^m$ (where m is the number of backcrosses). Vertical error bars show 95% Bonferroni corrected confidence intervals for the mean with errors pooled across the groups. Frequency and size of the introgressions were determined using barley consensus map consisting of ~3000 SNPs.

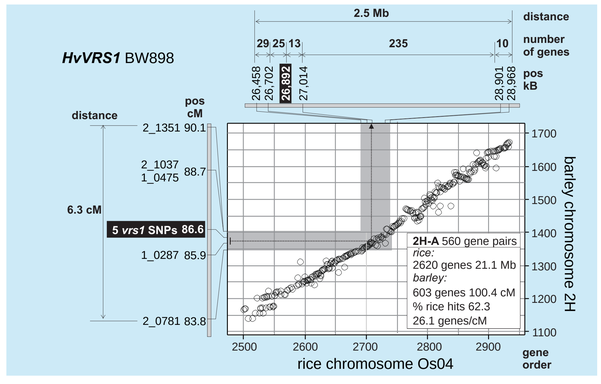
synteny-based gene identification

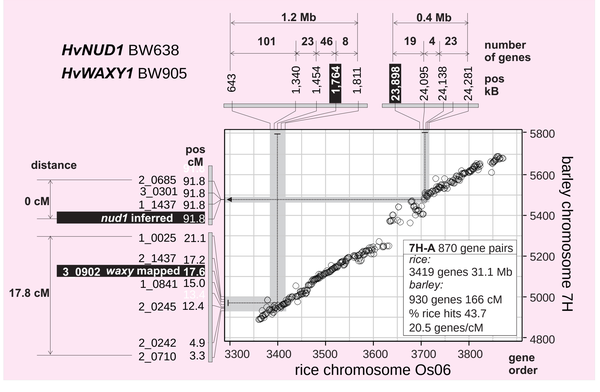
Predictions of the position and precision of locating HvVRS1, HvUZU, HvNUD1 and HvWAXY genes using Bowman NIL genotypic data, in conjunction with the current barley integrated gene map consisting of 2908 *cis*-eQTLs and 2787 SNPs, and barley-rice conservation of synteny models.

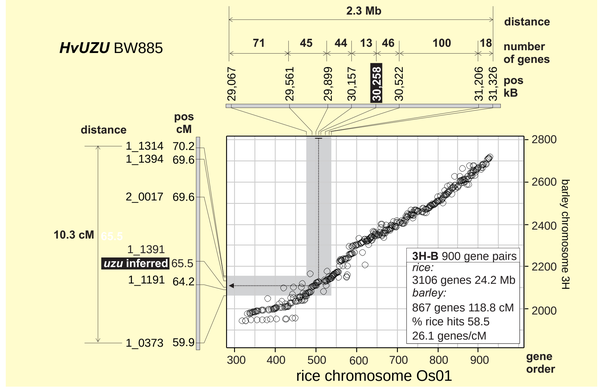
Scatterplots and the *Circos* diagram were based on 5695 barley-rice homolog pairs. For clarity, C*ircos* diagram shows only gene pairs from the barley chromosomes 2H, 3H and 7H. Scatterplots show genome-wide ordinal values where the x-axis = rice physical gene order, y-axis = barley genetic gene order. Insets show summaries of the model inputs.

Grey areas within the scatterplots indicate both the barley and the inferred rice regions as defined by SNPs that are polymorphic between cv Bowman and the corresponding NIL. Expansion of these regions on the physical and genetic scales is shown as graphs on the top and left of the scatterplots depicting polymorphic SNPs and their genetic positions (barley graph) and physical positions and number of genes in the intervals (rice graph). Positions of the actual genes and/or their inferred positions based on synteny are shown as black boxed white text. The direction of the arrow (the dotted line) within the scatterplot indicates how the position of each of the genes was predicted.

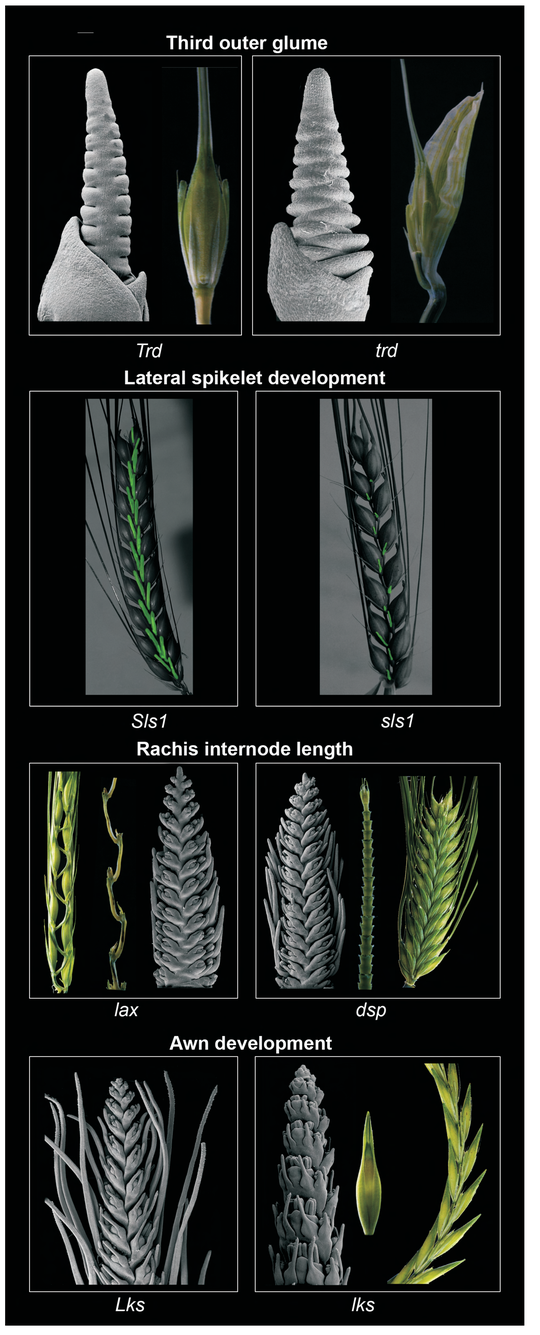








BARCODE cloning targets



Crosses

NIL	mutant group	allele	backcross	number of SNPs	number of introgressions	max interval size (cM)	chromosome	average position
BW371	*Angustifolium*	*Fol-b*	BC5	3	2	5.3	5H	180.25
BW370		*fol-a.1*	BC6	10	2	6	1H	124.1
BW010	*Awned palea*	*adp1.a*	BC3	26	2	74.5	3H	76.75
BW490	*Awnless*	*lks1.a*	BC5	4	1	4.5	2H	85.05
BW491		*lks1.b*	BC6	4	2	0.7	2H	72.65
BW076	*Brachytic*	*brh1.ae*	BC3	42	5	44.5	4H	99.55
BW082		*brh11.a*	BC5	34	2	34.1	5H	51.35
BW093		*brh.i*	BC6	26	1	34.1	5H	51.35
BW071	*Branched spike*	*brc1.5*	BC1	179	7	143.6	2H	78.9
BW059	*Broad leaf*	*blf2.b*	BC6	20	1	21	5H	143.1
BW605	*Compositum*	*mul.c*	BC6	4	3	4.4	5H	66.2
BW189		*com1.a*	BC6	28	1	42.3	5H	48.15
BW192		*com2.g*	BC7	12	1	15.9	2H	47.05
BW271	*Dense spike*	*dsp.ay*	BC2	29	2	19.5	7H	78.25
BW275		*dsp.bc*	BC3	20	2	31.4	3H	48.5
BW267		*dsp.at*	BC4	32	3	19.5	7H	78.25
BW652		*pyr.aa*	BC5	23	2	38.3	7H	68.85
BW555		*pyr.ai*	BC6	20	1	15.9	3H	59.65
BW253		*dsp.ab*	BC6	43	1	18.2	3H	50.8
BW935		*Zeo.f*	BC6	19	1	19.5	7H	78.25
BW937		*Zeo1.a*	BC6	7	1	21.4	2H	144.6
BW937		*Zeo1.a*	BC6	7	1	21.4	2H	144.6
BW277		*dsp1.a*	BC6	20	2	24.9	2H	144.25
BW661		*Pyr2.i*	BC6	37	2	26	3H	52.5
BW933		*Zeo.d*	BC6	17	1	26.2	2H	126.6
BW265		*dsp.ar*	BC6	47	2	49.8	3H	89.1
BW273		*dsp.ba*	BC6	36	1	51.8	3H	65.4
BW279		*dsp9.i*	BC6	18	2	85.3	6H	85.85
BW940		*Zeo3.h*	BC7	0	1	20.3	2H	139.45
BW262		*dsp.ao*	BC7	37	4	27.8	2H	68.9
BW938		*Zeo1.b*	BC8	10	1	10.4	2H	132.3
BW938		*Zeo1.b*	BC8	10	1	10.4	2H	132.3
BW237	*Desynapsis*	*des15.y*	BC4	7	3	6.4	2H	137.1
BW249		*des9.n*	BC4	12	3	10.6	7H	139.1
BW248		*des8.i*	BC4	56	3	76.8	3H	75.6
BW238		*des2.b*	BC4	56	3	94.8	3H	86.9
BW229		*des1.v*	BC5	3	1	27.7	7H	38.85
BW230		*des10.p*	BC5	10	2	9.1	5H	128.05
BW233		*des12.w*	BC5	19	2	32	7H	70.4
BW244		*des6.i*	BC5	56	3	38.1	5H	142.55
BW246		*des7.j*	BC5	17	1	40.8	3H	39.5
BW235		*des14.u*	BC5	27	2	49.7	7H	63.15
BW239		*des3.c*	BC5	52	2	51	2H	64.6
BW234		*des13.t*	BC5	32	3	82.6	3H	52.1
BW231		*des11.r*	BC5	39	1	87.1	3H	70.45
BW240		*des4.af*	BC6	3	1	44.1	7H	76.45
BW287	*Early maturity*	*eam7.g*	BC1	63	6	67.9	3H	36.25
BW288		*eam7.g*	BC2	57	2	92.4	6H	47.5
BW284		*eam10.m*	BC4	13	4	13	6H	83.1
BW508		*mat-c.19*	BC5	37	1	43.7	2H	60.95
BW290		*eam8.w*	BC6	6	2	2.2	1H	136.7
BW514		*mat-i.37*	BC6	6	1	4.2	7H	142.3
BW289		*eam8.k*	BC6	8	1	7.9	1H	135.85
BW507		*mat-b.7*	BC6	28	2	11.7	2H	57.65
BW285		*Eam5.x*	BC6	59	1	144.2	5H	89.5
BW282		*Eam1.f*	BC7	3	1	11.8	2H	33.2
BW281		*Eam1.d*	BC8	3	1	0	2H	28.4
BW401	*Eceriferum*	*gsh.bc*	BC2	17	3	42.6	4H	54.7
BW409		*gsh6.s*	BC6	15	2	29.8	3H	135.5
BW114		*cer-c.59*	BC3	32	1	93.9	5H	53.35
BW293	*Ligulum*	*eli-a.216*	BC2	17	3	17.8	3H	132.6
BW301	*Elongated outer glume*	*eog1.d*	BC2	110	6	123	2H	89.9
BW300		*eog1.c*	BC6	29	2	17	2H	66.7
BW299		*eog1.a*	BC6	21	1	18	2H	64
BW307	*Erectoides*	*ert-e.17*	BC6	5	1	6.7	6H	108.95
BW312		*ert-ii.79*	BC6	16	2	42.8	3H	64.6
BW368	*Extra floret*	*flo-b.3*	BC5	16	3	9.2	5H	106.2
BW367		*flo-a.1*	BC6	4	1	15.6	6H	57.2
BW369		*flo-c.5*	BC6	20	1	39.5	6H	62.15
BW375	*Fragile stem*	*fst3.c*	BC5	18	1	10.5	7H	78.25
BW372		*fst1.a*	BC5	8	1	26.7	5H	88.75
BW374		*fst2.b*	BC7	18	3	12.7	1H	53.85
BW376	*Gigas*	*gig.1*	BC2	98	7	111.7	3H	58.15
BW377		*gig.2*	BC5	13	1	29.4	1H	40.8
BW381		*gig1.a*	BC4	23	2	37.7	2H	137.85
BW381		*gig1.a*	BC6	23	2	37.7	2H	137.85
BW382		*gig2.b*	BC7	1	1	0	4H	96.6
BW392	*Globosum*	*glo-a*	BC6	3	1	94.2	4H	55.3
BW431	*Hooded lemma*	*Kap1.a*	BC7	19	1	27.2	4H	42
BW417	*Intense blue aleurone*	*ibl1.a*	inbred	257	7	187.5	5H	95.85
BW430	*Intermedium spike*	*int-m.la*	BC3	53	2	126.9	5H	109.65
BW424		*int-f.19*	BC5	15	2	6.4	2H	55.7
BW427		*int-k.47*	BC6	15	1	17.9	7H	77.45
BW429		*int-m.85*	BC6	5	1	18	5H	170.6
BW420		*int-b.3*	BC6	28	1	47.3	5H	129.85
BW904		*vrs5.n*	BC6	18	1	51.4	2H	74.7
BW425		*int-h.42*	BC6	27	1	56.3	5H	59.15
BW421		*int-c.5*	BC6	8	1	84.2	4H	50.3
BW002	*Laxatum*	*acr.1*	BC3	45	7	73.3	7H	107.75
BW003		*acr.2*	BC5	15	1	17.9	7H	77.45
BW008		*acr.c*	BC5	41	4	41.4	1H	76.2
BW457		*lox-a.8*	BC5	38	1	38.5	5H	46.25
BW439		*lax.ao*	BC6	64	4	85.5	2H	83.65
BW009		*acr1.a*	BC6	69	5	85.5	2H	83.65
BW477	*Leafless*	*lfs2.b*	BC1	99	4	61.7	2H	82.65
BW478	*Leafy bract*	*Lfb1.a*	BC6	2	1	14.8	5H	94.7
BW474	*Leafy lemma*	*lel1.a*	BC3	74	4	89.9	4H	78.35
BW475		*lel2.b*	BC4	24	3	42.9	4H	46.05
BW483	*Liguleless*	*lig1.my*	BC7	6	1	11.3	2H	135.65
BW471	*long basal rachis internode*	*lbi1.a*	BC5	56	2	40.7	1H	67.85
BW472		*lbi2.b*	BC6	2	1	6.6	4H	44.3
BW472		*lbi2.b*	BC6	2	1	6.6	4H	44.3
BW473		*lbi3.c*	BC6	5	1	14.7	7H	79.05
BW518	*Many noded*	*mnd1.a*	BC8	33	2	39.3	7H	141.75
BW636	*Narrow leafed dwarf*	*nld2.b*	BC5	84	3	32.7	5H	52.05
BW530	*Necrotic leaf spot*	*nec3.e*	BC4	3	1	106.1	6H	75.45
BW617		*nec.v*	inbred	1	1	0	2H	39.1
BW616		*nec.j*	inbred	315	7	194	5H	99.1
BW196	*Open crown*	*crown*	BC1	69	7	118.1	6H	62.15
BW640	*Opposite spikelets*	*ops.2*	BC4	13	1	18.9	5H	162.95
BW641		*ops1.3*	BC6	14	1	29.8	7H	14.9
BW765	*Reaction to BYDV*	*Ryd2.b*	BC6	433	7	167	3H	85.8
BW665	*Rough awn*	*raw6.f*	BC7	18	1	10.7	5H	127.35
BW774	*Scirpoides*	*scl.1*	BC3	19	1	47.8	1H	50
BW776		*scl.4*	BC4	7	3	11.7	2H	145.55
BW817	*Semidwarf*	*sdw.q*	BC3	71	6	117.6	2H	97.9
BW414		*Hcm1.a*	BC4	14	2	10	3H	53.6
BW782		*sdw.ad*	BC4	27	4	43.7	2H	60.95
BW787		*sdw.ai*	BC5	27	2	16.7	5H	57.15
BW049		*ari-k.504*	BC4	39	1	89.1	3H	81.75
BW056		*ari-r.14*	BC5	23	1	16.7	5H	57.15
BW057	*Short awn*	*Ari-s.265*	BC6	1	1	0	5H	132.6
BW486		*lks.n*	BC6	51	1	48.4	4H	65.2
BW769		*sca1.a*	BC7	48	1	28.3	3H	61.25
BW492		*lks2.b*	BC8	8	2	15.5	7H	63.35
BW849	*Single elongated internode*	*sid1.a*	BC6	9	1	11.9	4H	61.55
BW850		*sid1.b*	BC7	11	2	82.6	4H	46.9
BW851		*sid1.c*	inbred	233	7	125.3	2H	71.25
BW607	*Six-rowed spike*	*mul2.b*	BC6	3	1	2.1	2H	84.85
BW423		*int-e.58*	BC6	6	1	6.8	3H	40.6
BW401		*int-a.1*	BC6	15	2	21.9	1H	44.55
BW902		*vrs3.f*	BC6	20	2	31.6	1H	39.7
BW903		*vrs4.k*	BC6	13	1	72.3	3H	77.85
BW863	*Slender dwarf*	*sld3.e*	BC6	13	2	22.5	4H	14.95
BW867	*Small lateral spikelet*	*sls1.a*	BC7	5	1	3.4	1H	57.2
BW766	*Subjacent hood*	*sbk1.a*	BC3	8	3	5.3	6H	31.05
BW104		*cal-b.2*	BC3	25	2	16.7	5H	57.15
BW103		*cal-a.1*	BC5	7	2	2.1	5H	2.65
BW105		*Cal-c.15*	BC5	68	2	123.6	5H	110.6
BW767		*sbk1.b*	BC6	2	1	0.7	2H	6.75
BW106		*cal-d.4*	BC6	22	1	65	3H	69.7
BW872	*Subnodal bract*	*snb1.a*	BC1	107	7	101	6H	78.9
BW069	*Third outer glume*	*bra-c.1*	BC4	5	1	4.2	1H	137.7
BW880		*trd1.b*	BC7	4	1	6.6	1H	134.5
BW882	*Tip sterile*	*tst1.c*	BC3	54	3	55	6H	69.9
BW883		*tst2.b*	BC5	5	1	4.9	4H	89.95
BW881	*Triple awned lemma*	*trp1.a*	BC2	25	1	29.7	4H	54.65
BW041	*Unbranched style*	*ari-d.15*	BC7	9	2	8.2	7H	106.9
BW211	*Uniculm*	*cul4.3*	BC3	25	1	84.4	3H	131

Crosses that have been made using Bowman NILs (black and blue letters). 'BwMxBk' - Bowman lines that have been crossed to Bowman, Morex and Barke. Heatmap and the table on the right shows genotyping and mapping information for the Bowman lines that are in black. The color of the cell background varies from black-to-bright-to-white. Black - high BC levels, low values of the SNP count and low introgression number and size. Blue bright colour depicts the backcross levels, red SNP frequency, green number of introgressions, and yellow the introgression size.

acknowledgements

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