

# ZERGATIK EZ NUEN DIBULGATZEN

ETA ORAIN DIBULGAZIOAREN ASTUN BAT NAIZEN



**Koldo Garcia**

@koldotxu

#daitort bateria gabe gelditu naizela  
#ZientziazaleTopa txiokatzen ta aurkezpena  
moldatuko dudala gaurkoaz hausnartzeko  
#anitza #ui44

17:26 - 2016 uzt. 11

**BEREHALAKOTASUNEAN BIZI GARA**

**PROBESTU!**



Unibertsitatea net

Sarrera Ziztu bizian Blogak Ikasleen txokoa Otarrea Zer, non ikasi Txiotesia

Ingumak Laborategian **bloga**

Hasiara

← Aurrekoa Hurrengoa →

**Zientziaren dibulgazioa: esadazu dakizuna.**  
**Publish and market or perish**

2013/09/09-n Uxune Martinez-kargitaratuta



**Edonola**  
 IRAKURRIZ. IKUSIZ. DASTATUZ.



**Zergatik ez dut dibulgatzen?**

**Uxune**

Gogoz irakurri dut zure hausnarketa Koldo! Alpatzen dituzun hainbat arrazoi erreplikatu egiten dira ezagutzen ditudan ikerlari askoren ahotan: denbora, formaziorik ez, eginkizunetik at. Egia da.

Hala ere, gaur idatzi duzun hau bada lehen pausu bat. Horrela ikusten dit neuk behintzat.

Zure zalantzak eta galderek erantzuna dute (nire ustez). Foruari dagokionez, erabiltzen dituzun blog hau eta twitter iturri egokiak dira. Interesa, jendearen interesari dagokionez, ez badiguzu ezer esaten, nola jakin interesa dugun ala ez? 🤔

Eta zure, hitzak erabiliz! \^zientzia sukaldatzea bezala da: bakoitzak bere likutua ematen dio eta etxean maitasunez egina eta familia eta lagukin partekatuta zapora hobe du! Maitasunez egin eta etxean partekatzen duzun hori, partekatu gurekin ere... guk ere dastatu nahi dugu eta!

👉 ERANTZUN 📅 2013-09-10 AT 18:23

**Txoni Matxain**

Oso interesgarria, Koldo, botatzen dituzun hausnarketak. Bost arrazoi ematen dituzu, zergatik ez duzun gehiago dibulgatzen azaltzeko. Bai, gehiago diot, zeren eta artikulu hau dibulgazioari buruzkoa da, eta hortaz, zerbait idatzi duzu horren inguruan.

ORAIN DELA 3 URTE...

# 5 arrazoi

- \* Zailtasuna
- \* Denbora
- \* Foroa
- \* Interesa
- \* Formazioa



**Edonola**

IRAKURRIZ. IKUSIZ. DASTATUZ.



## Zergatik dibulgatzen dut?

Orain dela urtebete zergatik dibulgatzen ez nuen azaltzen saiatu **nintzen** . Orduetik blog honetan 52 sarrera idatzi ditut zientzia edo zientziarekin lotutako gaiak jorratuz, Ekaian artikulu bat **argitaratu** , Euskalnaturen erreportaje bat **idatzi** eta **#txiotesia** n **#kafepintxo** ekin zein ondo ikertzen den kontatu **dut** . Eta agertzeke daudenak. Zer dela eta aldaketa hau? Ezer ez kontatzenetik ia astero txapa ematera. Zer aldatu da?

**URTEBETERA...**

# 5 arrazoi

- \* ~~Zailtasuna~~. Trebezia irabazi
- \* ~~Denbora~~. Inbertsio bat da
- \* ~~Foroa~~. Gero eta plaza gehiago
- \* ~~Interesa~~. Zientziazaleak egon badaude
- \* ~~Formazioa~~. Idearik ez



# Zer gertatu da?

- \* Eroso nago
- \* Nire estiloa aurkitu dut
- \* Jende bikaina ezagutu dut
- \* Onuragarria da



**#KAFEPINTXO BATEKIN ZIENTZIA EGITEN**

ESTILOA





**#TXIOTESIA #WOLFRAMDEUNA**

JENDEA



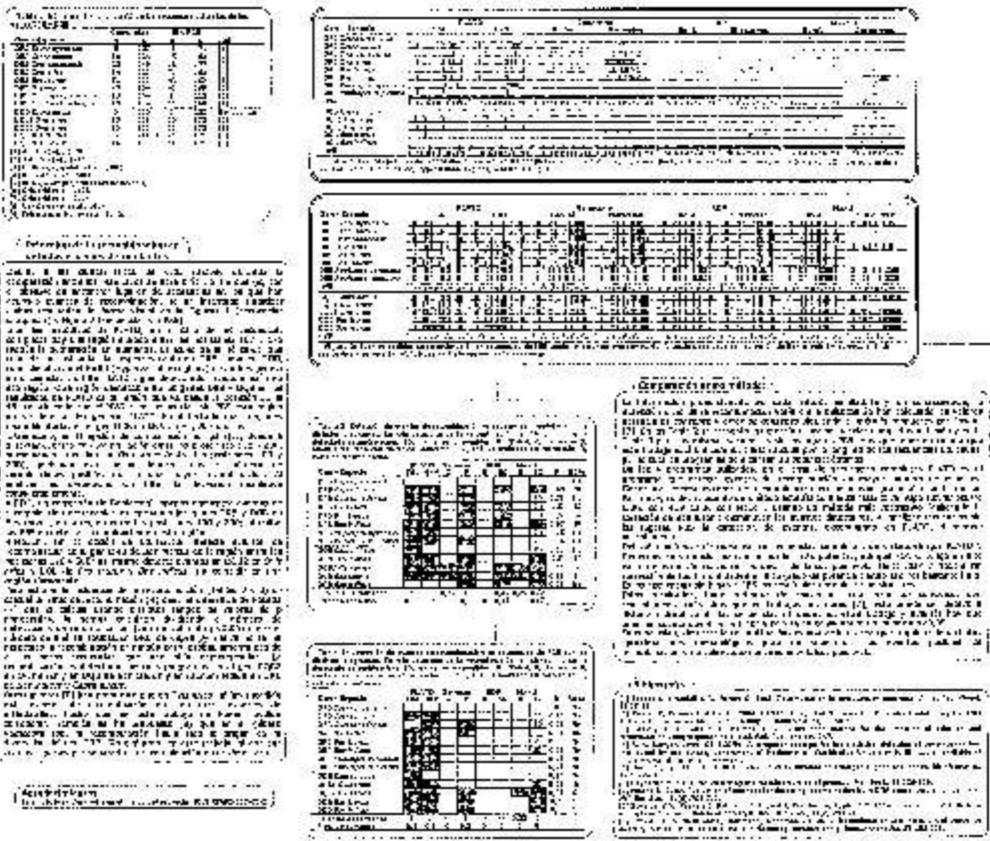
# Detección de recombinación en genes de clase II DRB y DQB del Complejo Principal de Histocompatibilidad (MHC) en rumiantes: comparación de métodos



García-Etxebarria, K. Jugo, B. M.

Genética, Antropología y Etología Animal, Facultad de Veterinaria, Universidad del País Vasco (UPV-EHU)

**Resumen:** El Complejo Principal de Histocompatibilidad (MHC) es una región genética altamente polimórfica que codifica proteínas que participan en la respuesta inmunitaria. En rumiantes, el MHC es crucial para la resistencia a enfermedades infecciosas. Este estudio compara dos métodos para detectar recombinación en los genes de clase II DRB y DQB del MHC en rumiantes. El primer método es el análisis de haplotipos, que implica la identificación de combinaciones únicas de alelos. El segundo método es el análisis de recombinación, que busca puntos de ruptura en la secuencia genética. Los resultados muestran que ambos métodos son efectivos para detectar recombinación, pero el análisis de recombinación proporciona información más detallada sobre la estructura genética del MHC. Este estudio contribuye a comprender mejor la diversidad genética y la evolución del MHC en rumiantes.



# Ancestry-based stratified analysis of Immuchip data identifies novel associations with celiac disease

Koldo García-Etxebarria<sup>1</sup>, Amaia Jauregi-Miguel<sup>1</sup>, Irati Romero-Garmendia<sup>1</sup>, Leticia Plaza-Izurrieta<sup>1</sup>, María Legarda<sup>2</sup>, Iñaki Irastorza<sup>2</sup>, Jose Ramon Bilbao<sup>1</sup>

<sup>1</sup>University of the Basque Country (UPV-EHU) & BioCruces Health Research Institute; <sup>2</sup>Cruces University Hospital  
e-mail: koldo.garcia@ehu.es

## Background

- Celiac disease (CD) is an autoimmune disease that is developed in the presence of gliadin in the diet.
- It is a complex genetic disease whose 40% of genetic component is known.
- Immunchip analysis was made using geographical origin as covariant.
- It is difficult to conciliate association results and expression analyses in CD.

## Material and methods

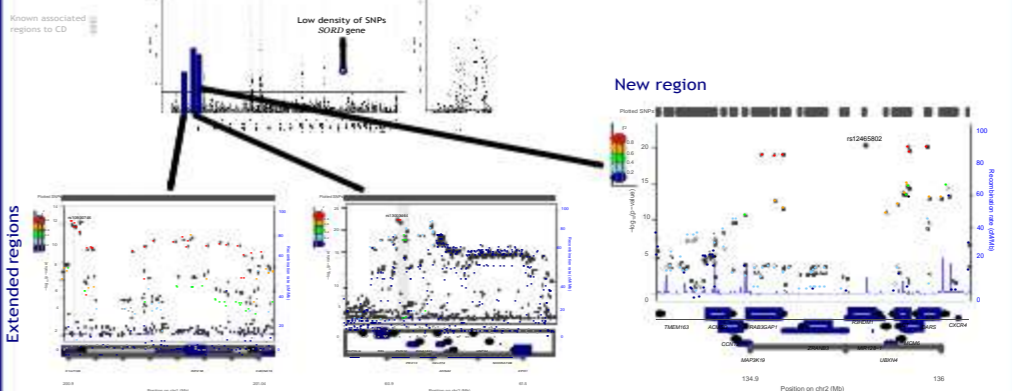
- Stratification analysis (discovery)**
- 12041 cases from Wellcome Trust
  - 12228 controls Case-Control Consortium.
  - 139553 SNPs from the Immunchip microarray.
  - Clustering of individual: Plink&Admixture
  - Stratified association analysis: Plink
- Expression analysis (validation)**
- Biopsies of 15 Active CD, 15 Treated CD and 15 controls
  - Expression of selected genes using Fluidigm

## What if there is a stronger stratification independent from geographical origin?

## Main findings

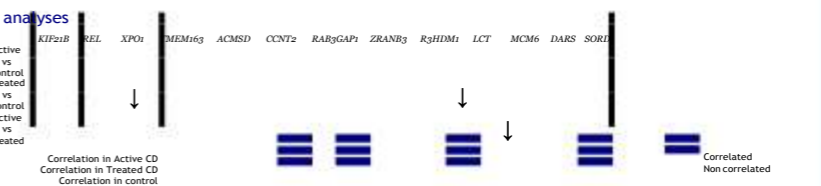
### Stratified association analysis

- 30 groups based on their ancestry



### Differential expression analyses

- ↑ Overexpressed
- ↓ Underexpressed



- New region associated to CD
- 2 known regions extended
- 9 out 13 analysed genes have differential expression in CD

**Acknowledgements**  
This work was funded by Research Project grants from the Spanish Ministry of Science and Innovation (12/1101) and Basque Department of Health (201111034).  
A.J.M. and I.R.G. are supported by grants from UPV/EHU and GV/EJ.  
This study makes use of data generated by the Wellcome Trust Case-Control Consortium. A full list of the investigators who contributed to the generation of the data is available from www.wtccc.org.uk. Funding for the project was provided by the Wellcome Trust under award 076113, 080675 and 090355.

Stratified analysis based on the ancestry is a useful tool to find new functional candidates in complex diseases



# Evolutionary history of bovine endogenous retroviruses in the Bovidae family

Koldo Garcia-Etxebarria & Begoña M. Jugo

Genetika, Antropologia Fisikoa eta Animalien Fisiologia Saila. Zientzia eta Teknologia Fakultatea. Euskal Herriko Unibertsitatea (UPV/EHU), 644 Postakutza, E-48080 Bilbao  
Contact e-mail: koldo.garcia@ehu.es



## Previously...

Endogenous retroviruses (ERV): remains of exogenous retroviruses that become incorporated into host genome.



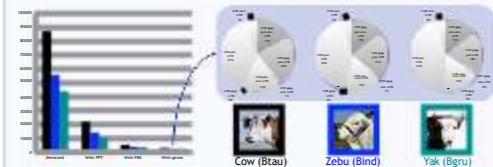
Genome-Wide Detection and Characterization of Endogenous Retroviruses in *Bos taurus*<sup>a</sup>

24 families (groups of copies from precursor infection) of bovine ERVs detected in cow.

Are present these families of bovine ERVs in other *Bos* species (zebu and yak)? And in other ruminants?

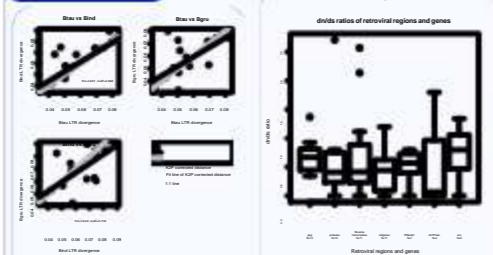
## Detection of ERVs in *Bos* genus

Detection of ERVs using LTRharvest & LTRdigest.



- More ERVs detected in cow using new methods.
- More ERVs detected in cow than zebu and yak, maybe due to better assembly or more retroviral infections.

## Clustered ERVs



Doubts in the use of LTR divergence to estimate the insertion time due to the break of molecular clock.

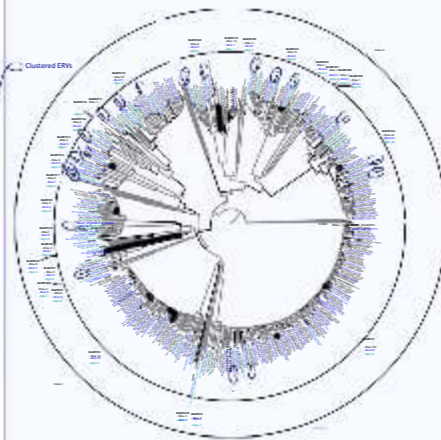
dn/ds < 1 in most genes. Purifying selection acting in retroviral genes. Reservoir for co-option?

- New methods allow the discovery of new bovine families.
- Most bovine ERV families are present in other species of ruminants.

More information: Koldo Garcia-Etxebarria, Begoña M Jugo. 2013. Evolutionary history of bovine endogenous retroviruses in the Bovidae family. BMC Evolutionary Biology. In press.  
Acknowledgements: K.G.-E. is funded by UPV/EHU (Vice-Rectorate of Research, "Specialization of

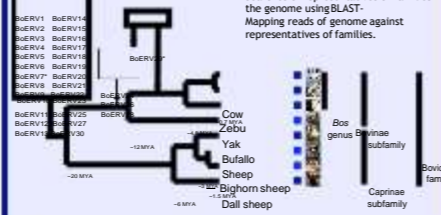
## Phylogenetic relationship of ERVs

Search of pol sequences using BLAST. Alignment using MAFFT. Neighbor-joining tree (p-distance, 1000 bootstrap).



- Previously known 24 ERV families present in *Bos* genus.
- 6 new ERV families. 3 of Class II, active in mammals?

## Other ruminants



- Most families (26/30) detected in (almost) all ruminants.
- boERV24/26/28 specific of Bovinae subfamily.
- boERV29 specific of Bosgenus?

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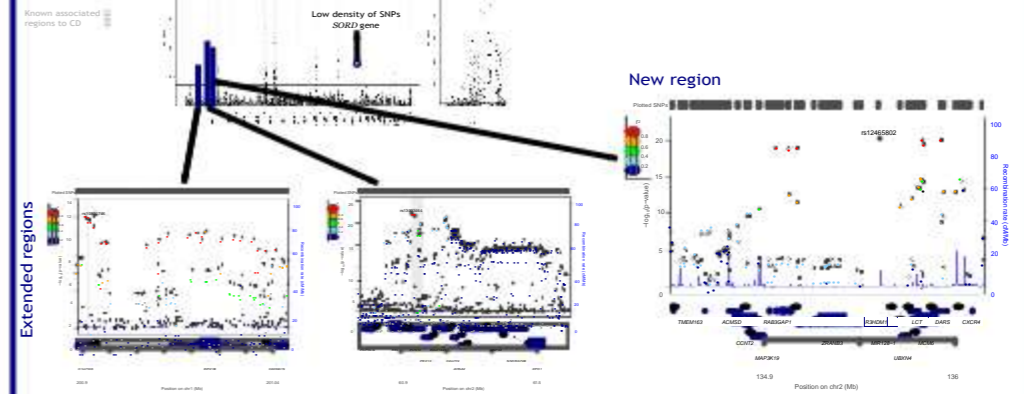
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## Stratified analysis based on the ancestry

is a useful tool to find new functional candidates in complex diseases



# Txiripaz!

- \* Zoria
- \* (Balía)bideen gida behar dugu!
  - \* Atomizatua/sare isolatuak
  - \* Ikusgarritasuna
- \* Militantea baina eskertua



EUSKARAZKO ZIENTZIA

- Tesu euskaratu ✓
- Ekuazio ✓
- Kolore Nitulatu ✓
- Sozia ✓
- Zientzia - kateia ✓
- Luluosatu ✓
- Zientzia, atelea ✓
- Zientzalaria ✓

- Trioksinu bitleri ✓
- Trioksinu epuratu ✓
- Itengaitza ✓
- Udale kurtisa

- COF - Elhuyon Sozia
- Alvia karia ✓
- Woffman deuna ✓
- Norokoa ✓
- Telenopolis ✓

- k7 daia orziti ✓
- Di2lyso 300 ✓
- Medoelun
- Zago ✓
- Bilbohiu ✓

BALIABIDE BATZUK

IA DENETARIK EGIN OSTEAN...

**BAI!**



# BAI!

(Beno, ez beti...)





# PERTSONA ARRUNTAK GARA

EZ IZAN BELDURRIK GAUZAK DIREN BEZALA AZALTZEKO



# Nola?

- \* Norberak bere estiloa dauka
- \* Ahal den neurrian
- \* Gozaten baduzu hori transmitituko duzu
  - \* ZIENTZIAZ MAITEMINDUTA GAUDE!!!!



# Aukeren leihoa

- \* Masa kritikoa dago
- \* #KZJaia3 (3 hilabete): 144 ekarpen
- \* #Dazientziat (15 hilabete)
  - \* 2745 txio
  - \* 278 txiolari
  - \* 1456 esteka



# Baina...

- \* Profesionalak behar ditugu
- \* Ezin daiteke (bakarrik) borondate onean oinarritu





# ZIENTZIA JALGI HADI PLAZARA!

(EUSKAL) ZIENTZIAZALETASUA INDARTU INGURUAN ERAGINDA