

EL PODOCITO

HERNÁN TRIMARCHI

**HOSPITAL BRITÁNICO DE BUENOS AIRES
ARGENTINA**

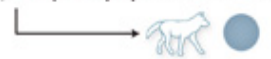
2015

Peak Fitz Roy & Cerro Torre Santa Cruz Argentina





Mammals
5,600 species estimated
5,501 (98%) species discovered



Birds
10,500
10,064 (96%)



Reptiles
12,000
9,547 (80%)



Amphibians
15,000
6,771 (45%)



Fish
45,000
32,400 (72%)



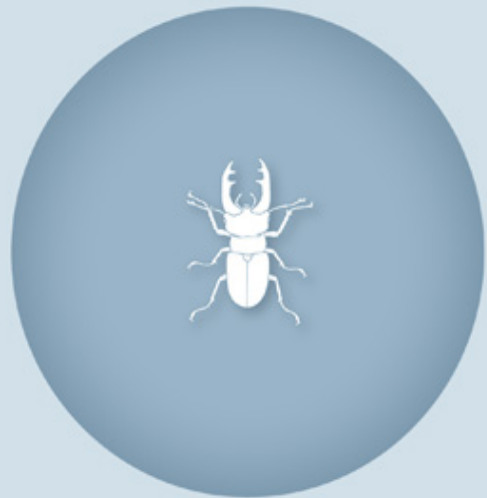
Crustaceans
150,000
47,000 (31%)



Mollusks
200,000
85,000 (43%)



Arachnids
600,000
102,248 (17%)



Insects
5,000,000
1,000,000 (20%)

REVIEW

Between a chicken and a grape: estimating the number of human genes

Mihaela Pertea and Steven L Salzberg*

Abstract

Many people expected the question 'How many genes in the human genome?' to be resolved with the publication of the genome sequence in 2001, but estimates continue to fluctuate.

Ever since the discovery of the genetic code, scientists have been trying to catalog all the genes in the human genome. Over the years, the best estimate of the number of human genes has grown steadily smaller, but we still do not have an accurate count. Here we review the history of efforts to establish the human gene count and present the current best estimates.

The first attempt to estimate the number of genes in the human genome appeared more than 45 years ago, while the genetic code was still being deciphered. Friedrich Vogel published his 'preliminary estimate' in 1964 [1], based on the number of amino acids in the alpha- and beta-chains of hemoglobin (141 and 146, respectively). Knowing that three nucleotides corresponded to each amino acid, he extrapolated to compute the molecular weight of the DNA comprising these genes. He then made several assumptions in order to produce his estimate: that these proteins were typical in size (they are actually smaller than average); that nucleotide sequences were uninterrupted on the chromosomes (introns were discovered more than 10 years later [2,3]); and that the entire genome was protein coding. All these assumptions were reasonable at the time, but later discoveries would reveal that none of them was correct. Vogel then used the molecular weight of the human haploid chromosomes to correctly calculate the genome size as 3×10^9 nucleotides, and dividing that by the size of a 'typical' gene, came up with an estimate of 6.7 million genes.

Even at the time, Vogel found this number 'disturbingly high', but no one suspected in 1964 that most human genes were interrupted by multiple introns, nor did anyone know that vast regions of the human genome would turn out to contain seemingly meaningless repetitive sequences. Since Vogel's initial attempt, many scientists have tried to estimate the number of genes in the human genome, using increasingly sophisticated molecular tools. Over the years, the number has gradually come down, in a process that has been humbling at times, as we realized that many other species - even plants - are predicted to have more genes than we do (Figure 1). An estimate of 100,000 genes appeared in the 1990 joint National Institutes of Health (NIH)/Department of Energy (DOE) report on the Human Genome Project [4]; this was apparently based on a very rough (and incorrect) calculation that typical human genes are 30,000 bases long, and that genes cover the entire 3-gigabase genome.

Many people, including many geneticists, expected that we would have a definitive gene count when the human genome was finally completed, and indeed one of the main surprises upon the initial publication of the human genome in February 2001 [5,6] was that the number had again dropped, quite precipitously. However, as we shall see, the publication of the human genome did not come anywhere close to producing a precise gene list or even a gene count, and in the years since the number has continued to fluctuate. As a result, even today's best estimates still have a large amount of uncertainty associated with them.

In order to count genes, we need to define what we mean by a 'gene', a term whose meaning has changed dramatically over the past century. For our discussion, we will restrict the definition of gene to a region of the genome that is transcribed into messenger RNA and translated into one or more proteins. When multiple proteins are translated from the same region due to alternative mRNA splicing, we will consider this collection of alternative isoforms to be a single gene. In this respect, our definition of a gene is equivalent to what may also be called a chromosomal locus. We will exclude non-protein-coding RNA genes (such as microRNAs (miRNAs) and small nuclear RNAs (snRNAs)), in part

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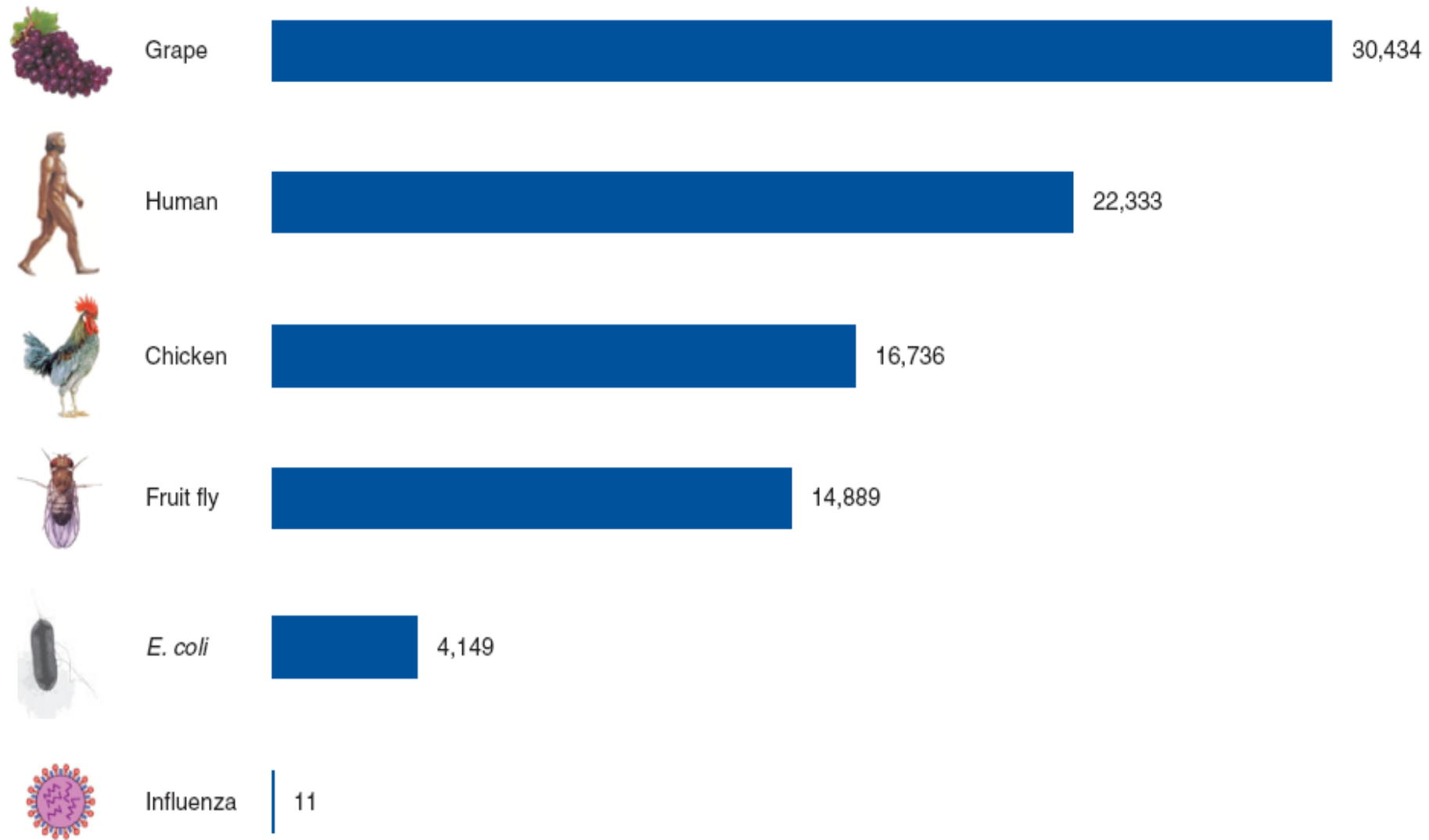


Figure 1. Gene counts in a variety of species. Viruses, the simplest living entities, have only a handful of genes but are exquisitely well adapted to their environments. Bacteria such as *Escherichia coli* have a few thousand genes, and multicellular plants and animals have two to ten times more. Beyond these simple divisions, the number of genes in a species bears little relation to its size or to intuitive measures of complexity. The chicken and grape gene counts shown here are based on draft genomes [50,51] and may be revised substantially in the future.

Fruit Fly
44%



Mouse
92%



85%

Yeast
26%



24%

Chimp
98%

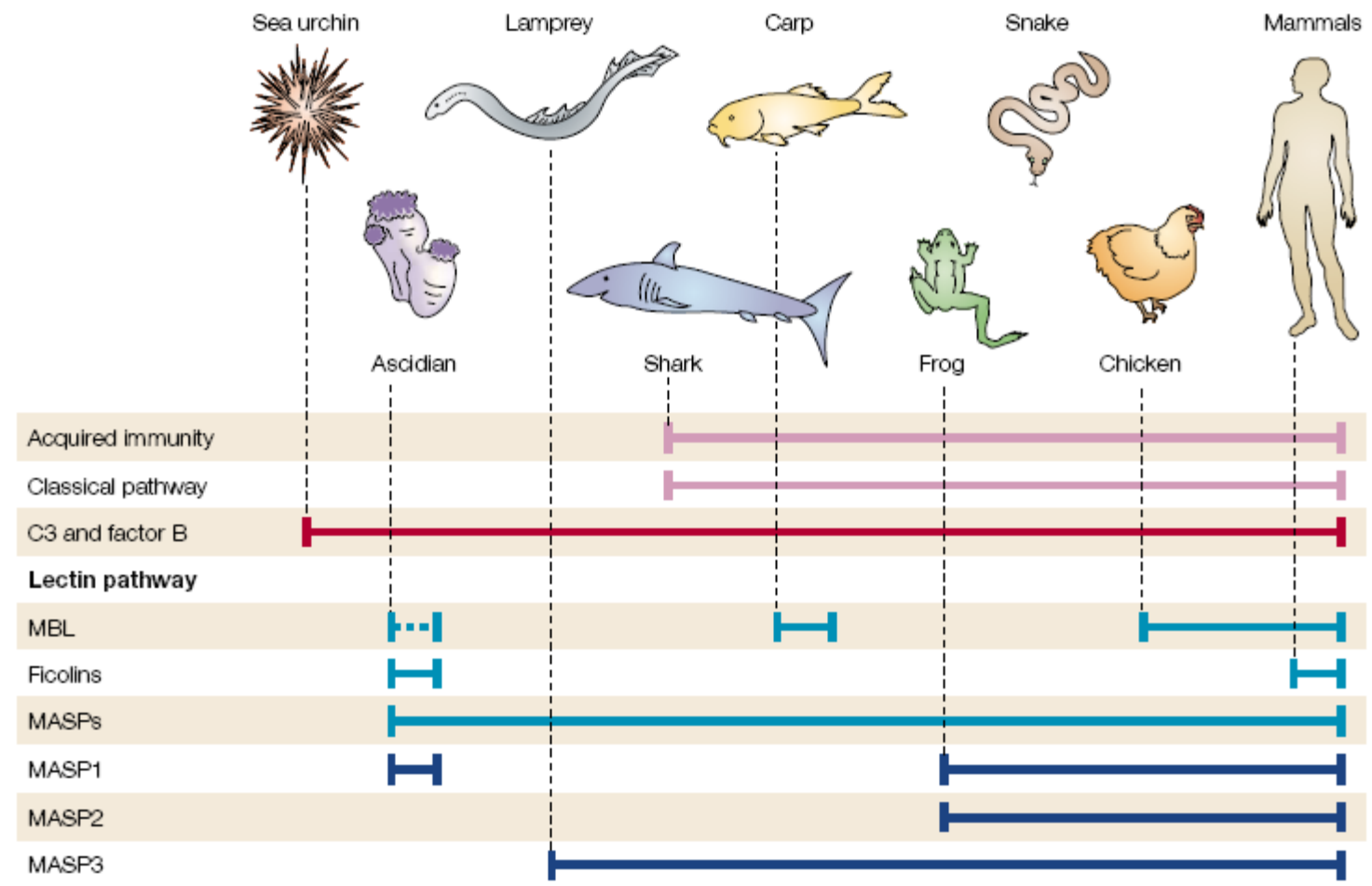


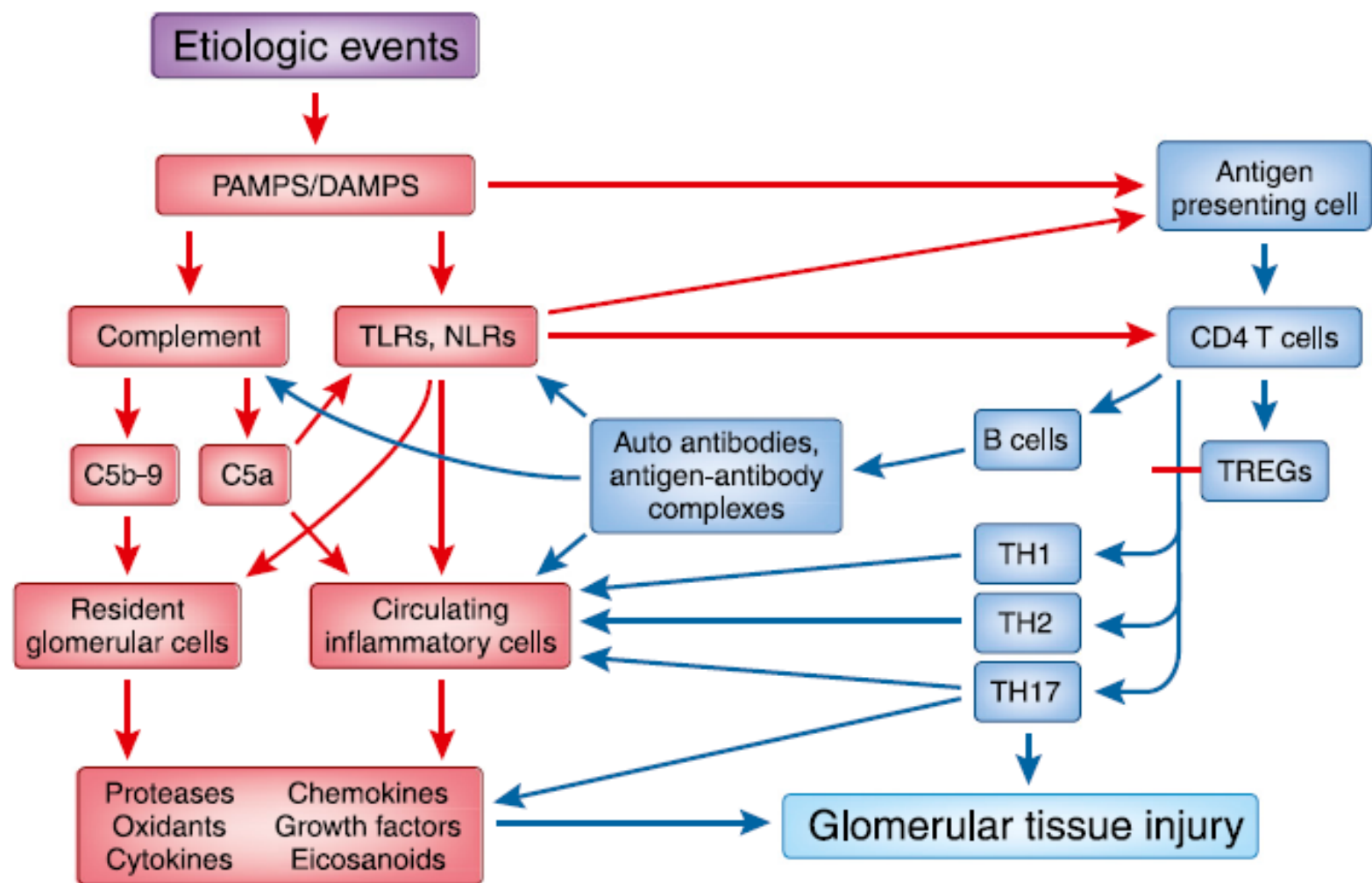
47%

Plant
18%



**What percent
of your genes
do you share?**



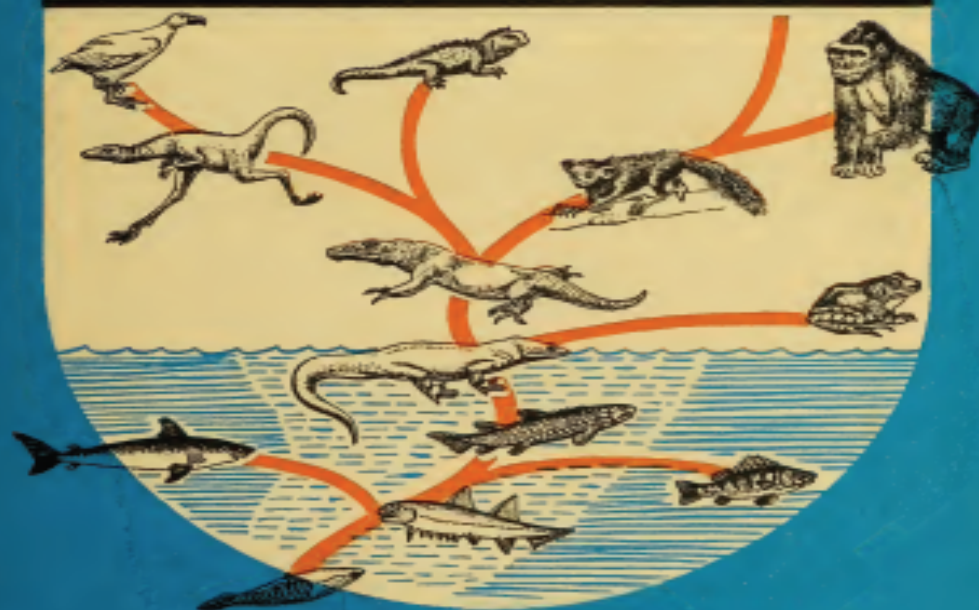


The Natural History Library

\$1.45
N10

From Fish to Philosopher

HOMER W. SMITH



A Doubleday Anchor Book

The American Museum of Natural History

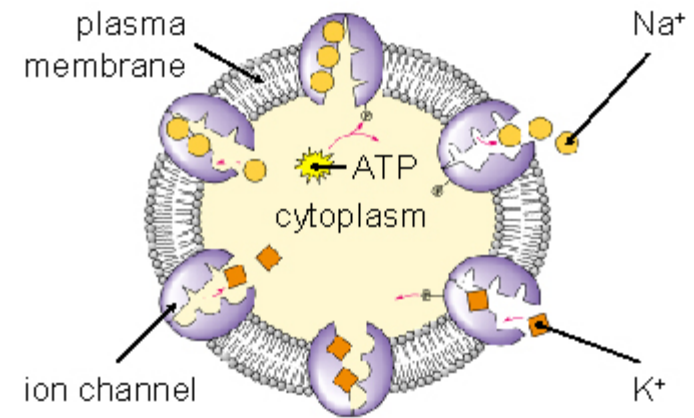
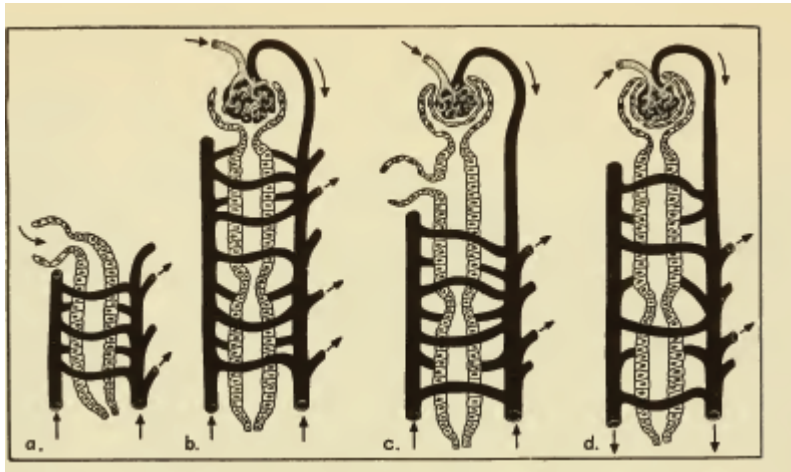


FIGURE 5. Four Stages in the Evolution of the Vertebrate Nephron—(a) In the protovertebrate the renal tubule drained the coelom or body cavity by means of an open mouth or coelomostome. (b) The glomerulus was evolved in the earliest vertebrates as a device to excrete water, and was at first only loosely related to the coelomostome. (c) Later the glomerulus became sealed within the end of the tubule, the coelomostome persisting in some species. (d) In the higher vertebrates, the coelomostome has disappeared entirely, leaving the typical vertebrate nephron. The primitive blood supply to the protovertebrate tubule persists as the “renal-portal system” in the fishes, Amphibia, reptiles and birds (a to c), but disappears in the mammals (d), leaving the tubules supplied only by post-glomerular blood.

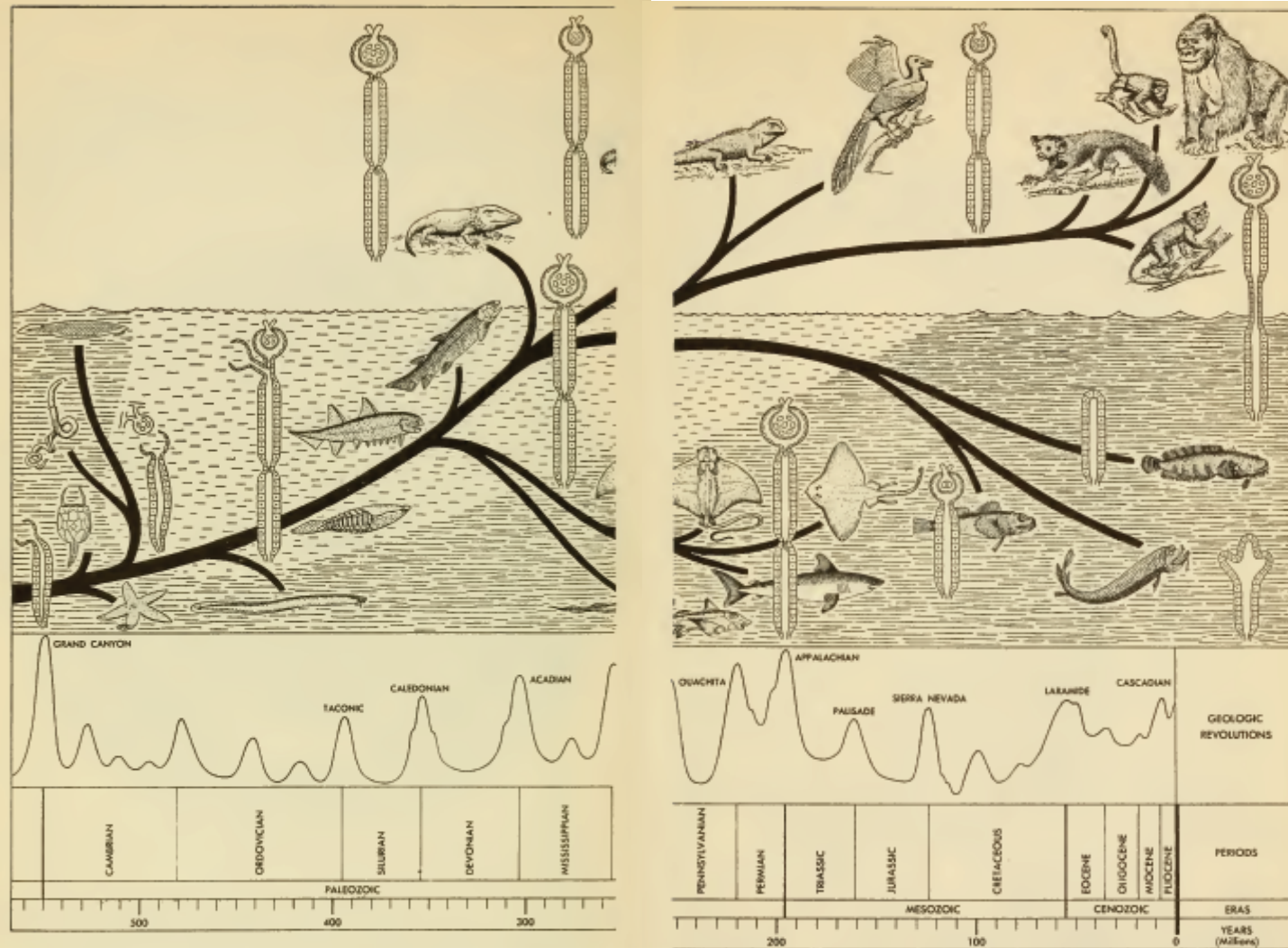


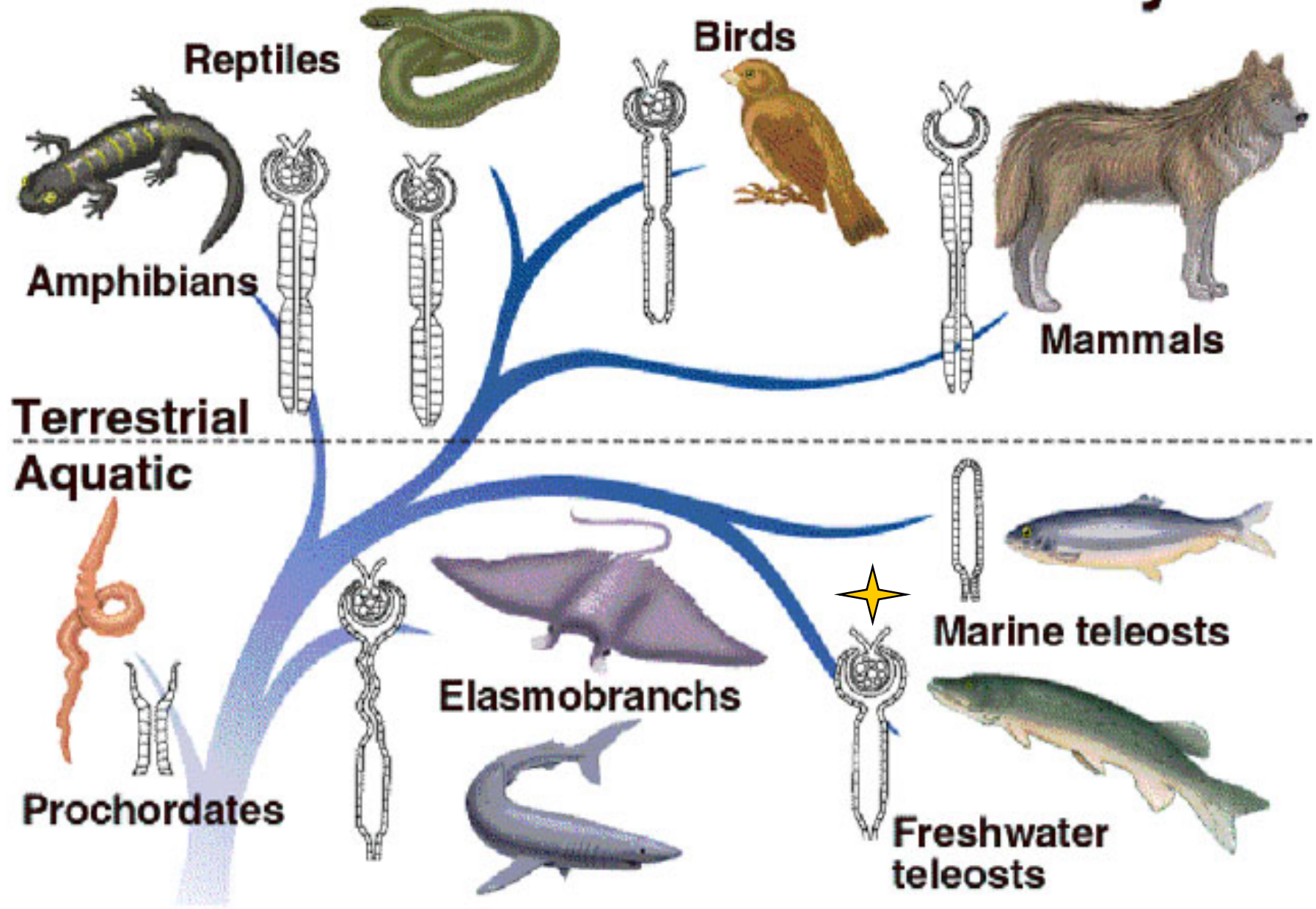
FIGURE 2. Synopsis of the Evolution of Vertebrates—showing the evolution of the vertebrates in relation to a salt-water (darkly shaded) and fresh-water (lightly shaded) habitat. The irregular curve illustrates mountain-building episodes (geologic revolutions) which have importantly influenced this evolutionary history.

The time scale is such that the Pleistocene era (one million years in length) and Recent Time (about twenty-five thousand

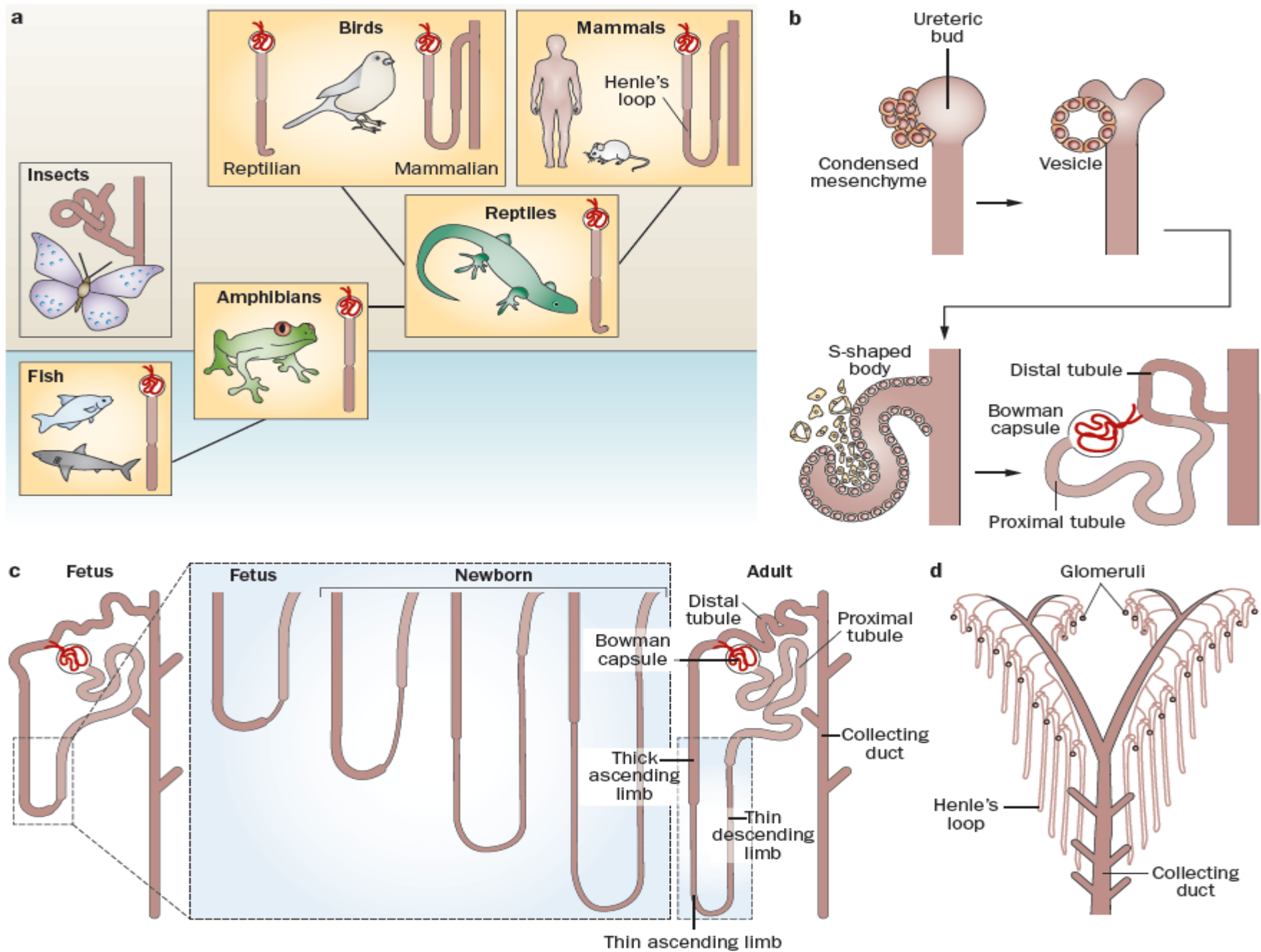
years) could not be included, and these are merely suggested by the heavy line at zero time.

The entire period encompassed by documented history is only about six thousand years, or one hundred-thousandth of the interval elapsing since the opening of the Paleozoic era (Cambrian period), when fossilized animals first begin to appear in the sedimentary rocks.

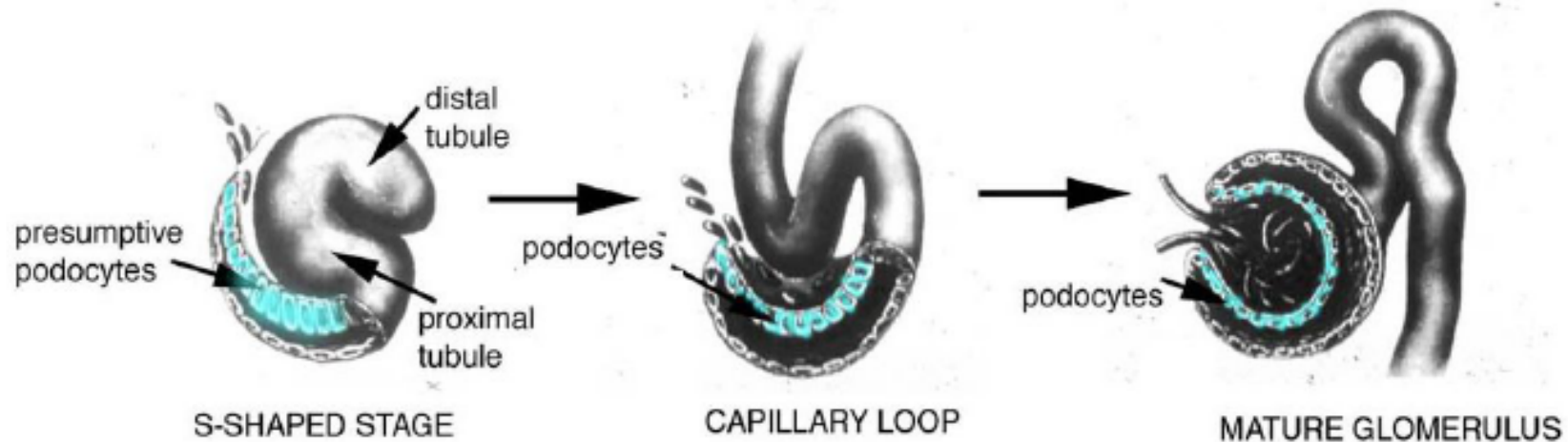
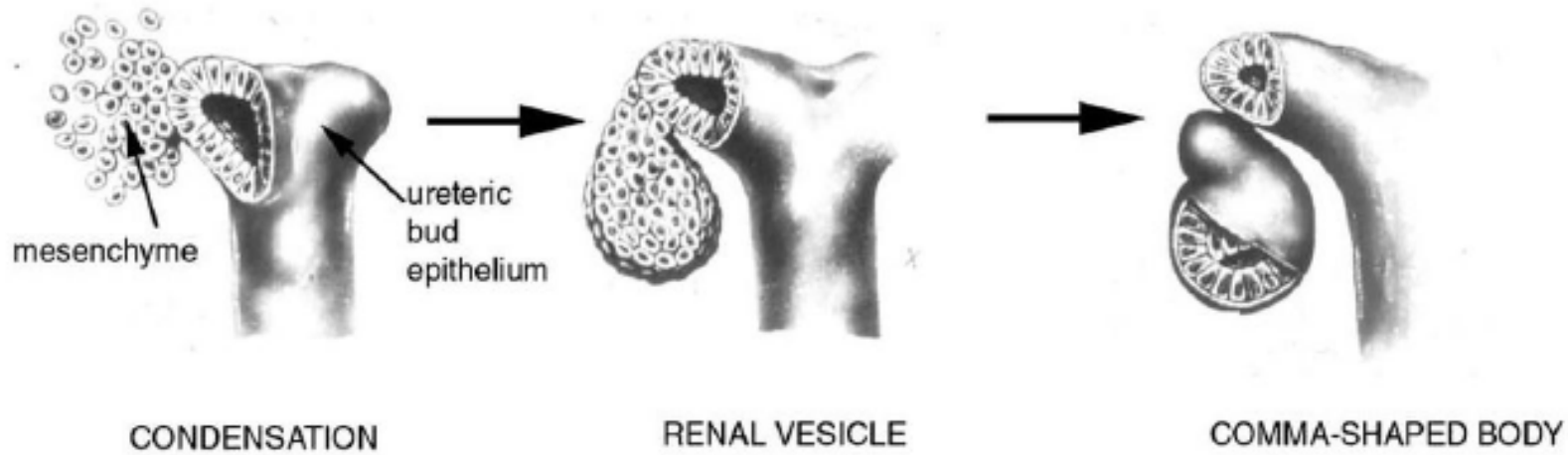
Evolution of Vertebrate Kidneys

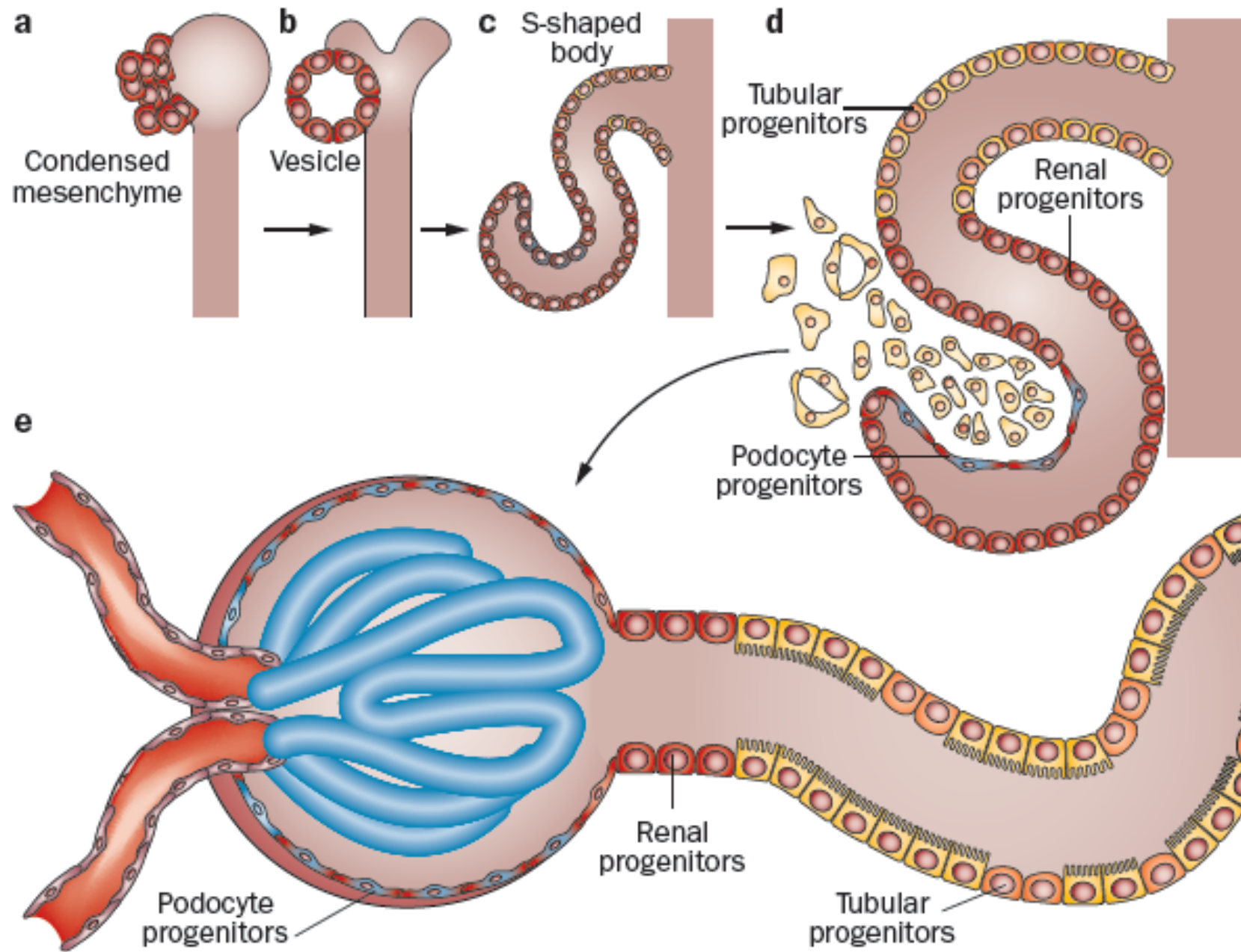


teleostos de agua dulce

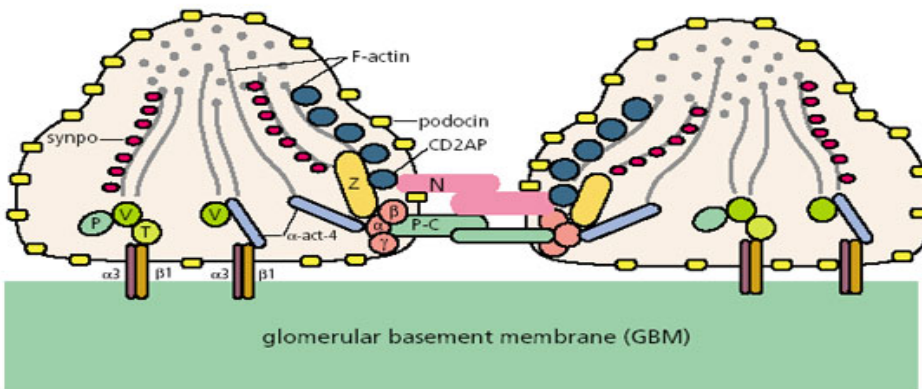
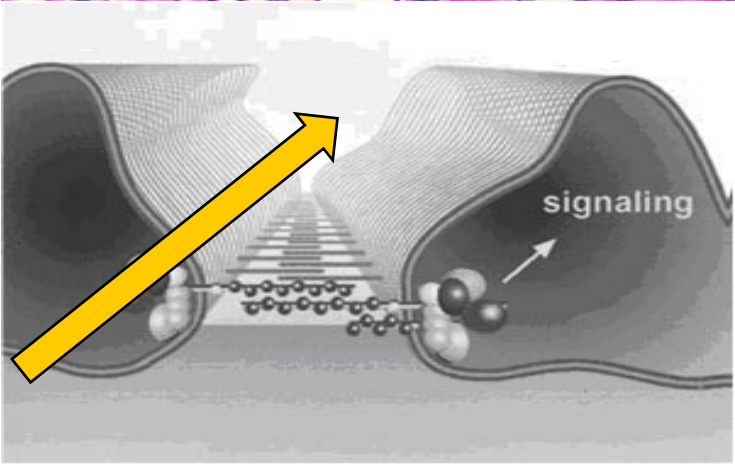
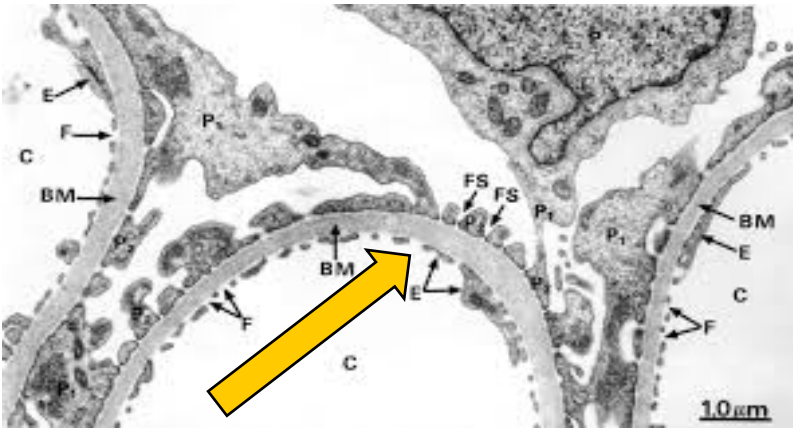
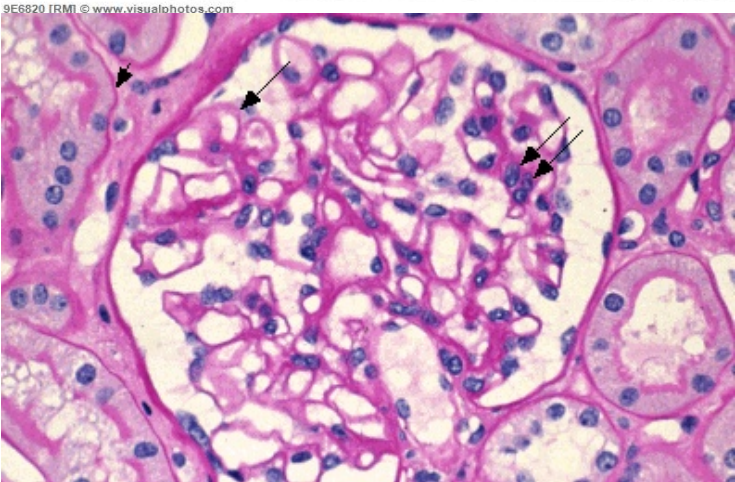
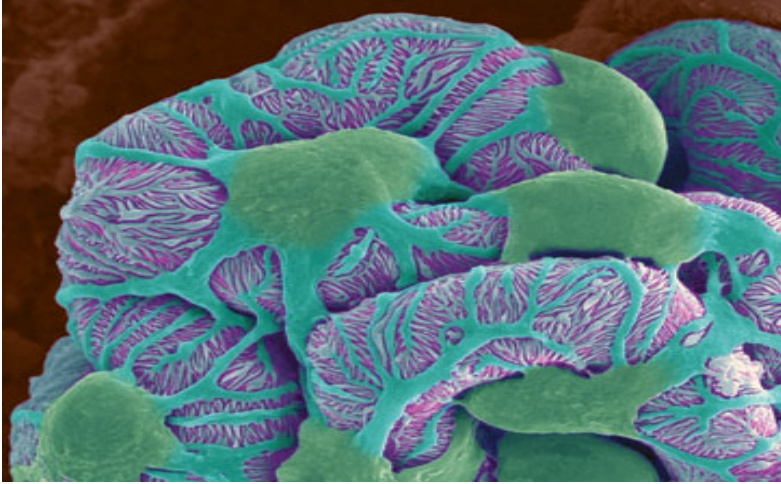


Development of the glomerular tuft

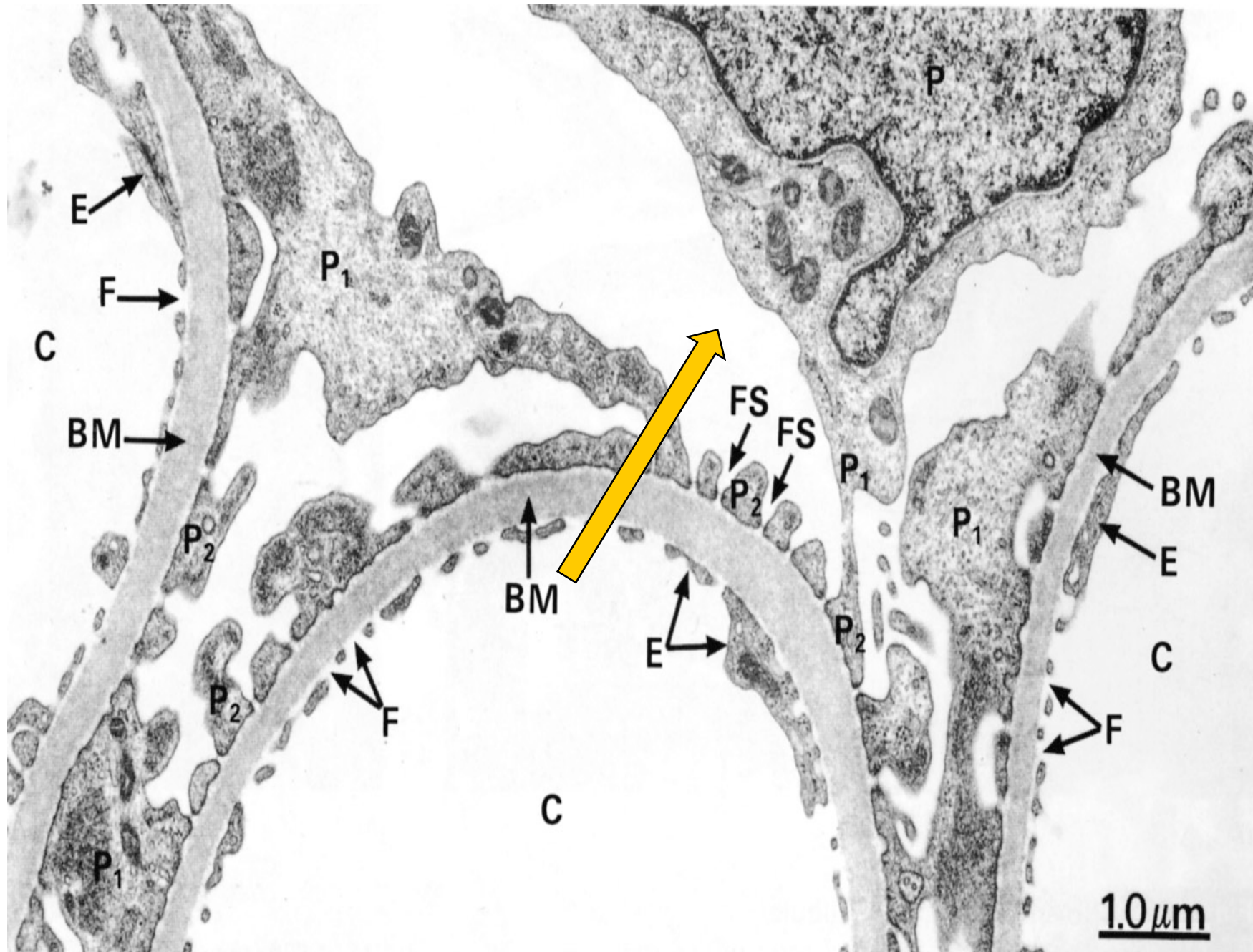


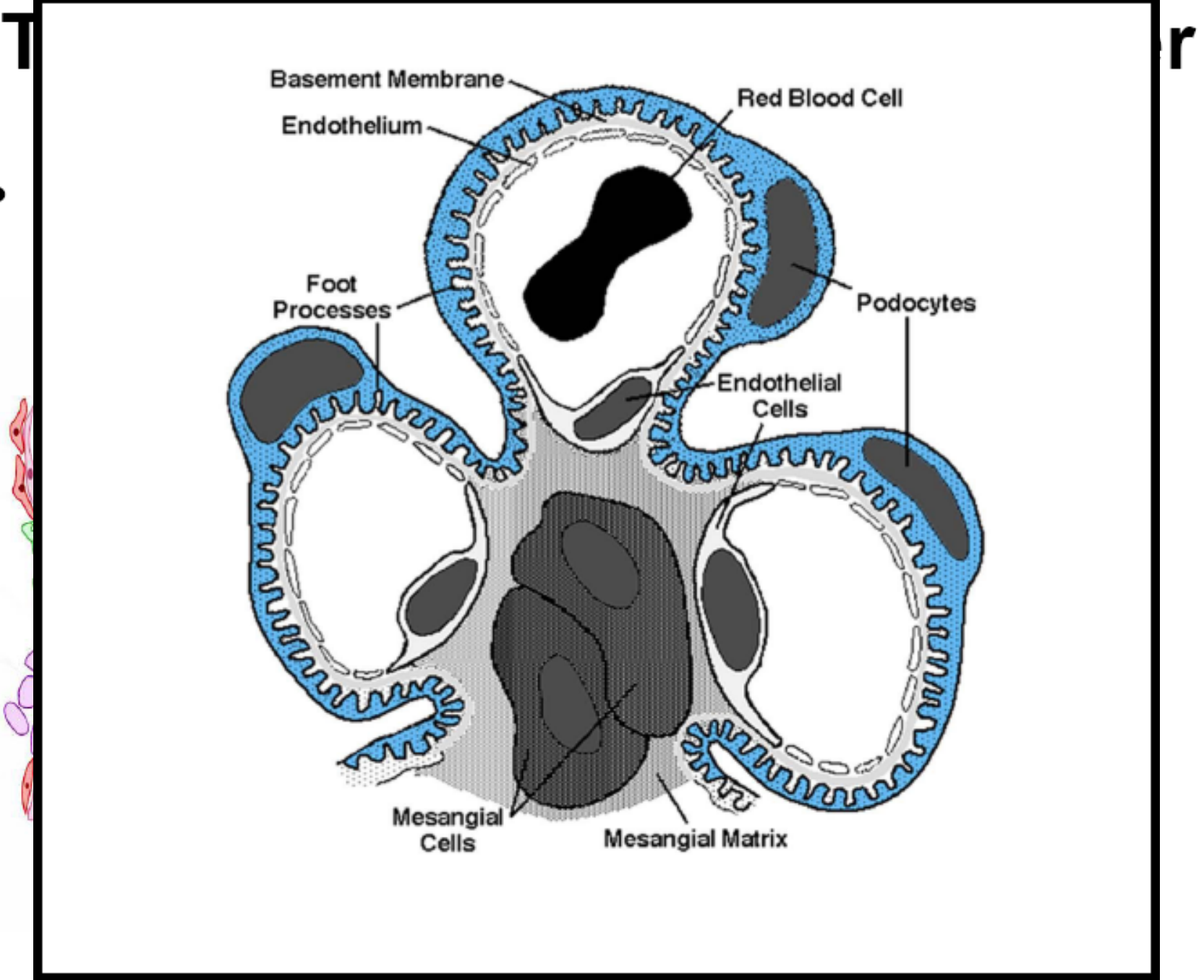


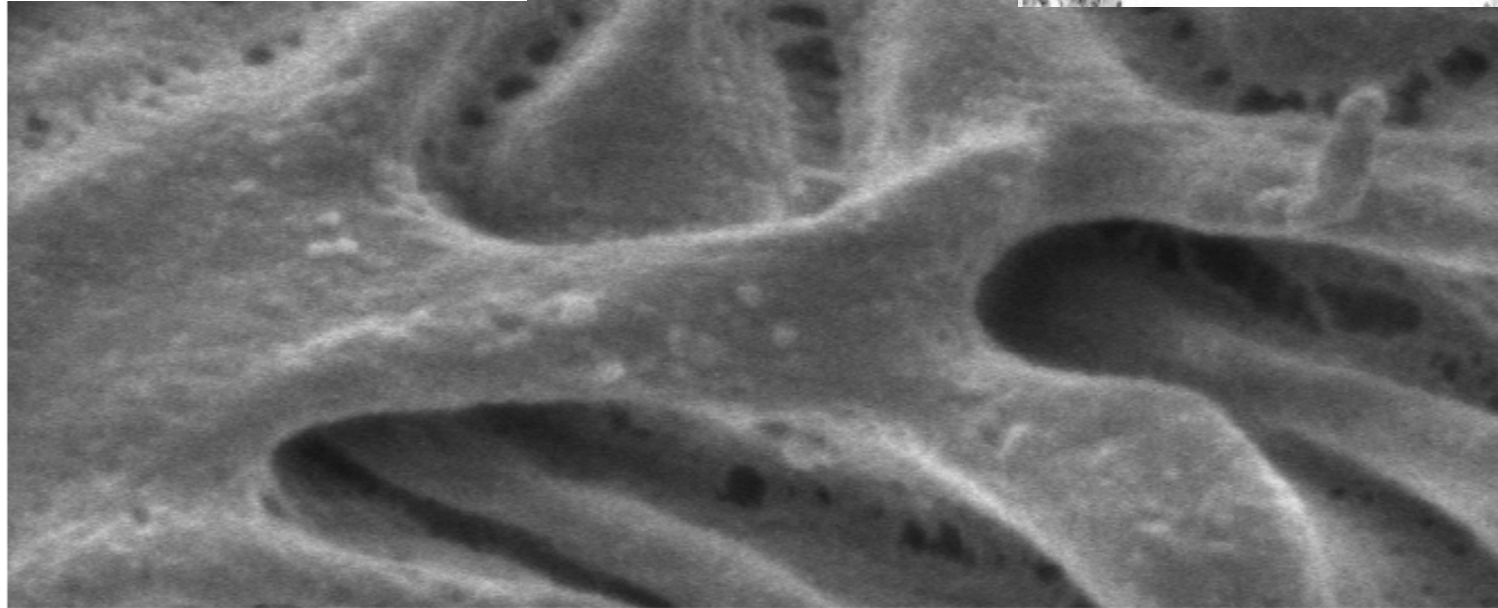
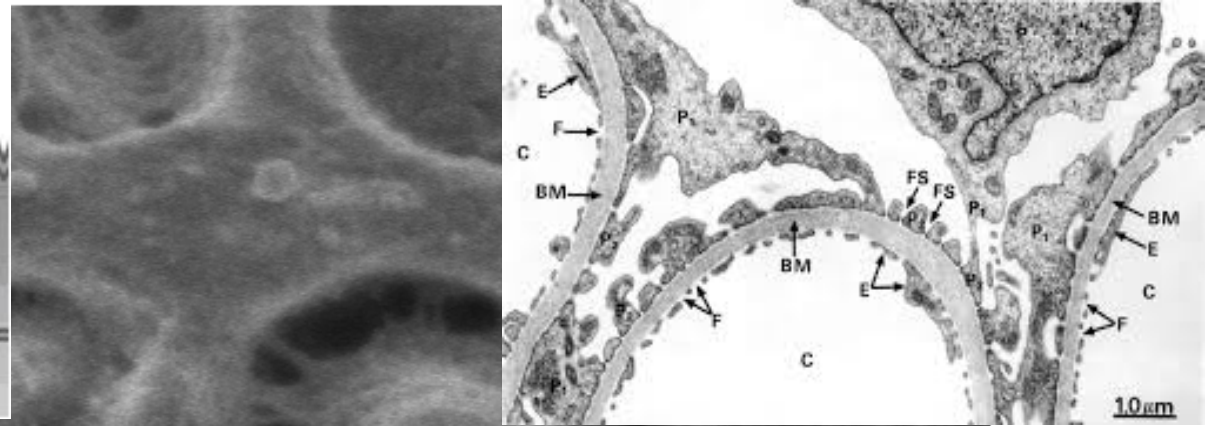
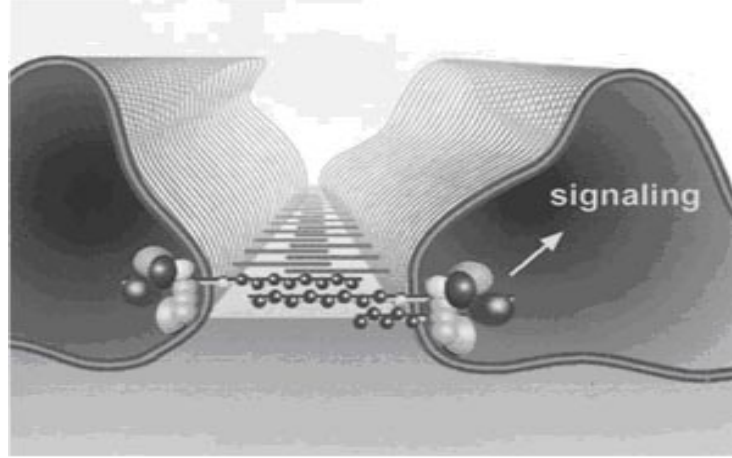




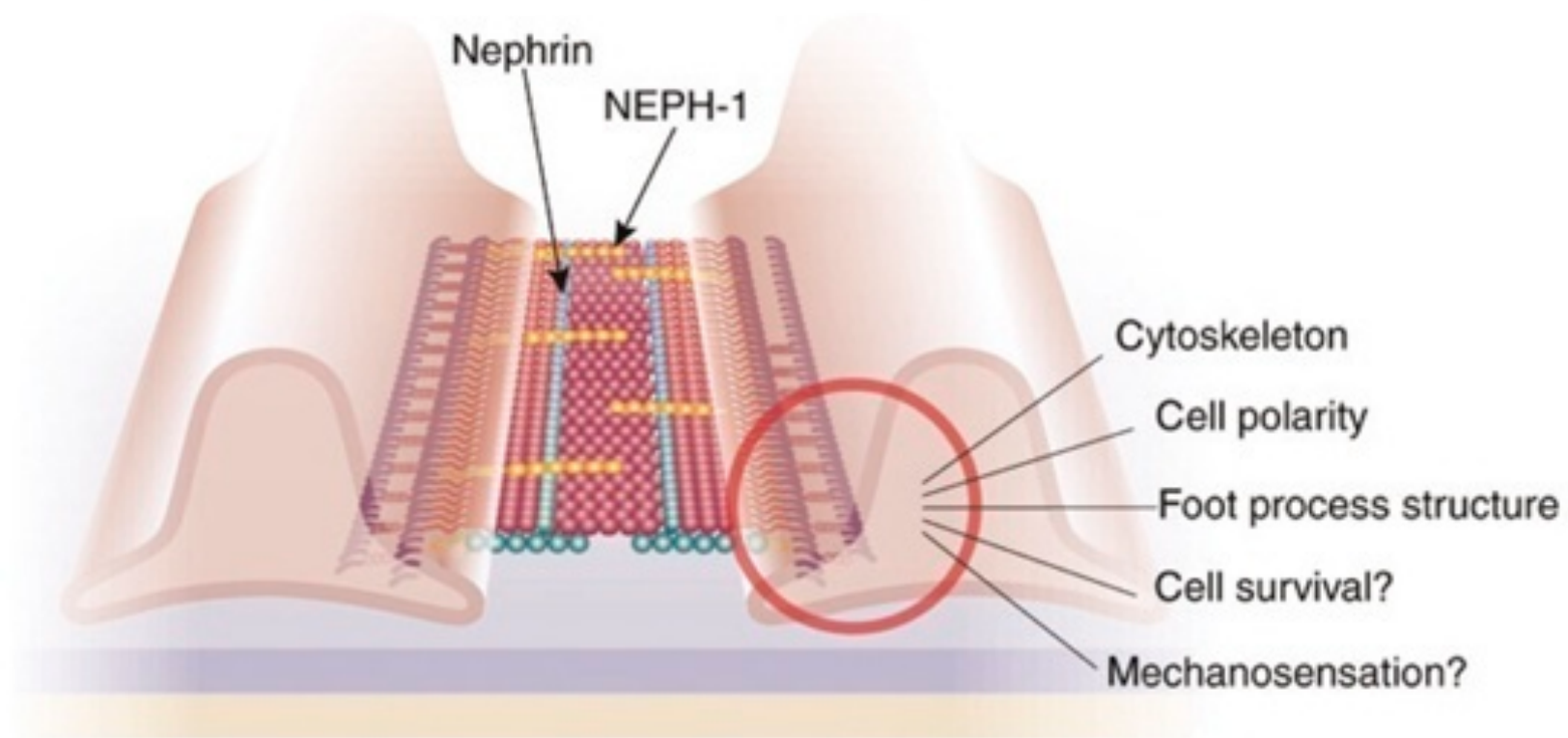


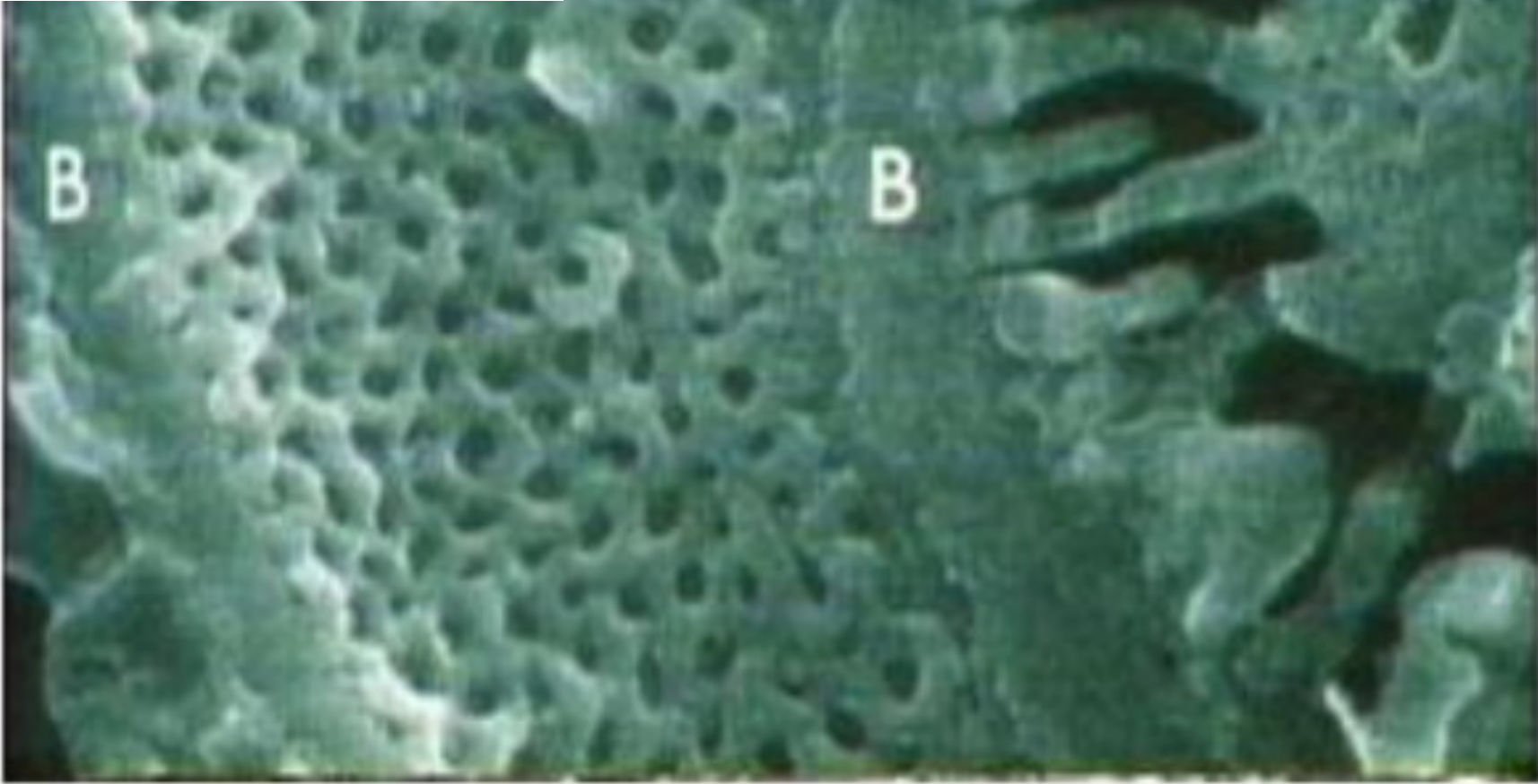
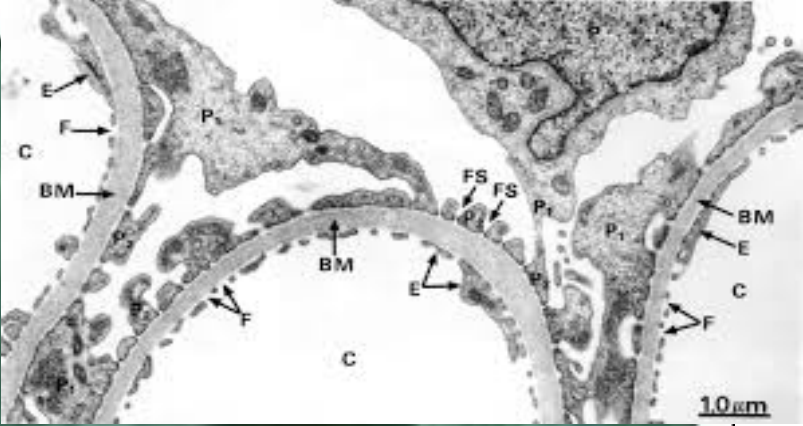
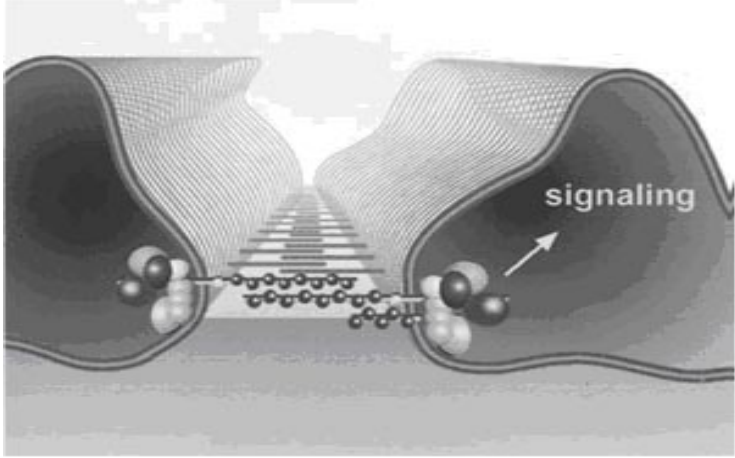






Scanning electron photomicrographs from Wistar rat, taken at high magnification (x140,000). Visualization of epithelial filtration pores by an innovative SEM technique based on a new detector, called in-lens, more sensitive than conventional one, that captures more efficiently the secondary electrons from the sample surface, due to its position closer to the sample. This approach allowed us to observe the deepest regions of the filtration slits.

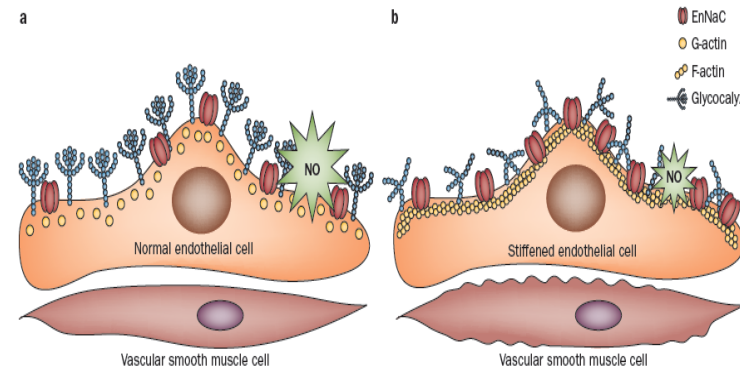




The glomerular barrier – an integrative view

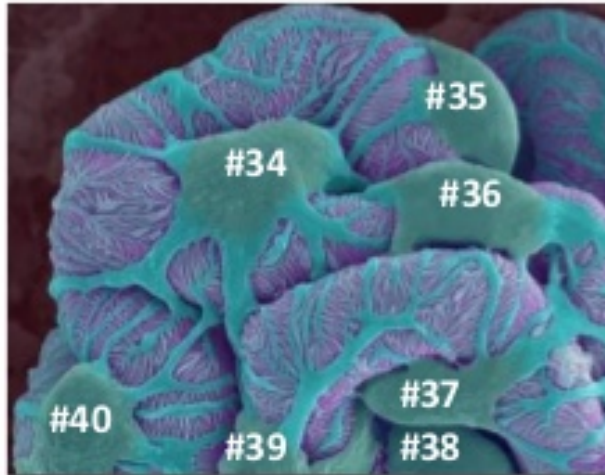
The podocytes, GBM and the endothelium

- are all important for an intact barrier
- They represent barriers in series
- There is intense communication between the podocyte, the mesangial and the endothelial cells
- The **endothelium** is of paramount importance to prevent albuminuria since it is the *'first line of defense'*



Each Podocyte Counts!

2%
Tryggvason 2011



1,200,000,000 de podocitos

Each glomerulus has 500-600 podocytes.

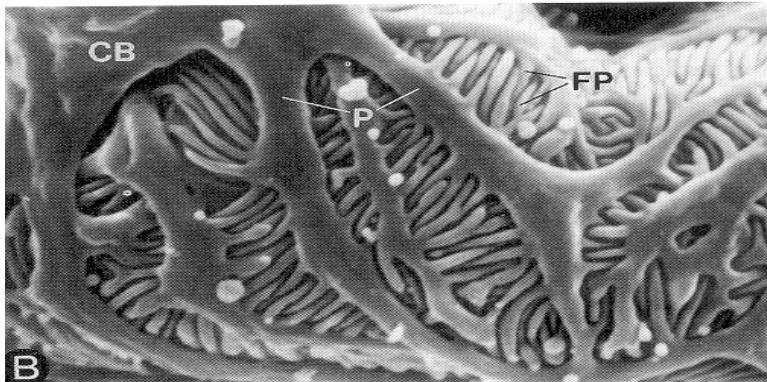
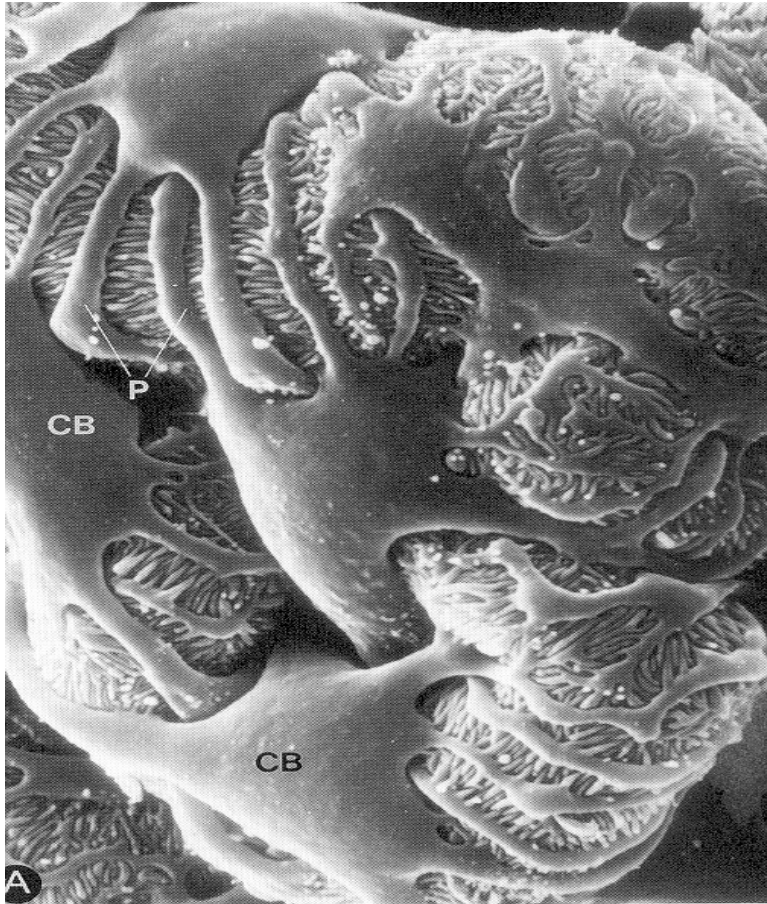
Podocytes do not efficiently proliferate.

Podocyte loss is cumulative in time

Once a glomerulus loses more than ~20% of its podocytes, it scars down. This injury is irreversible.

120 podocitos/glomérulo

200,000,000 de podocitos



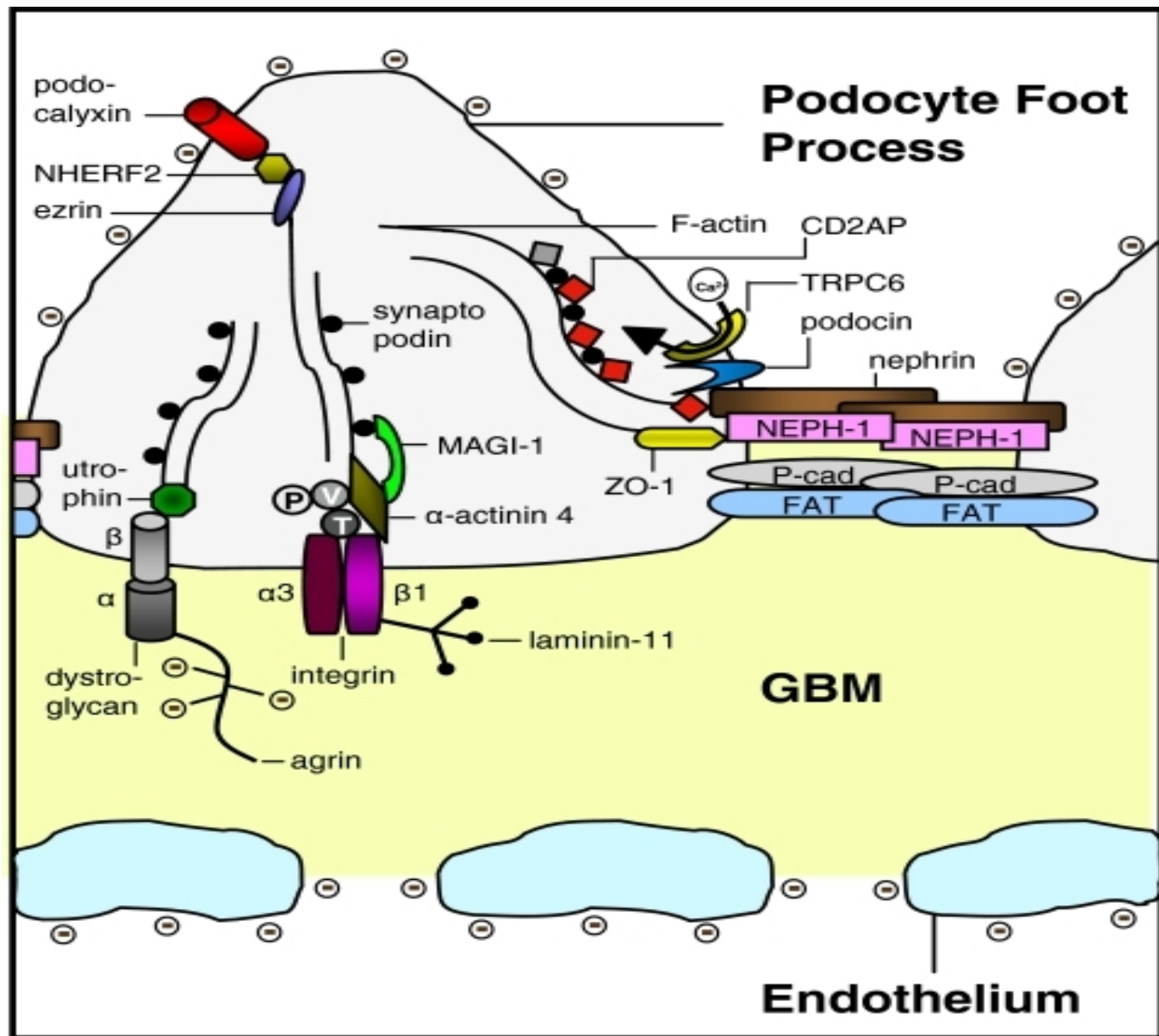
PODOCITO

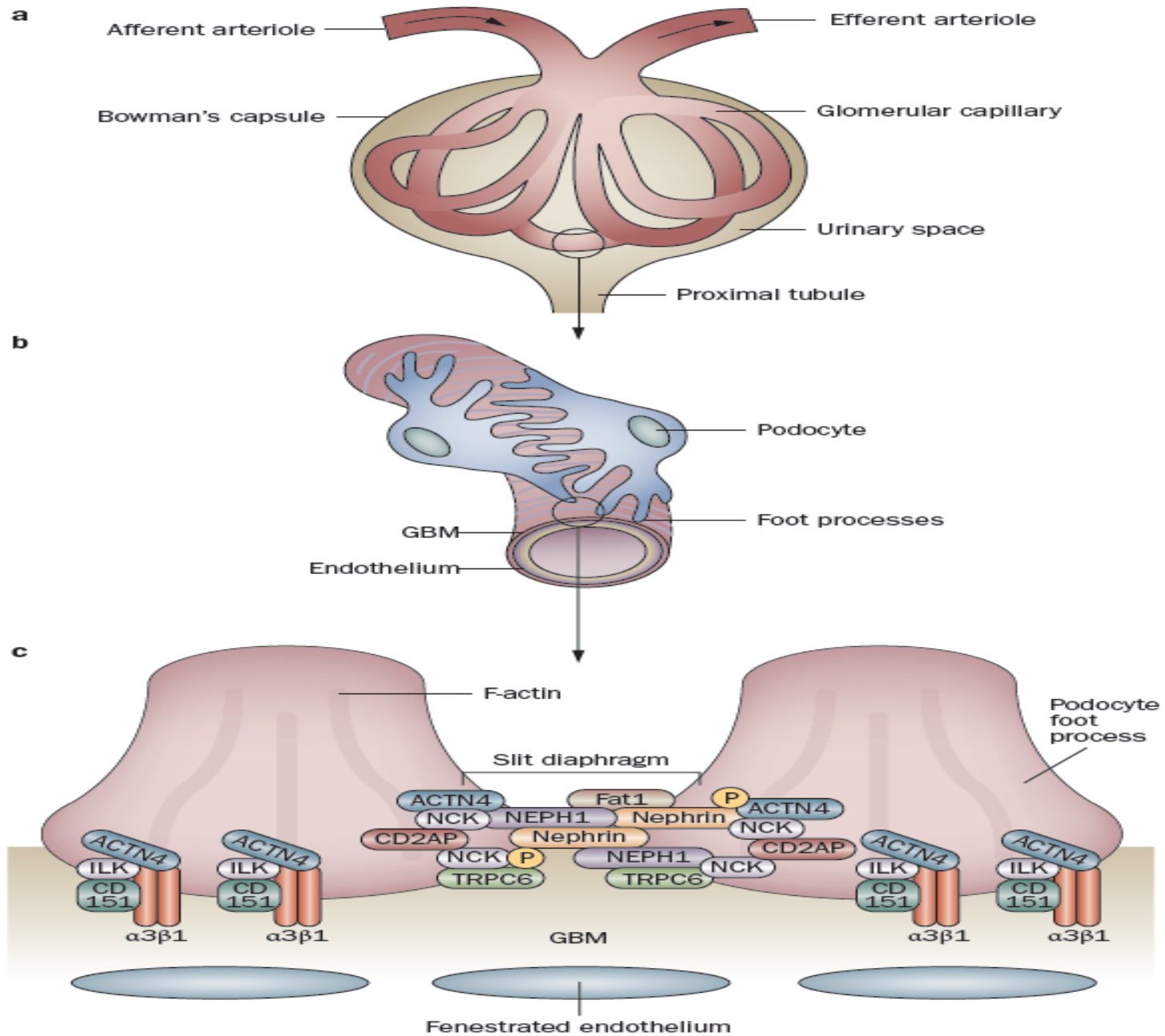
LA CÉLULA MÁS GRANDE
DEL GLOMÉRULO

ALTAMENTE DIFERENCIADA

INCAPAZ DE DIVIDIRSE

MANTENIMIENTO
(*síntesis y degradación*)
DE LA
MEMBRANA BASAL





PODOCITO

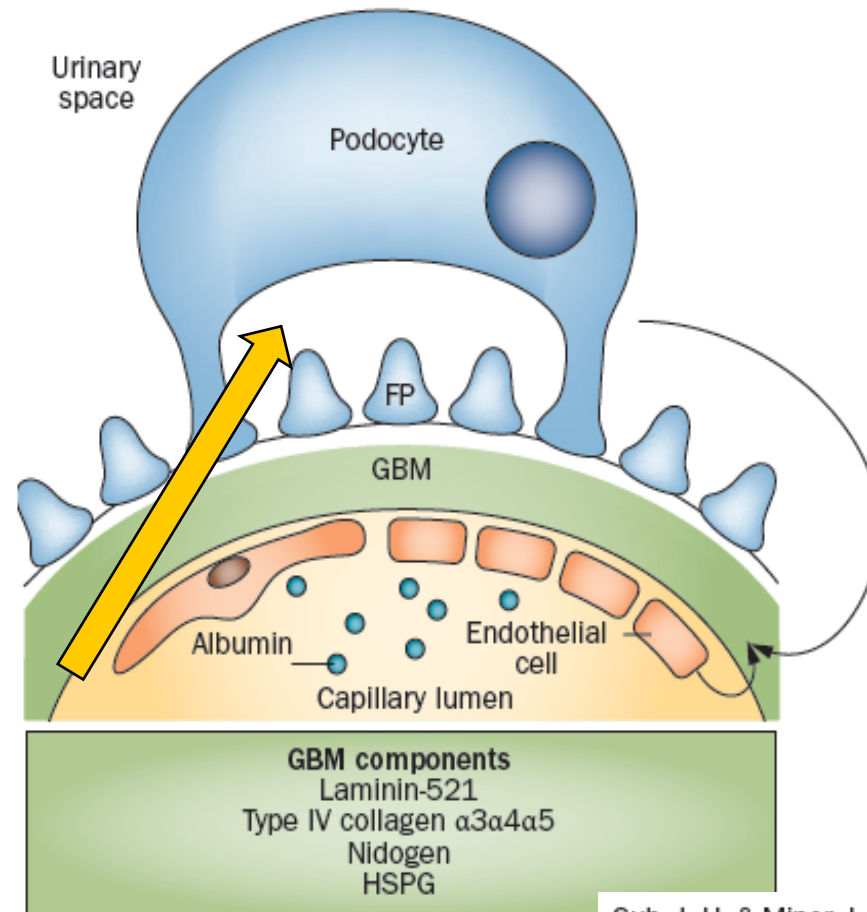
- **1. Barrera de permeabilidad**
- **2. Mantenimiento de la arquitectura glomerular**
- **3. Biosíntesis**
- **4. Interacción con el medio**

1. BARRERA DE PERMEABILIDAD

Es una barrera a la filtración de macromoléculas al cubrir la membrana basal con citoplasma.

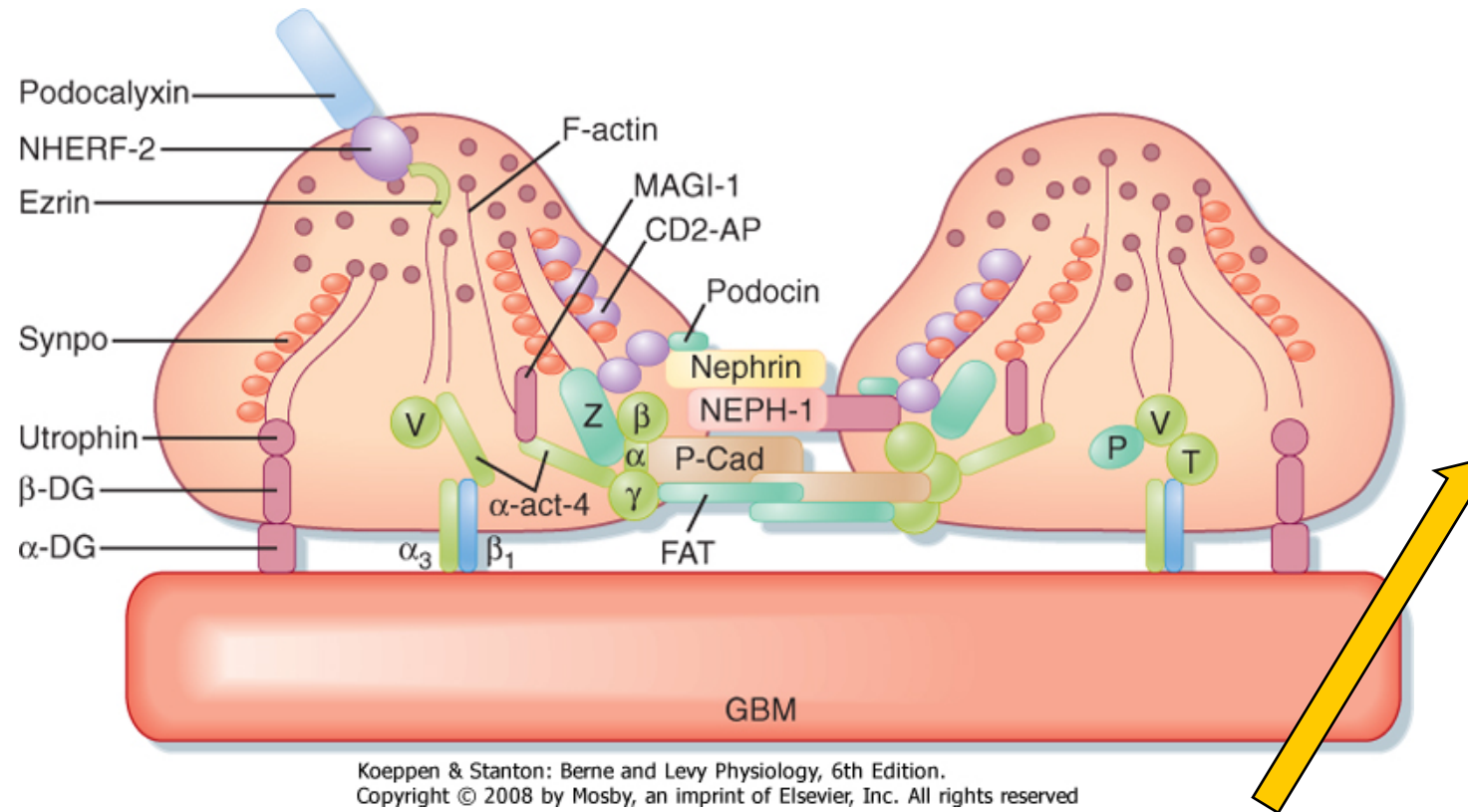
Las abundantes cargas negativas del glicocálix actúan como una barrera electrostática.

Los residuos filtrados y atrapados en la membrana basal son fagocitados por el podocito



2. MANTENIMIENTO DE LA ARQUITECTURA GLOMERULAR

Contrarrestan las fuerzas hidrostáticas propias de los capilares glomerulares valiéndose de integrinas y distroglicanos.



3. BIOSÍNTESIS

Síntesis y degradación de la membrana basal:

Colágeno tipo IV

Fibronectina

Laminina

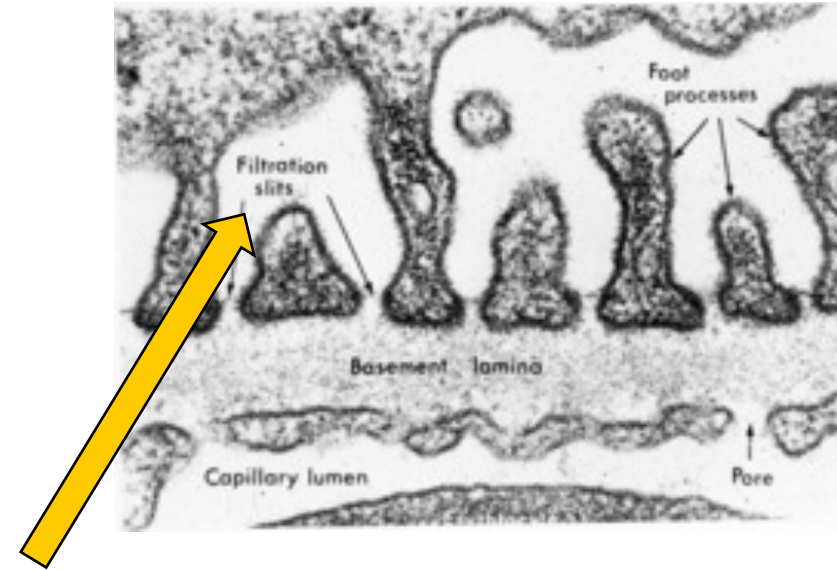
Heparán sulfato

Prostaglandinas

Factores de crecimiento

VEGF

Epoetinas



4. INTERACCIÓN CON EL MEDIO

Con proteínas reguladoras del complemento,

Receptores IgG-Fc

Receptores de las LDL

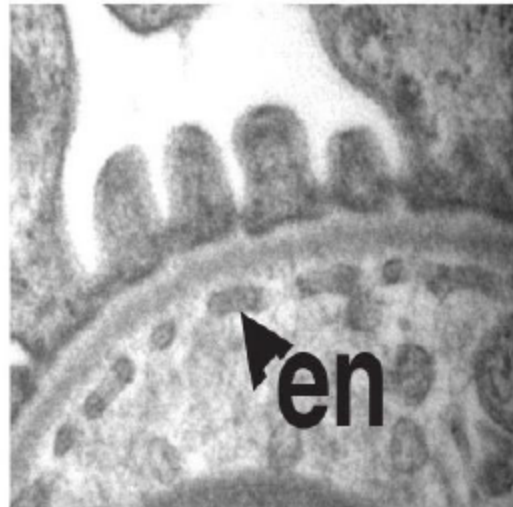
Interacción con el sistema plasminógeno-plasmina



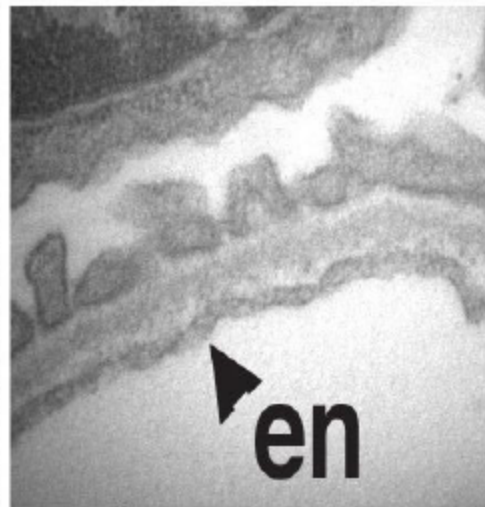
- Exquisite sensitivity of glomerular barrier to VEGF levels – dysregulation = proteinuria
- Crosstalk between glomerular cells critical for barrier integrity (endothelium!)
- Multiple angiogenic factors are expressed in glomerulus (Ang1 and VEGF) –play very different roles

VEGF-A is required for fenestration & survival of ECs

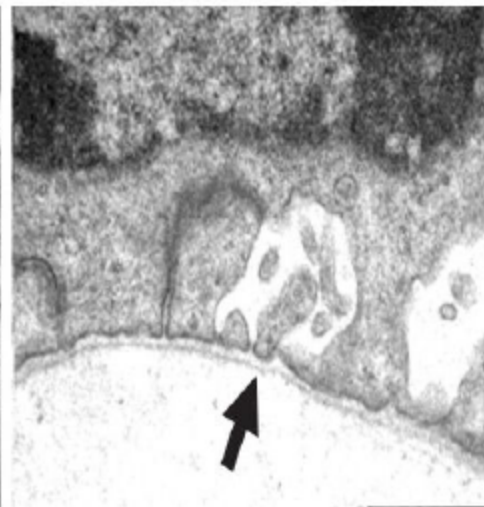
+/+

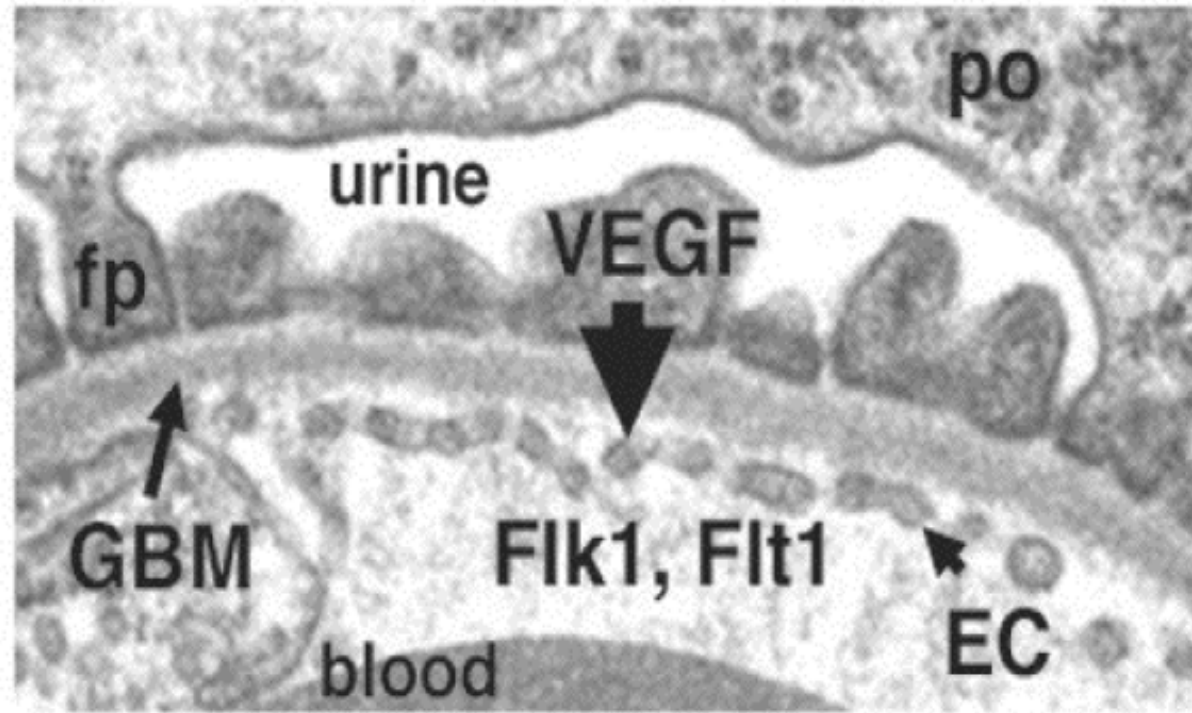


-/-, immature



-/-, mature





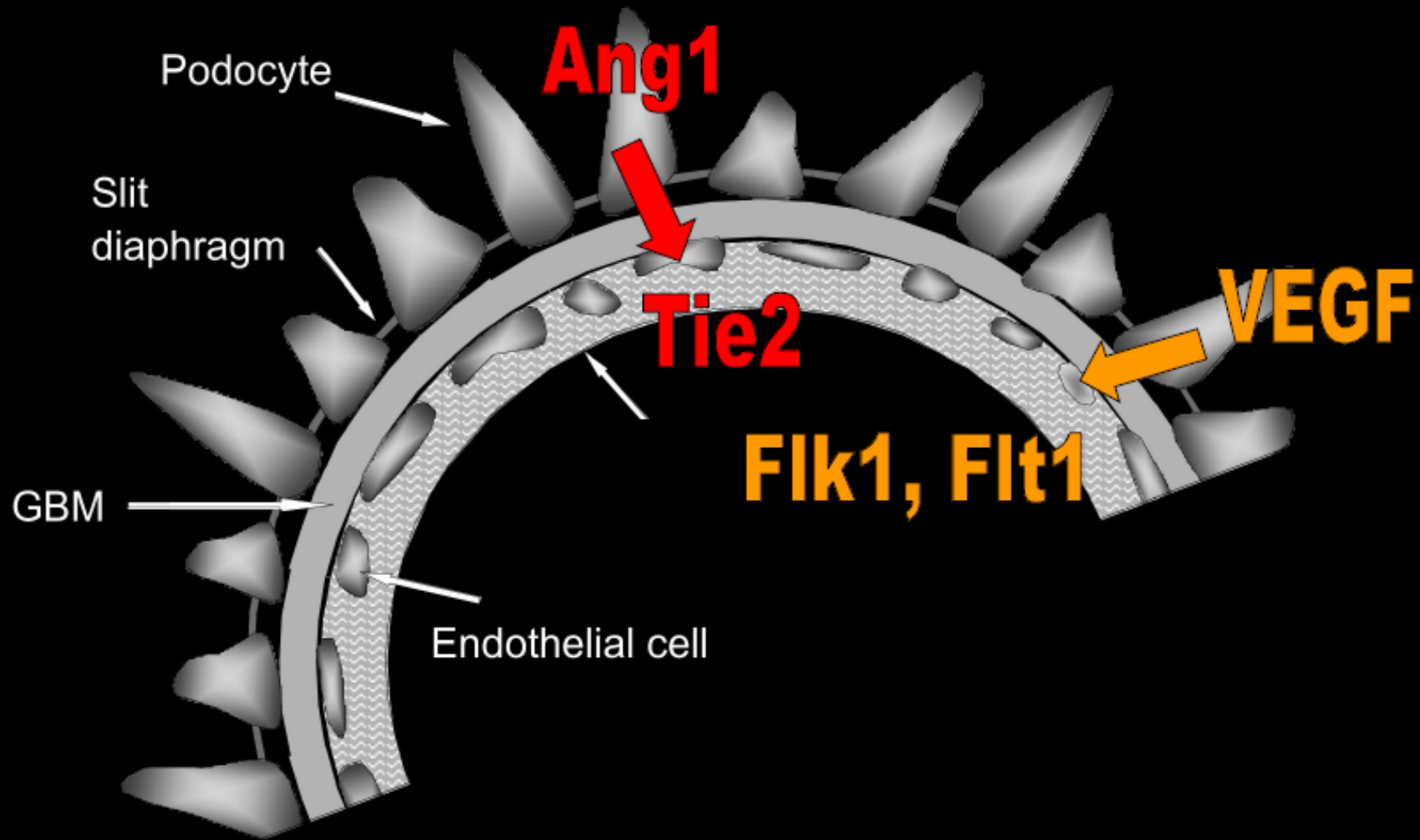
Hypothesis

VEGF inhibitors cause proteinuria and

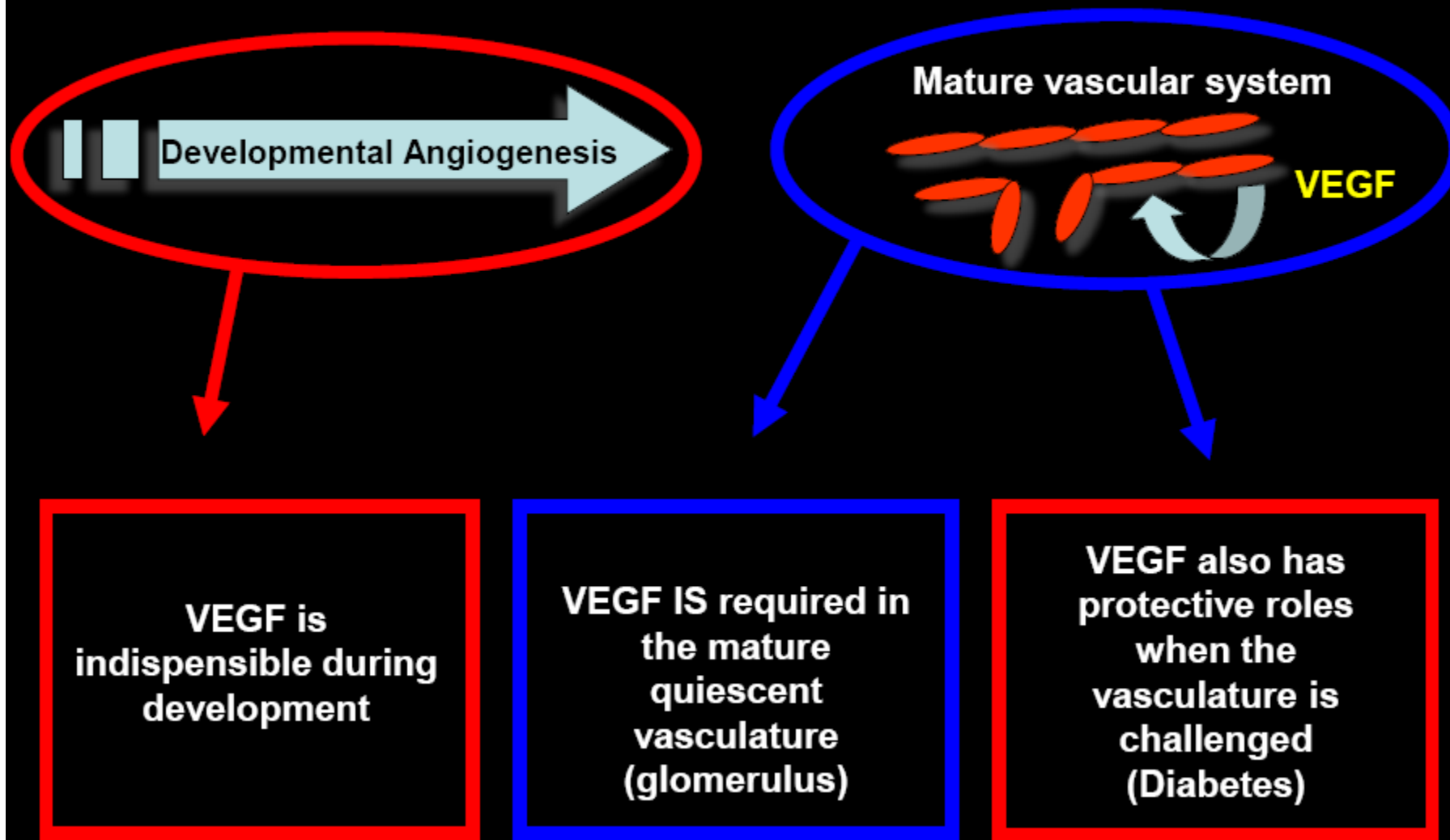
glomerular injury by local reduction of VEGF

(“on target effect”)

Ang1 and VEGF in the glomerulus

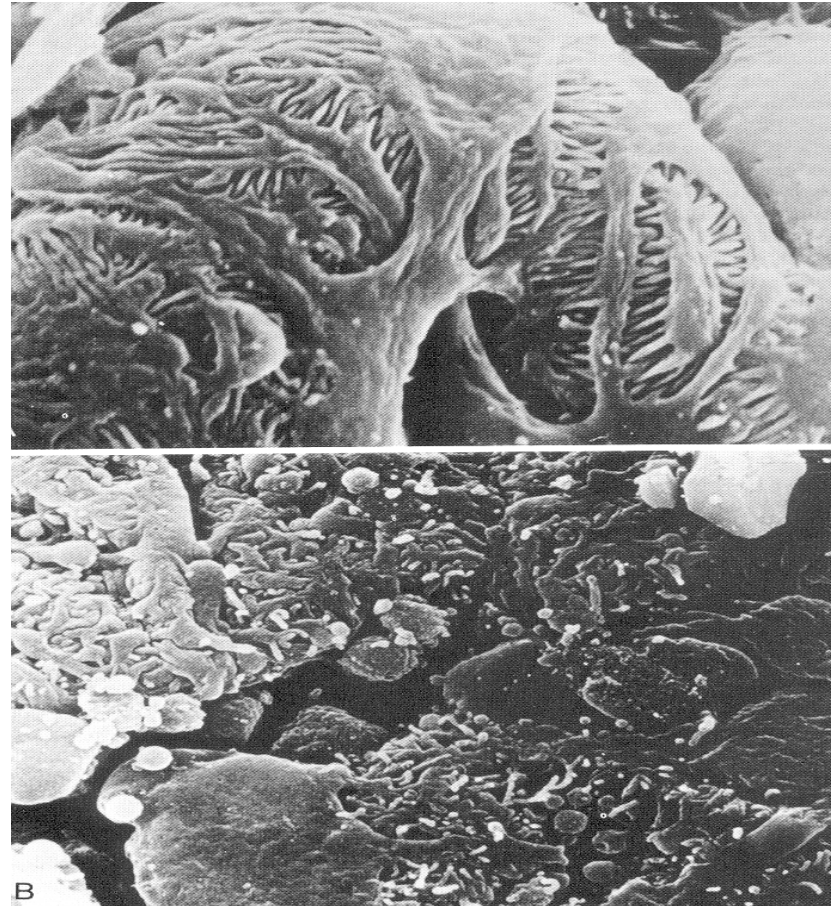


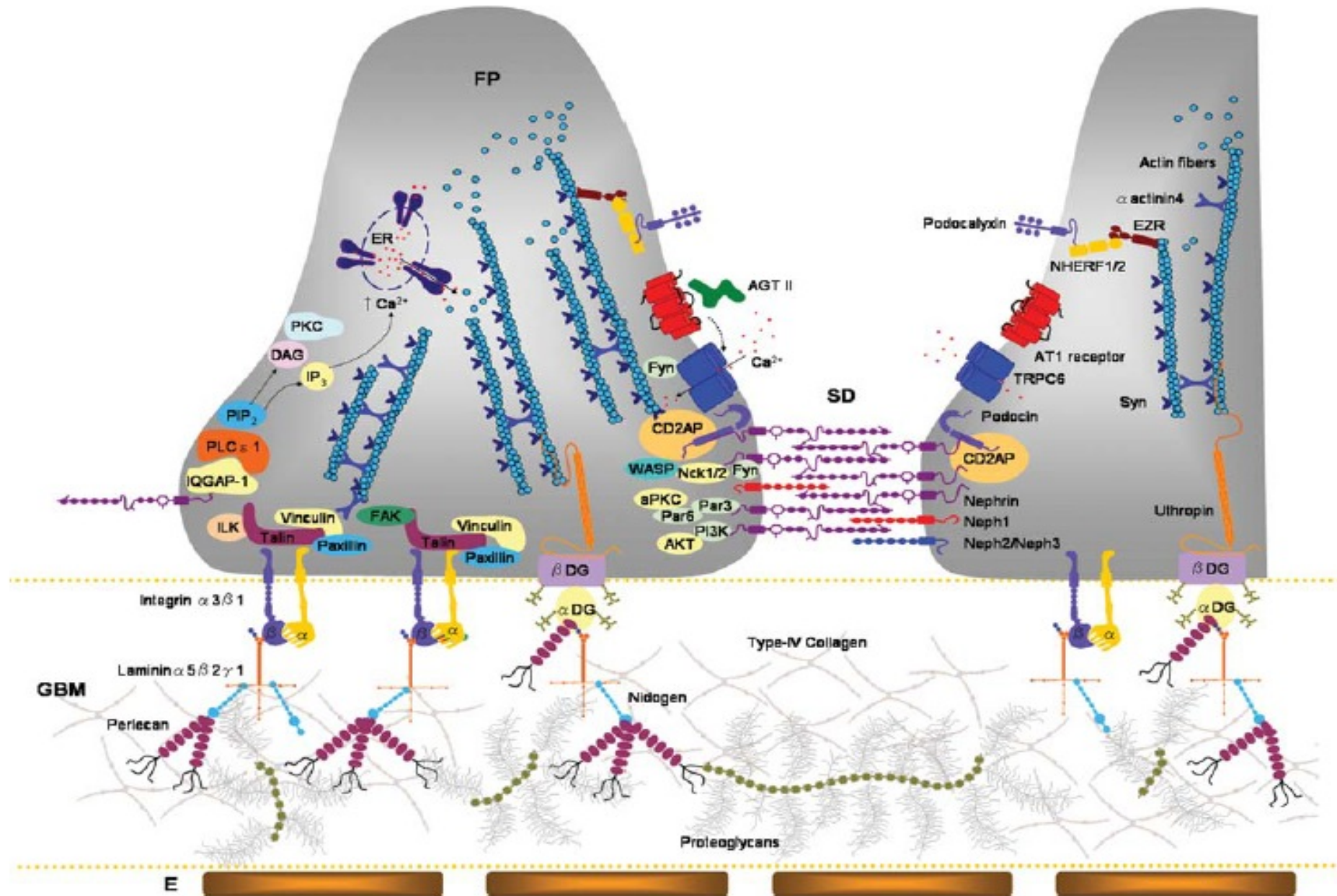
VEGF



PODOCITO: Injuria

- La injuria y la disfunción del podocito se manifiestan clínicamente por sólo dos signos principales:
- **PROTEINURIA** POR DESDIBUJAMIENTO DE LOS PEDICELOS, VACUOLIZACIÓN Y/O DESPRENDIMIENTO DE LOS PODOCITOS
- **DISMINUCIÓN DE LA FILTRACIÓN GLOMERULAR** POR ESCLEROSIS





Nephrin-interacting protein *nePH1*

Esta proteína también conecta al diafragma a la actina.

Su fosforilación aumenta la polimerización de la actina luego de la fosforilación de la nefrina.

Tanto las proteínas CD2aP y nCK son fundamentales en la conexión funcional de la actina al diafragma.

La interacción con CD2aP predominaría en estados estables, mientras que con las proteínas nCK lo sería en el desarrollo y en la injuria podocitaria.

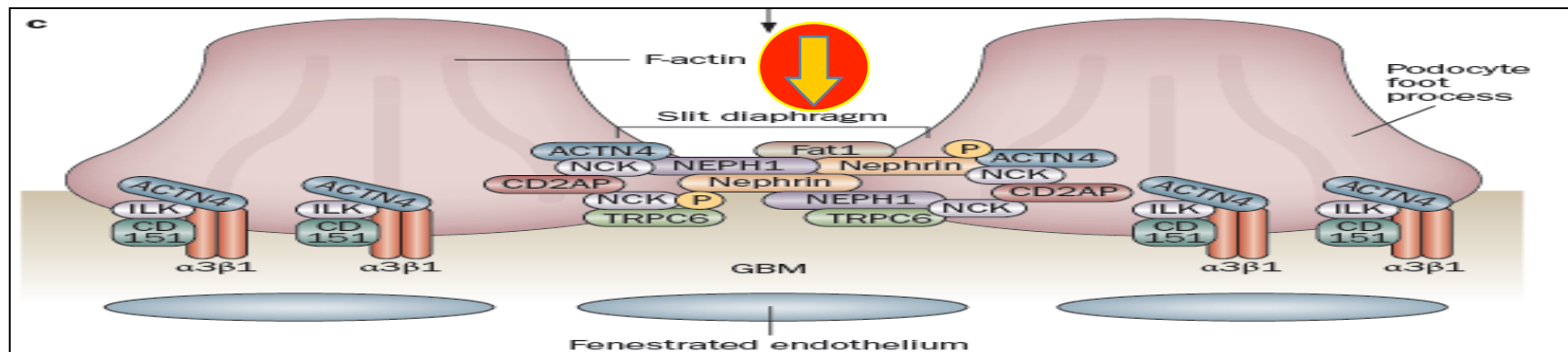


Figure 1 | Structure of the glomerular filtration barrier. **a** | Glomerular filtration occurs through the capillary wall into the urinary space, which empties into the proximal tubules. **b** | The capillary wall contains an innermost fenestrated endothelium, the GBM, and a layer of podocytes with interdigitating foot processes. **c** | Podocyte foot processes, interconnected by slit diaphragms, form the final barrier for filtration. Proteins that anchor the foot processes to the GBM ($\alpha 3\beta 1$ integrin, ACTN4, ILK and the tetraspanin CD151) as well as those that are associated with the slit diaphragm (nephrin, NEPH1, podocin, Fat1, ACTN4, the adaptor protein NCK, CD2AP and TRPC6) are crucial for normal function of the filtration barrier. Abbreviations: ACTN4, α -actinin-4; CD2AP, CD2-associated protein; GBM, glomerular basement membrane; ILK, Integrin-linked kinase; P, podocin; TRPC6, transient receptor potential cation channel 6.

Rol del TRPC6 Transient receptor potential cation channel 6 (trPC6)

Sobreexpresada en familias con FsGs autosómica-dominante.
Estos canales regulan la entrada de calcio intracelular.

En los podocitos, el trPC6 se localiza en la hendidura del diafragma,
y participa en la señalización.

Su sobreexpresión resulta en proteinuria.

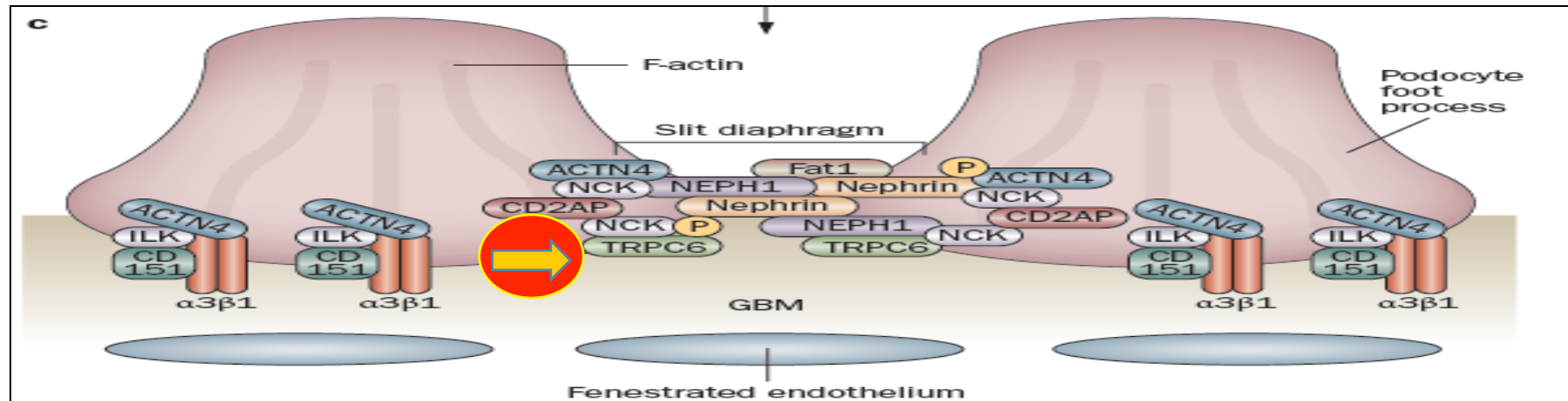


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LA VIA NOTCH

La vía notch ha sido involucrada en la patogenia de la proteinuria.

Las moléculas notch son proteínas de transmembrana que al activarse por ligandos extracelulares, sufren clivaje proteolítico y liberan el dominio notch intracelular.

Este dominio luego se transloca al núcleo, donde estimula la transcripción de diversos genes.

Su activación se ve en podocitos dañados, y la expresión de notch1 resulta en apoptosis podocitaria, albuminuria, y glomeruloesclerosis.

La supresión de la vía notch atenúa la proteinuria.

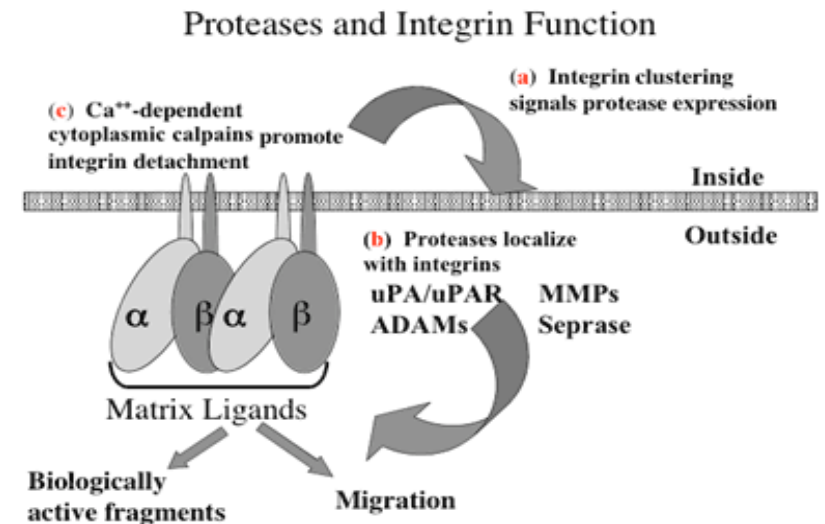
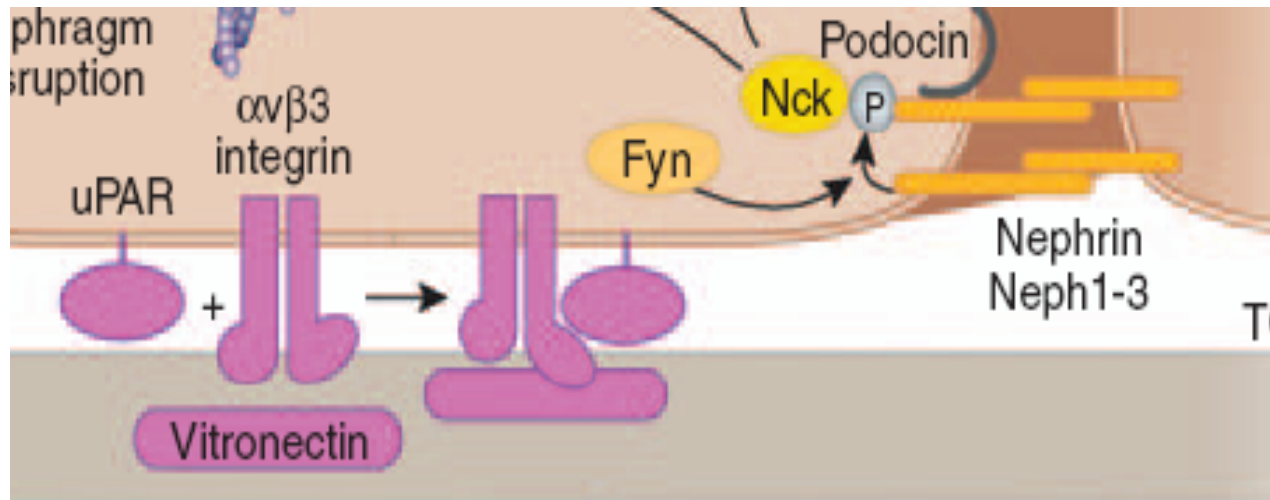
Receptor de Urokinasa

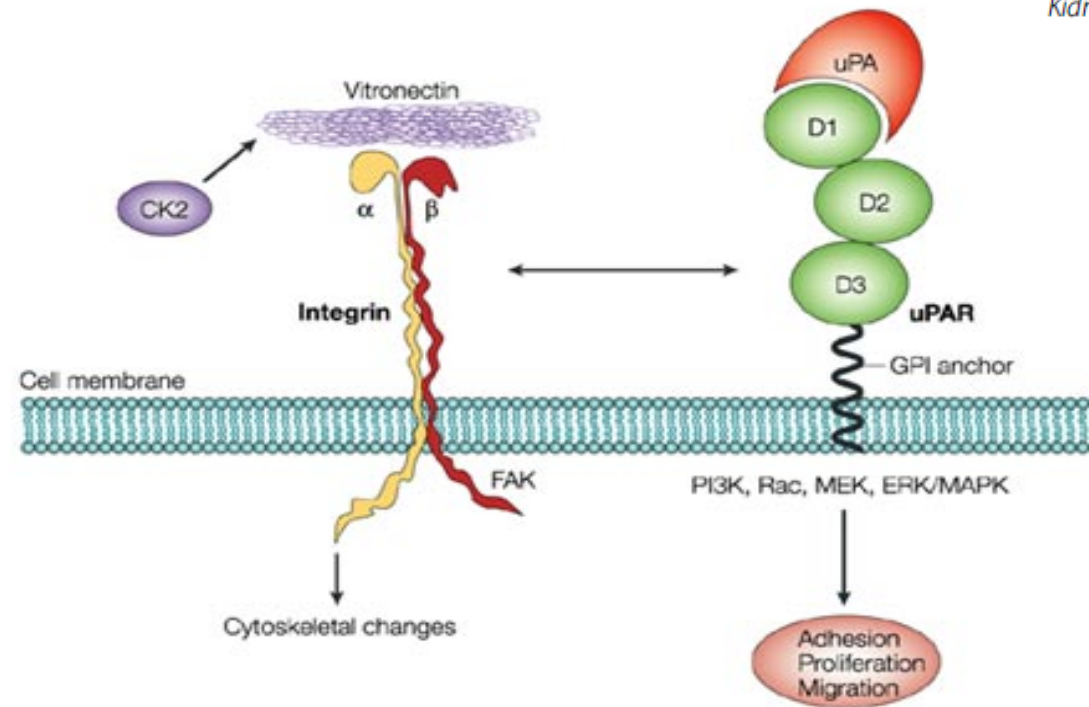
Este receptor ha sido implicado en la patogenia de la proteinuria.

Es una proteinasa, pero también presenta interacciones con otras proteínas de membrana como las integrinas.

Durante la injuria podocitaria, el receptor (uPar) promueve el desdibujamiento de los pedicelos por su interacción con la integrina $\alpha\beta3$.

La expresión de la vitronectina, el ligando extracelular de la integrina $\alpha\beta3$, está estimulado en la proteinuria.





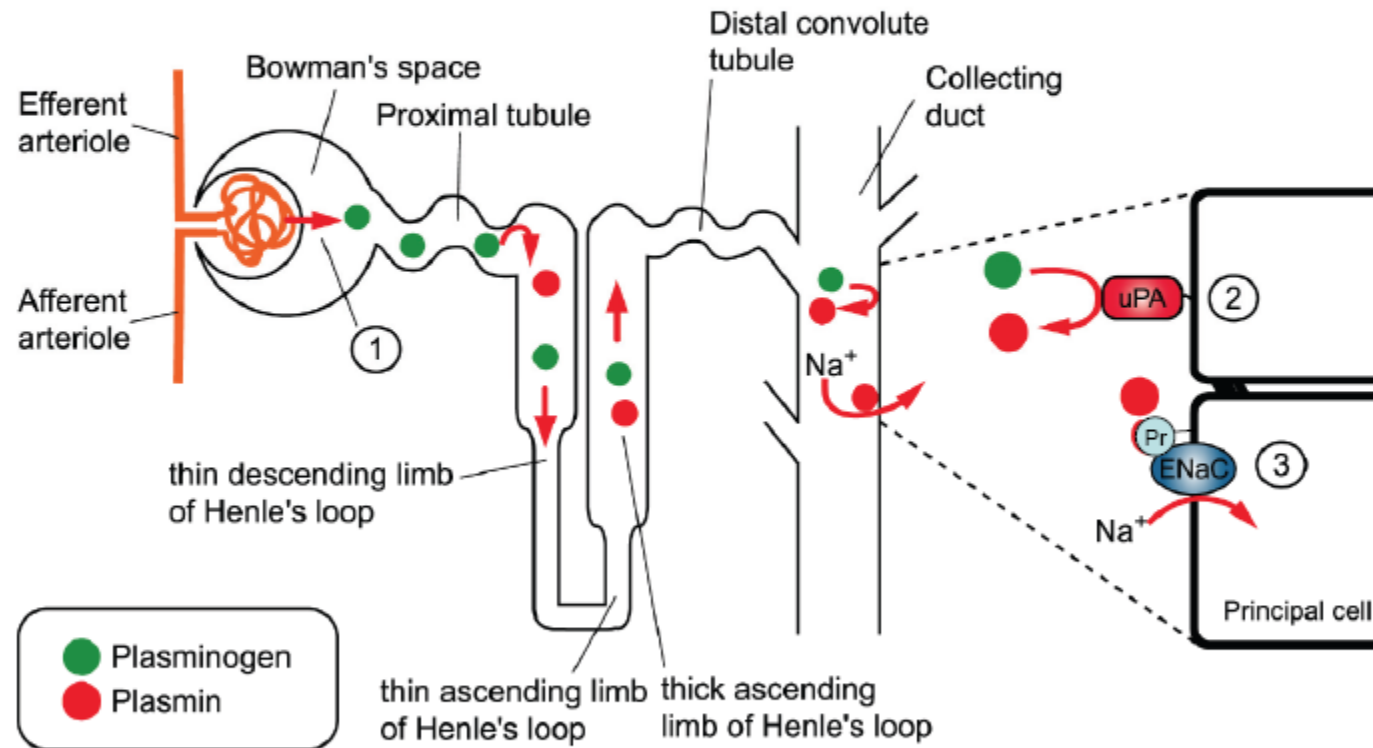
El uPAR se une tanto a la urokinasa (uPA) como a la vitronectina, que es a su vez el receptor del PAI-1.

La Proteín kinasa CK2 fosforila a la vitronectina y regula la adhesión celular uPA-dependiente a la vitronectina.

El uPAR carece de un dominio citosólico pero transmite señales intracelulares por su asociación con las integrinas de transmembrana.

ERK, extracellular-signal-regulated kinase FAK, focal adhesion kinase MAPK, mitogen-activated protein kinase.

A novel model for stimulation of sodium reabsorption in nephrotic syndrome



Proteinuria may promote distal sodium reabsorption

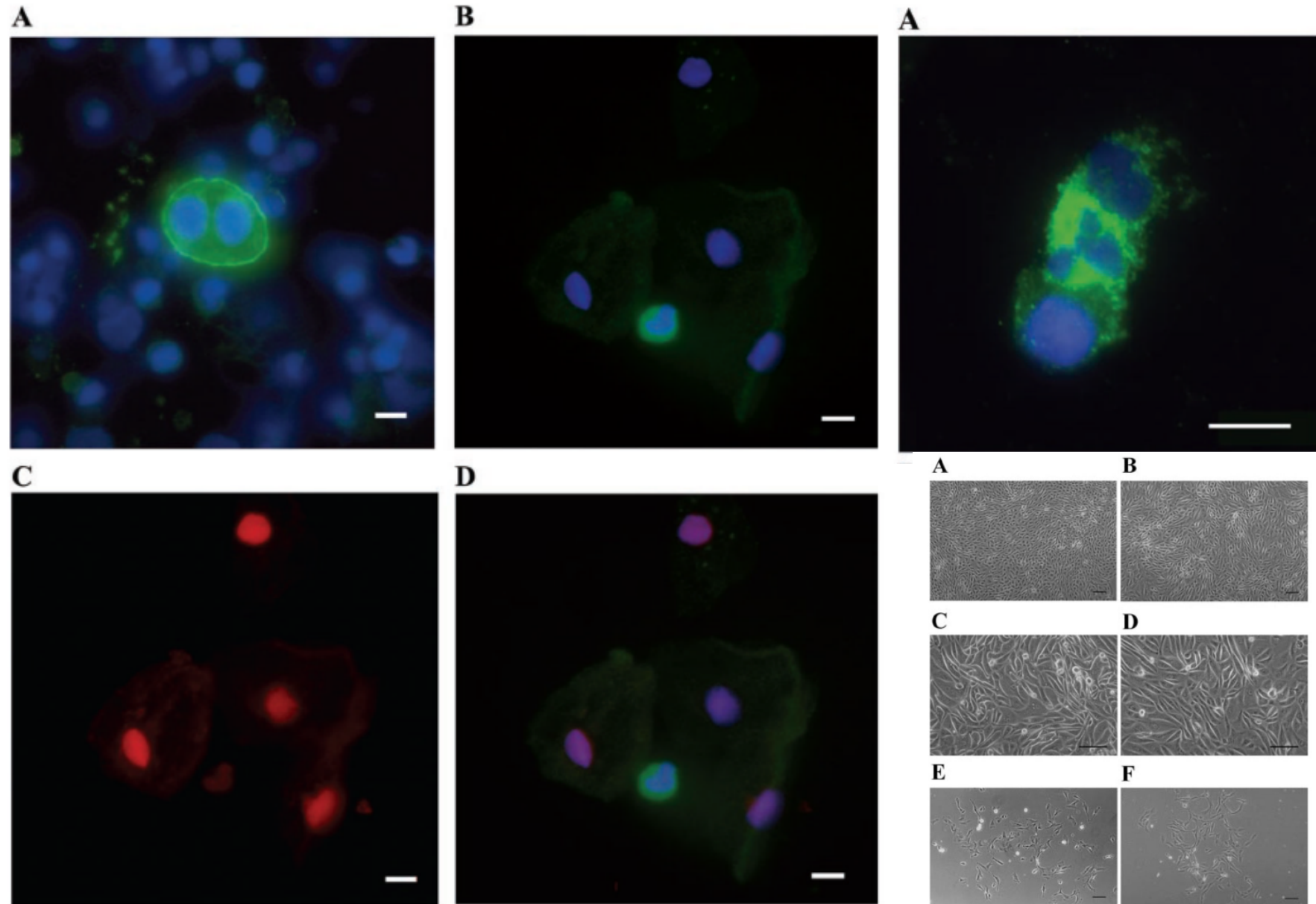
Table 1 | Pathways involved in acquired glomerular diseases

Molecular pathways	Human diseases
<i>Transmembrane receptors</i>	
Nephrin	DNP, MCD
B7-1	LN
uPAR	FSGS, DNP
Notch	FSGS, DNP
PLA ₂ R	MN
<i>Ion channels</i>	
TRPC6	MCD, MN
<i>Growth factors</i>	
VEGF-A	Preeclampsia
TGF- β	DNP
<i>Proteases</i>	
Cathepsin L \rightarrow dynamin, synaptopodin	MN, FSGS, DNP

Abbreviations: DNP, diabetic nephropathy; FSGS, focal segmental glomerulosclerosis; LN, lupus nephritis; MCD, minimal change disease; MN, membranous nephropathy; TGF- β , transforming growth factor- β ; TRPC6, transient receptor potential cation channel-6; uPAR, urokinase plasminogen-activator receptor; VEGF-A, vascular endothelial growth factor A.

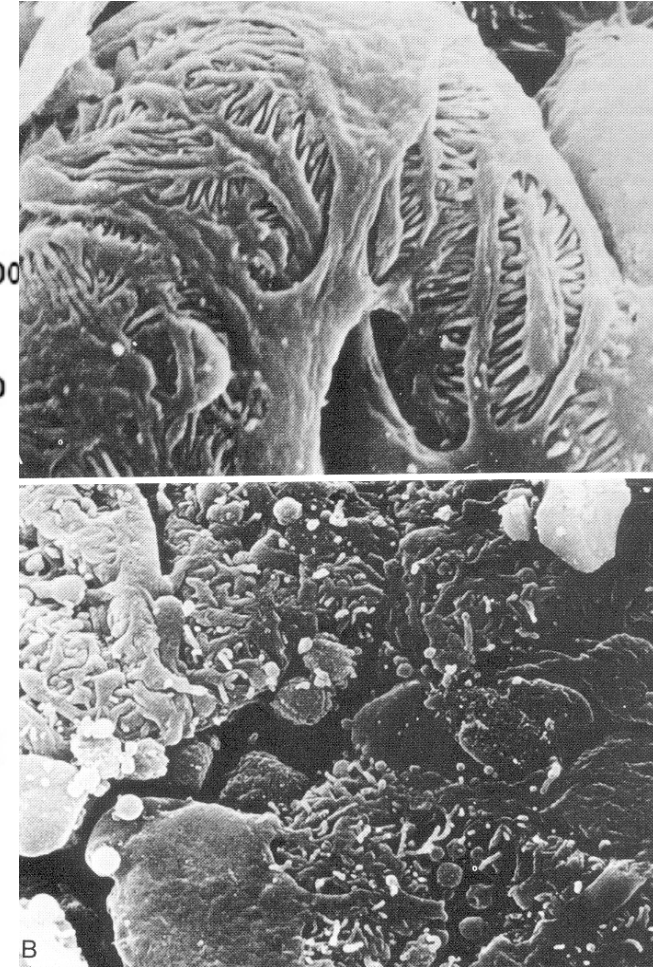
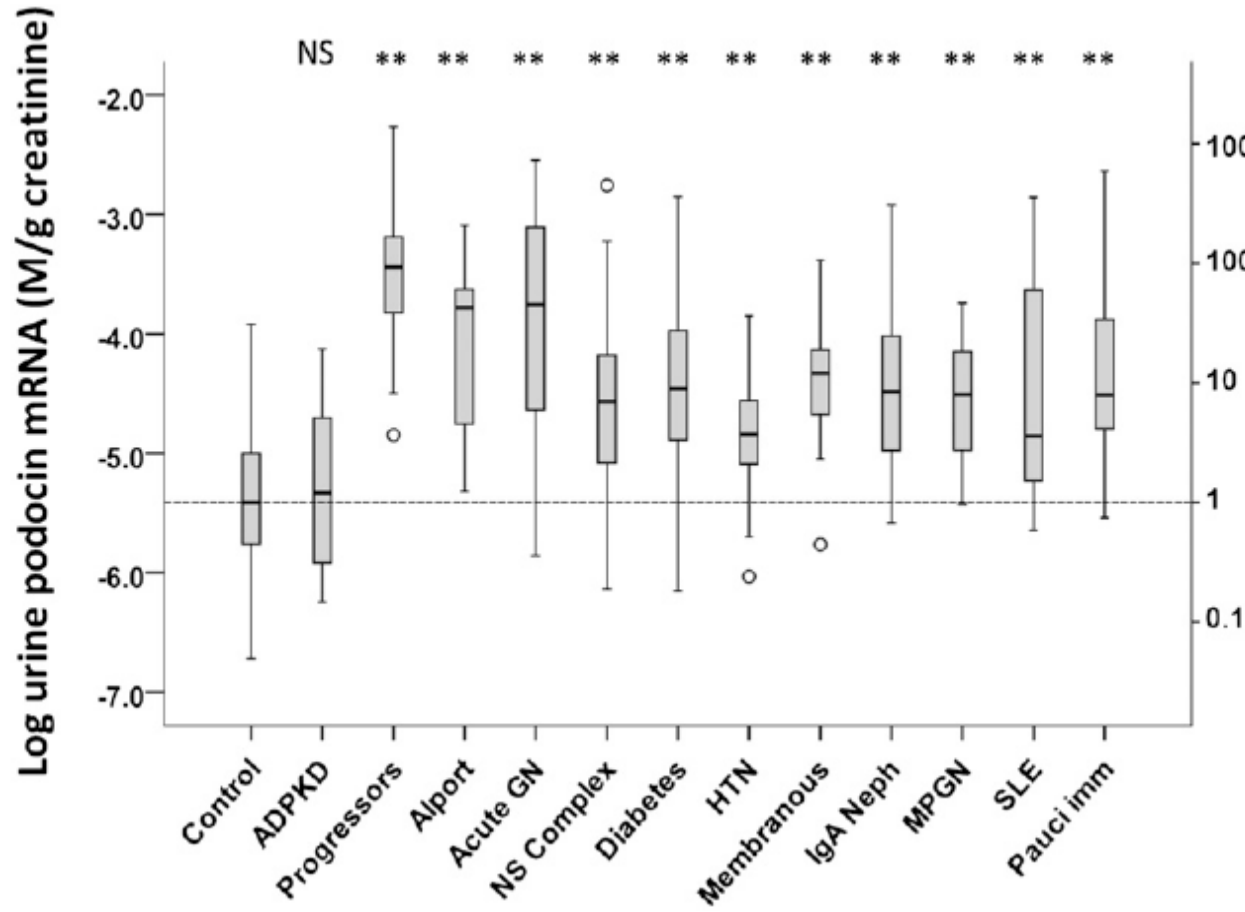
Only those pathways that have been shown to be involved in acquired human glomerular diseases are listed.

ACT 2: GOING, GOING, GONE... THE ROLE OF PODOCYTE DEPLETION

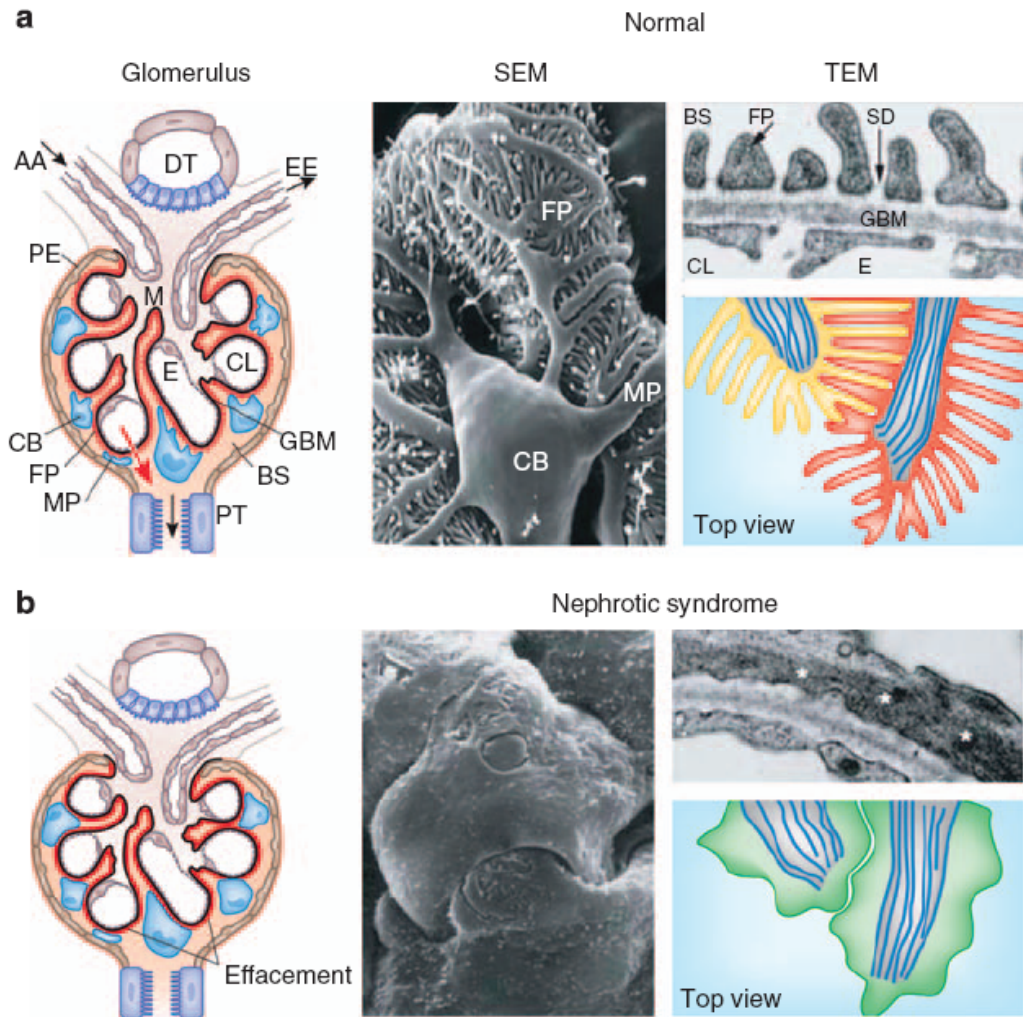


Urine Podocyte mRNAs, Proteinuria, and Progression in Human Glomerular Diseases

Larysa Wickman,* Farsad Afshinnia,[†] Su Q. Wang,[†] Yan Yang,[†] Fei Wang,[‡]
Mahboob Chowdhury,[†] Delia Graham,* Jennifer Hawkins,[†] Ryuzoh Nishizono,[†]
Marie Tanzer,* Jocelyn Wiggins,[†] Guillermo A. Escobar,[§] Bradley Rovin,^{||} Peter Song,[‡]
Debbie Gipson,* David Kershaw,* and Roger C. Wiggins[†]



ACT 5: THE MISSING LINK: HOW IRREVERSIBLE FOOT PROCESS EFFACEMENT AND PODOCYTE LOSS PROMOTE GLOMERULOSCLEROSIS



Podocyte injury owing to specific disease

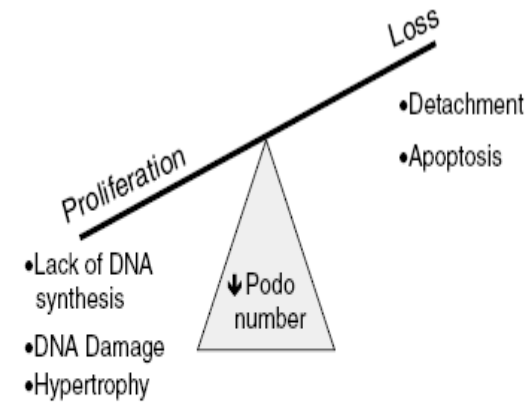
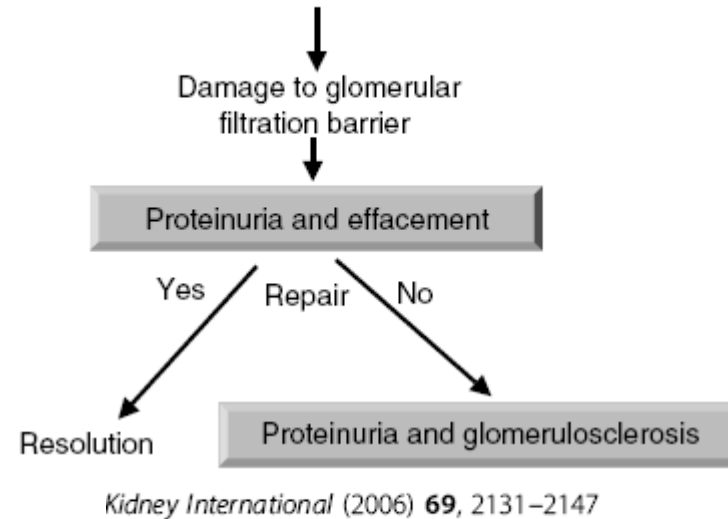
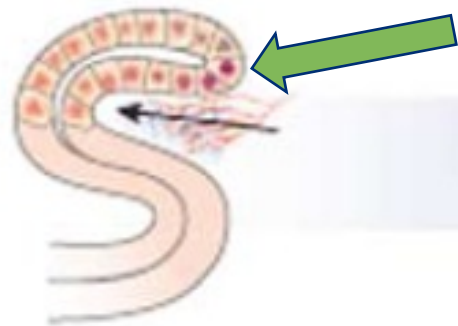
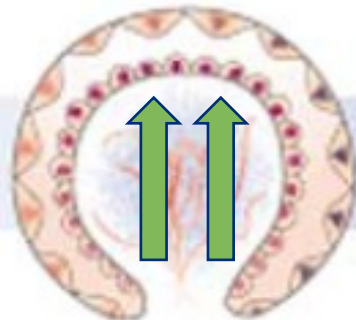


Figure 2 | Factors governing podocyte number. Total podocyte (podo) number is a balance between proliferation and loss. Podocyte number is reduced by either a decrease in proliferation owing to lack of DNA synthesis, DNA damage or hypertrophy, and/or an increase in podocyte loss owing to detachment and apoptosis.

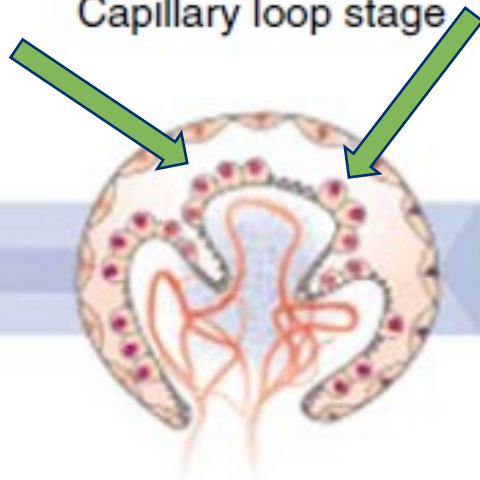
S-shaped stage



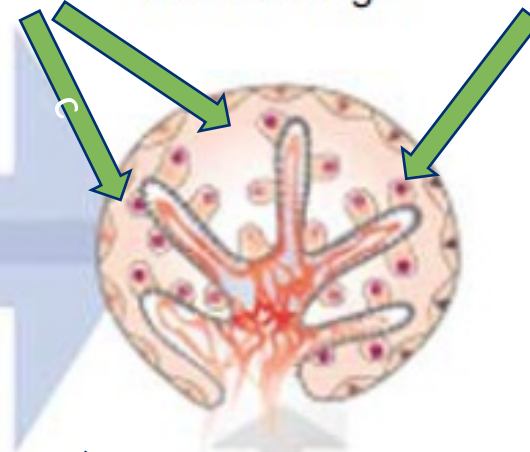
Head-shaped stage



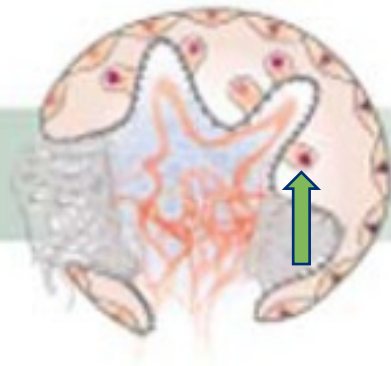
Capillary loop stage



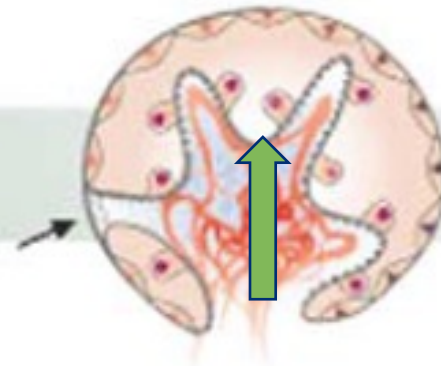
Mature stage



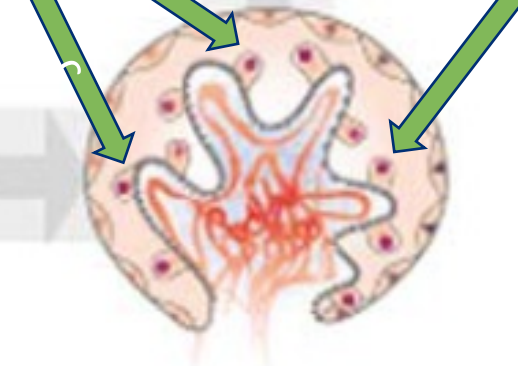
Global sclerosis



Segmental sclerosis



Adhesion



Mesangial expansion

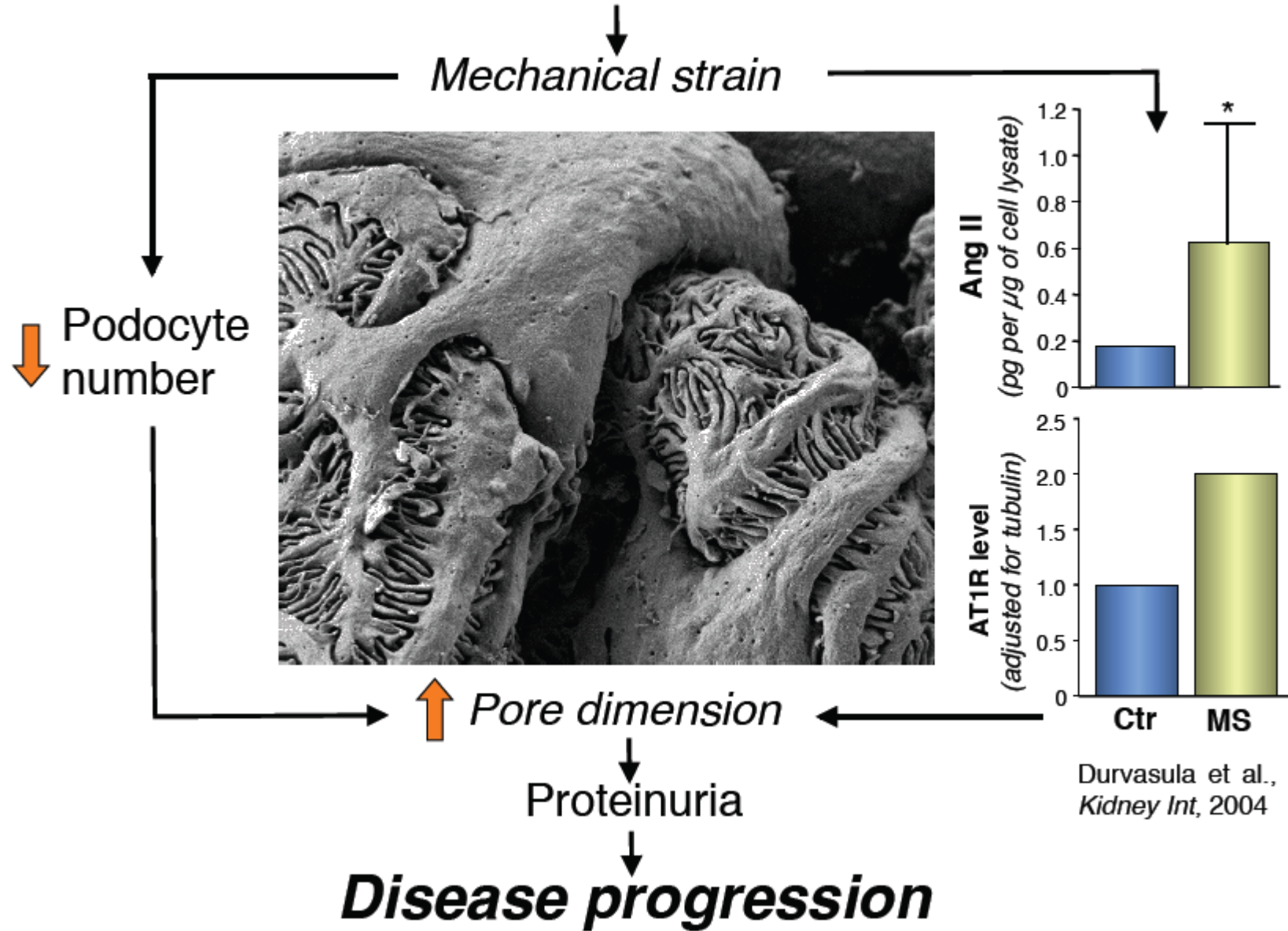
Loss of podocytes beyond a critical level results in a fibrotic glomerular response in that part of the glomerulus

Loss of some podocytes (20%) is associated with mesangial expansion possibly as an attempt to reduce the filtration surface area

Loss of podocytes beyond a critical level results in widespread scarring of that glomerulus

Loss of podocytes resulting in appearance of bare areas of filtration surface results in adhesion of the bare surface to Bowman's capsule (synechia)

Glomerular hypertension



TIPOS DE PROTEINURIA

En condiciones normales, la excreción urinaria de proteínas no excede los 150 mg/día y consiste principalmente de proteínas filtradas (60%) y de la proteína tubular de Tamm-Horsfall (40%).

La proteína urinaria más importante es la albúmina, constituyendo el 20% de la proteinuria diaria, a razón de hasta 20 mg/día (13.8 mg/min).

La proteinuria usualmente refleja un aumento en la permeabilidad glomerular a la albúmina y otras macromoléculas plasmáticas

Hay varios tipos básicos de proteinuria:

Glomerular

Tubular

Sobreflujo

Dinámica (inducida por ejercicio)

Algunos conceptos

La variante glomerular la forma más frecuente de proteinuria (alrededor del 90%).

Proteínas de bajo peso, como la β 2-microglobulina, aminoácidos, y cadenas livianas, tienen un peso molecular de hasta 25 kDa (albúmina: 69 kDa).

Estas proteínas cruzan libremente la membrana basal glomerular y luego son completamente reabsorbidas por las células proximales tubulares.

Recordar que la enfermedades glomerulares, al progresar, se acompañan de injuria tubular y proteinuria tubular.

Table 1 | Types of proteinuria

Types	Characteristics
Glomerular	Most common form, up to 90% Feature of chronic kidney disease Loss of albumin and higher molecular weight proteins
Tubular	Low molecular weight proteins, such as β 2-microglobulin
Overflow	Increased production, that is, light chains in multiple myeloma
Post-exercise	Transient benign Can be up to 10 g/day
Post-prandial	Transient physiological proteinuria Possibly through insulin action in podocytes
Infection-associated	Physiological response Mediated by toll-receptors Possibly involved in clearing pathogens from the circulation

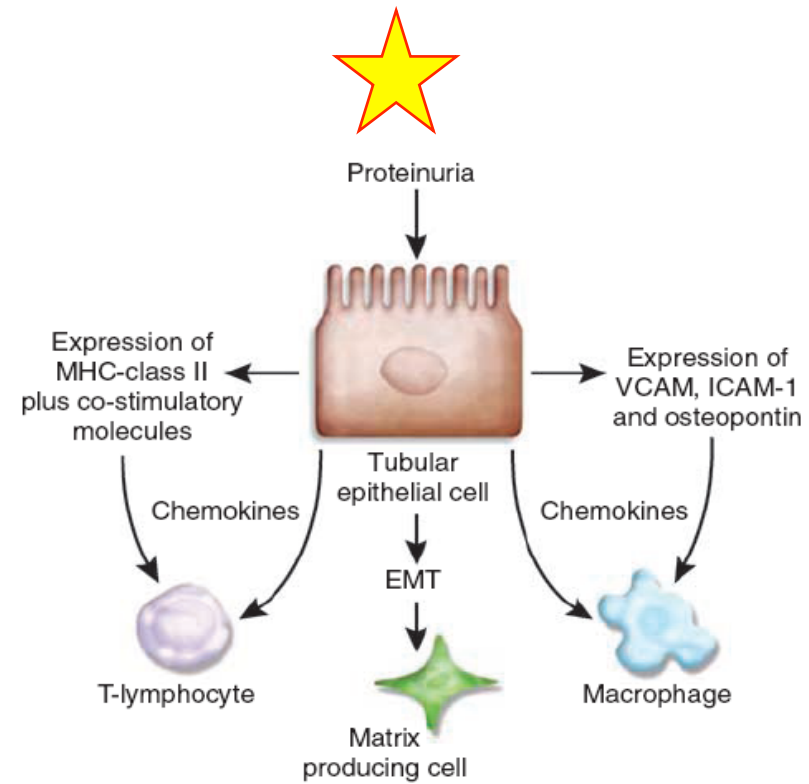
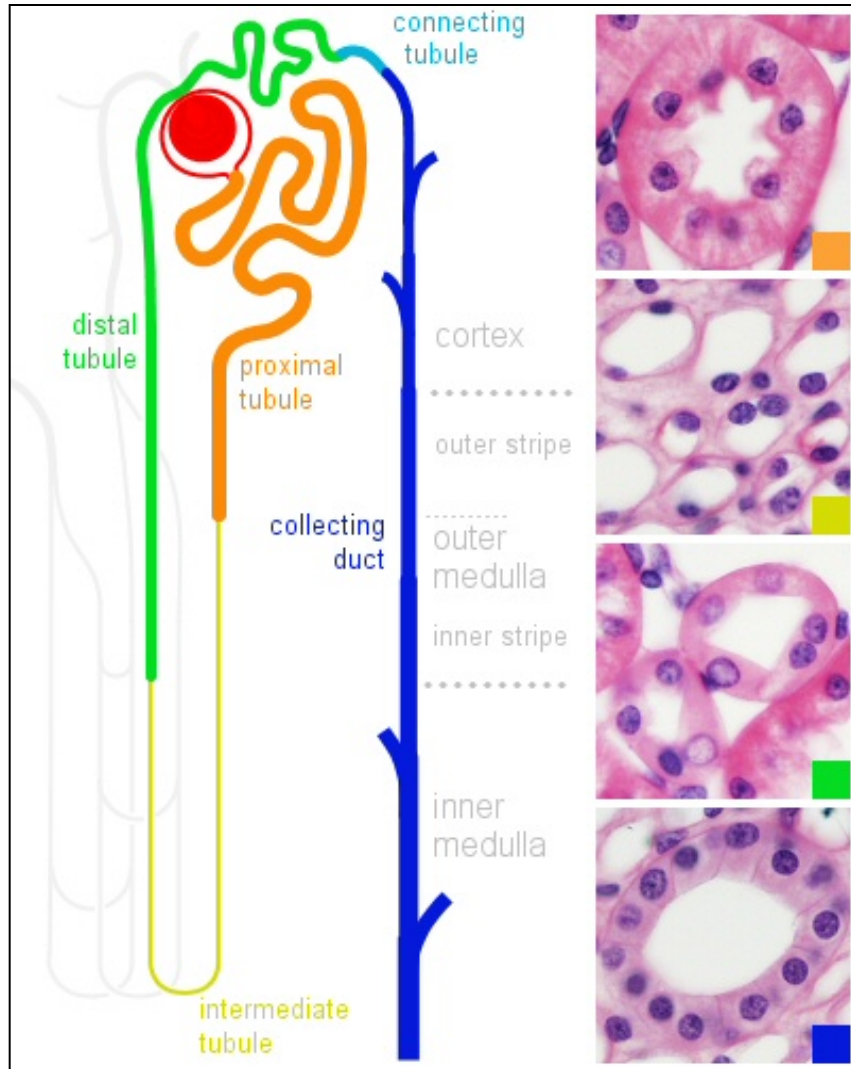
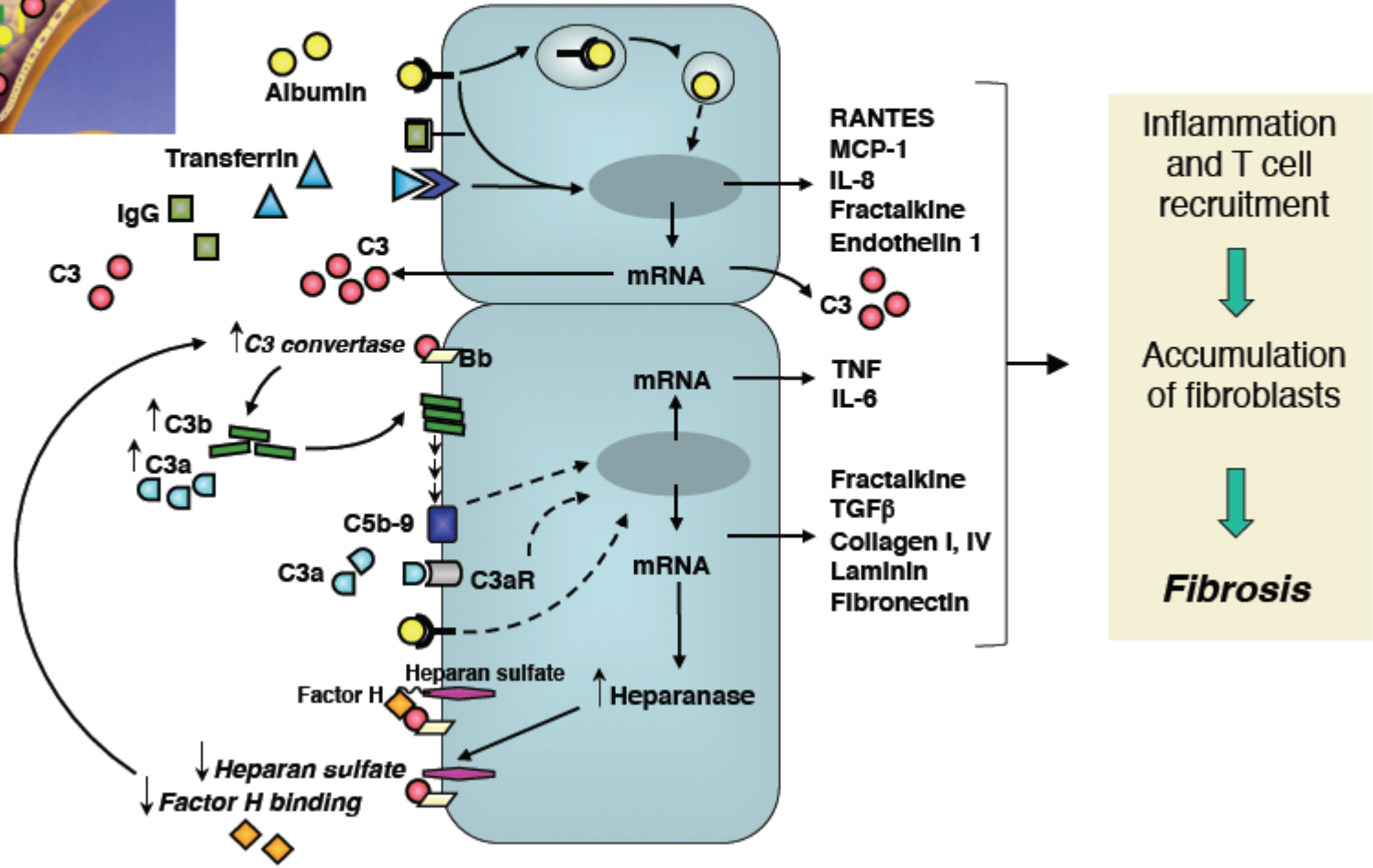
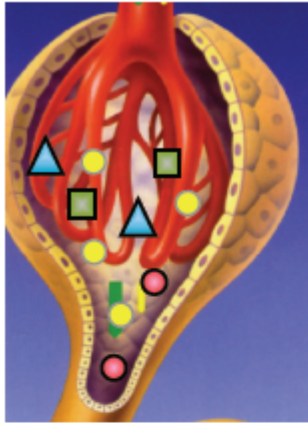
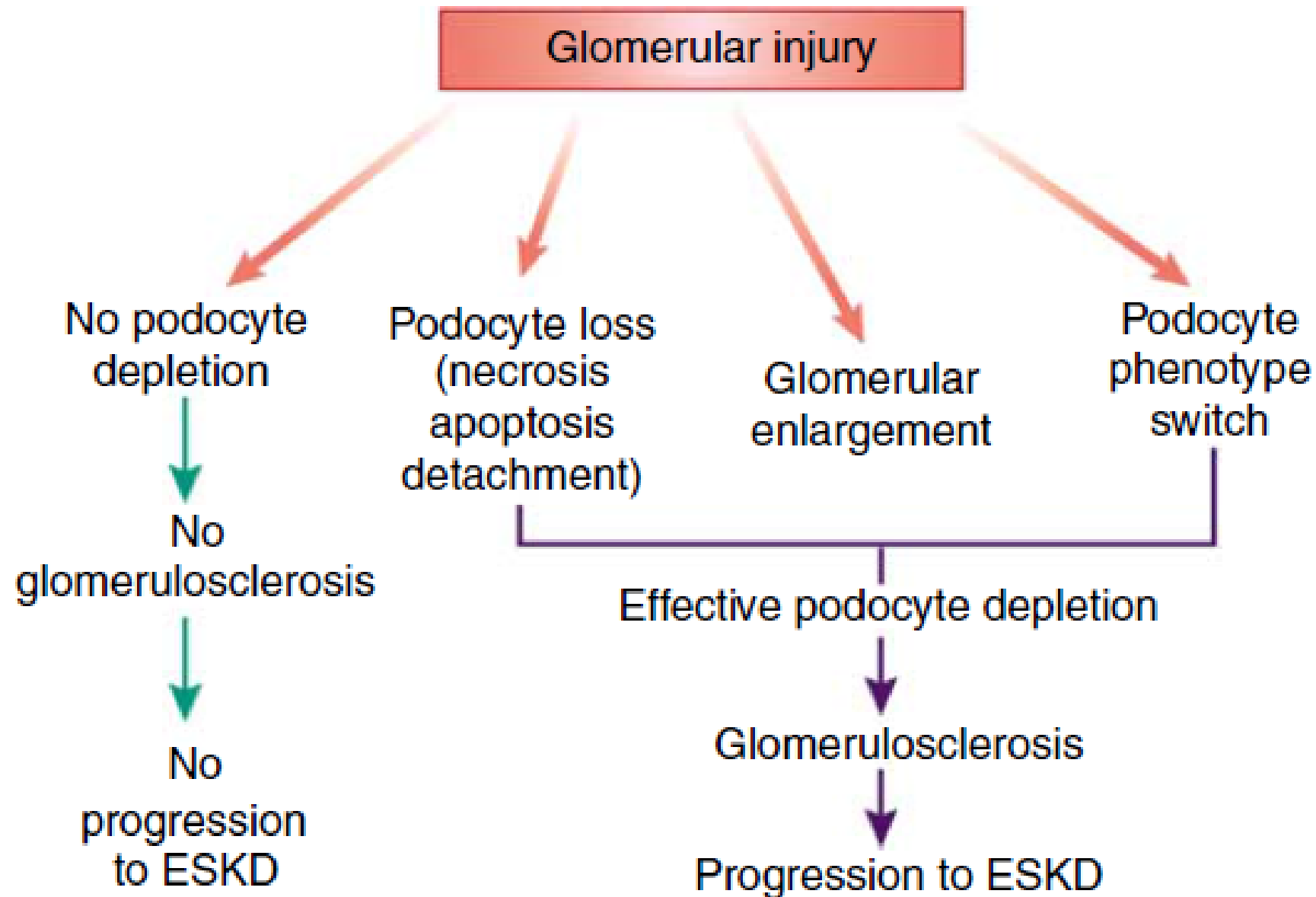


Figure 1 | Effects of proteinuria on tubular epithelial cells. Increased protein absorption by tubular cells may result in direct tubular toxicity, release of chemokines and cytokines, increased expression of adhesion and MHC class II molecules along with co-stimulatory molecules. The net effect is an increased influx of mononuclear inflammatory cells. The evidence for direct proteinuria induced EMT is weak.



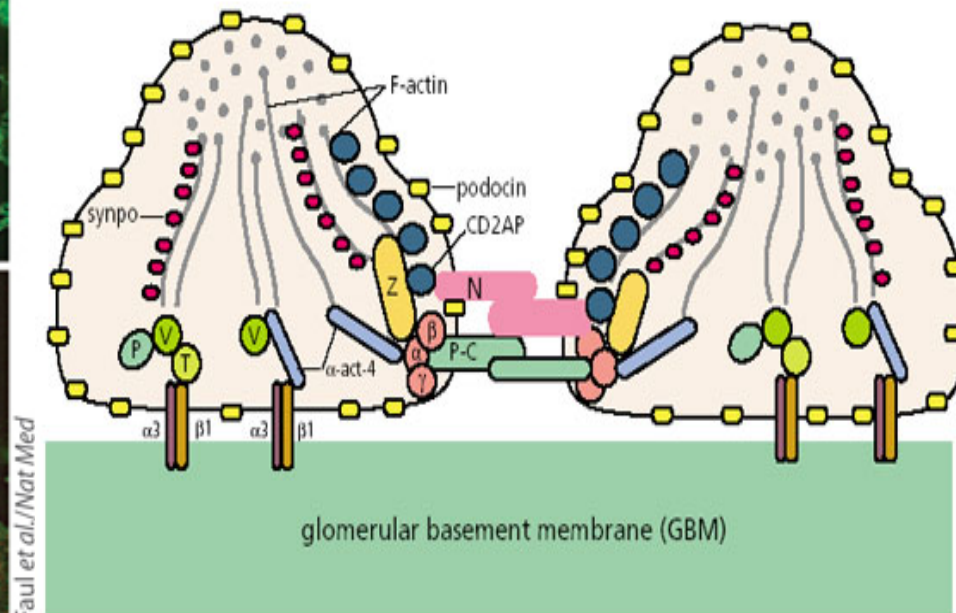
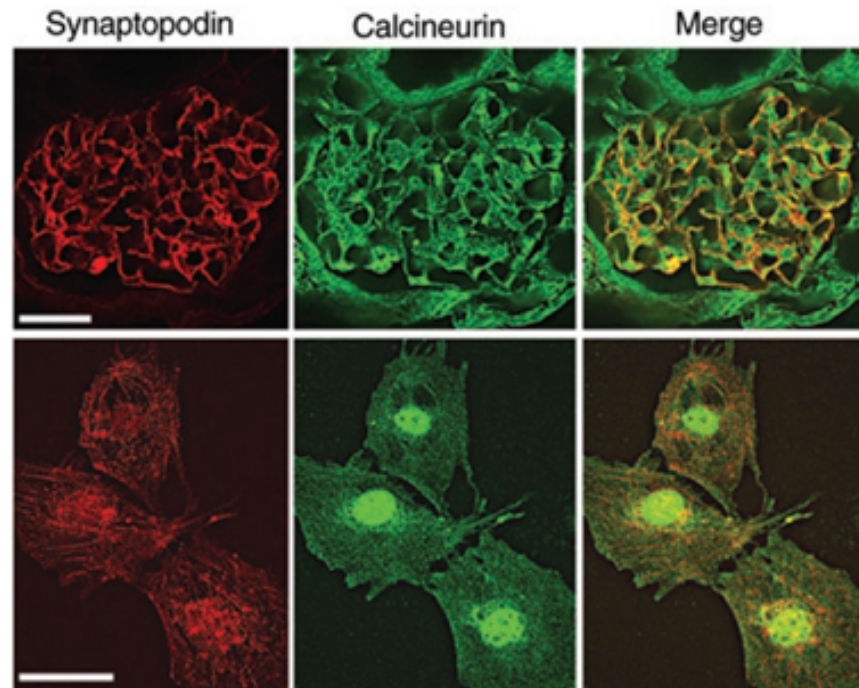


CICLOSPORINA

La CsA bloquea la defosforilación de la sinaptopodina, una proteína organizadora de la actina del podocito. Este bloqueo inhibe la proteólisis de la sinaptopodina, estabilizando las hendiduras diafragmáticas y la contracción-relajación normal del podocito.

Este efecto es independiente de la acción sobre las células B y T.

Interesante: La expresión de calcineurinas en el podocito resulta en la degradación de la sinaptopodina y el desarrollo de proteinuria.



Rol del TRPC6 Transient receptor potential cation channel 6 (trPC6)

Sobreexpresada en familias con FsGs autosómica-dominante.
Estos canales regulan la entrada de calcio intracelular.

En los podocitos, el trPC6 se localiza en la hendidura del diafragma,
y participa en la señalización.

Su sobreexpresión resulta en proteinuria. Es blanco del Tacrolimus

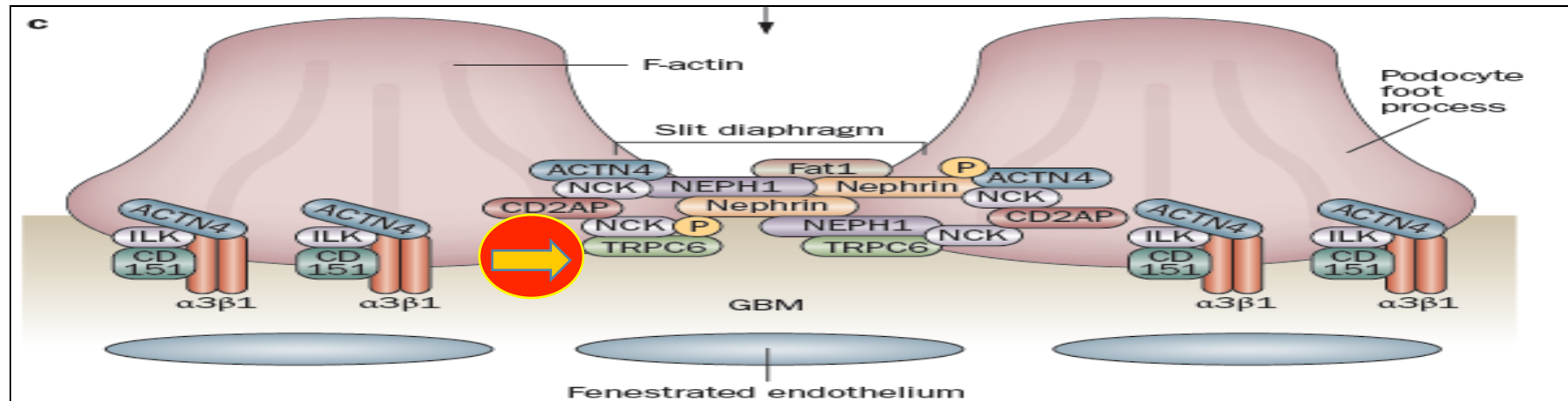


Figure 1 | Structure of the glomerular filtration barrier. **a** | Glomerular filtration occurs through the capillary wall into the urinary space, which empties into the proximal tubules. **b** | The capillary wall contains an innermost fenestrated endothelium, the GBM, and a layer of podocytes with interdigitating foot processes. **c** | Podocyte foot processes, interconnected by slit diaphragms, form the final barrier for filtration. Proteins that anchor the foot processes to the GBM ($\alpha 3 \beta 1$ integrin, ACTN4, ILK and the tetraspanin CD151) as well as those that are associated with the slit diaphragm (nephrin, NEPH1, podocin, Fat1, ACTN4, the adaptor protein NCK, CD2AP, and TRPC6) are crucial for normal function of the filtration barrier. Abbreviations: ACTN4, α -actinin-4; CD2AP, CD2-associated protein; GBM, glomerular basement membrane; ILK, integrin-linked kinase; P, podocin; TRPC6, transient receptor potential cation channel 6.

Table 2 Effects and target structures of new anti-proteinuric strategies on podocytes

New anti-proteinuric strategies	Target structures/pathways on podocytes
Abatacept (CTLA-4-Ig)	B7-1, integrin signalling [4, 93, 96]
Adalimumab (Anti-TGF- β)	TGF- β /SMAD, apoptosis [111]
Amiloride (suPAR blocker)	β 3-integrin signalling [99, 100]
Oral ManNAc	Angptl 4 [116]
Ruboxistaurin (selective PKC- β inhibitor)	(Among others) extracellular matrix synthesis/turnover [120, 121]
Saquinavir (protease inhibitor)	NF- κ B/I κ B α [122, 123]
TRPC6 siRNA	Ca ²⁺ levels, actin cytoskeleton rearrangement [107–110]

Ig, Immunoglobulin; TGF- β , transforming growth factor beta, MAnNAc, *N*-acetyl-D-mannosamine; protein kinase C beta; TRPC6, transient receptor potential cation channel, subfamily C, member 6; siRNA, small interfering RNA; Angptl 4, angiotensin-like 4; NF- κ B/I κ B α , nuclear factor kappa-light-chain-enhancer of activated B cells/inhibitor of kappa B

Abatacept and Glomerular Diseases: The Open Road for the Second Signal as a New Target is Settled Down

Nephrol Dial Transplant (2012) 27: 1746–1755

doi: 10.1093/ndt/gfr612

Advance Access publication 9 November 2011

Amiloride off-target effect inhibits podocyte urokinase receptor expression and reduces proteinuria

Bin Zhang^{1,2,*}, Shaoting Xie^{1,2,*}, Wei Shi¹ and Yun Yang¹

Podocyte directed therapy of nephrotic syndrome—can we bring the inside out?

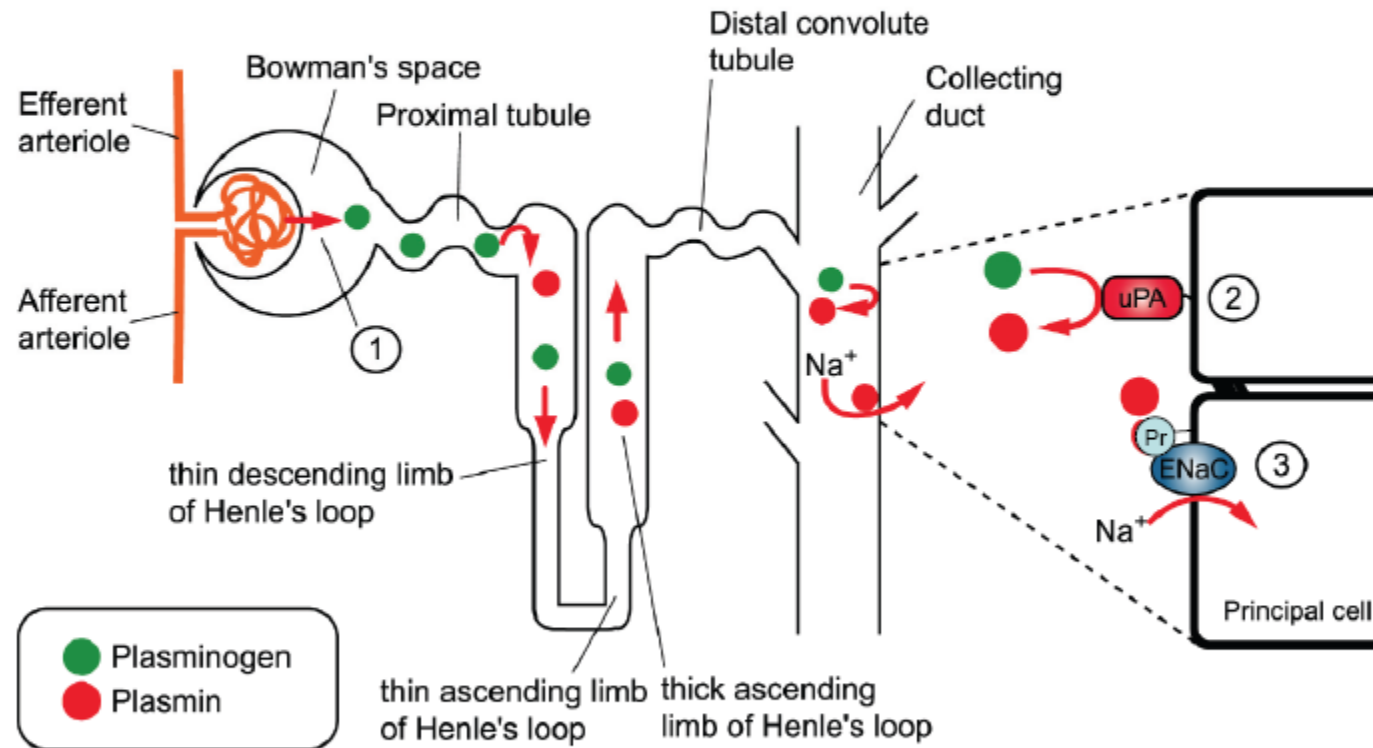
Janina Müller-Deile¹ • Mario Schiffer¹

Case Report

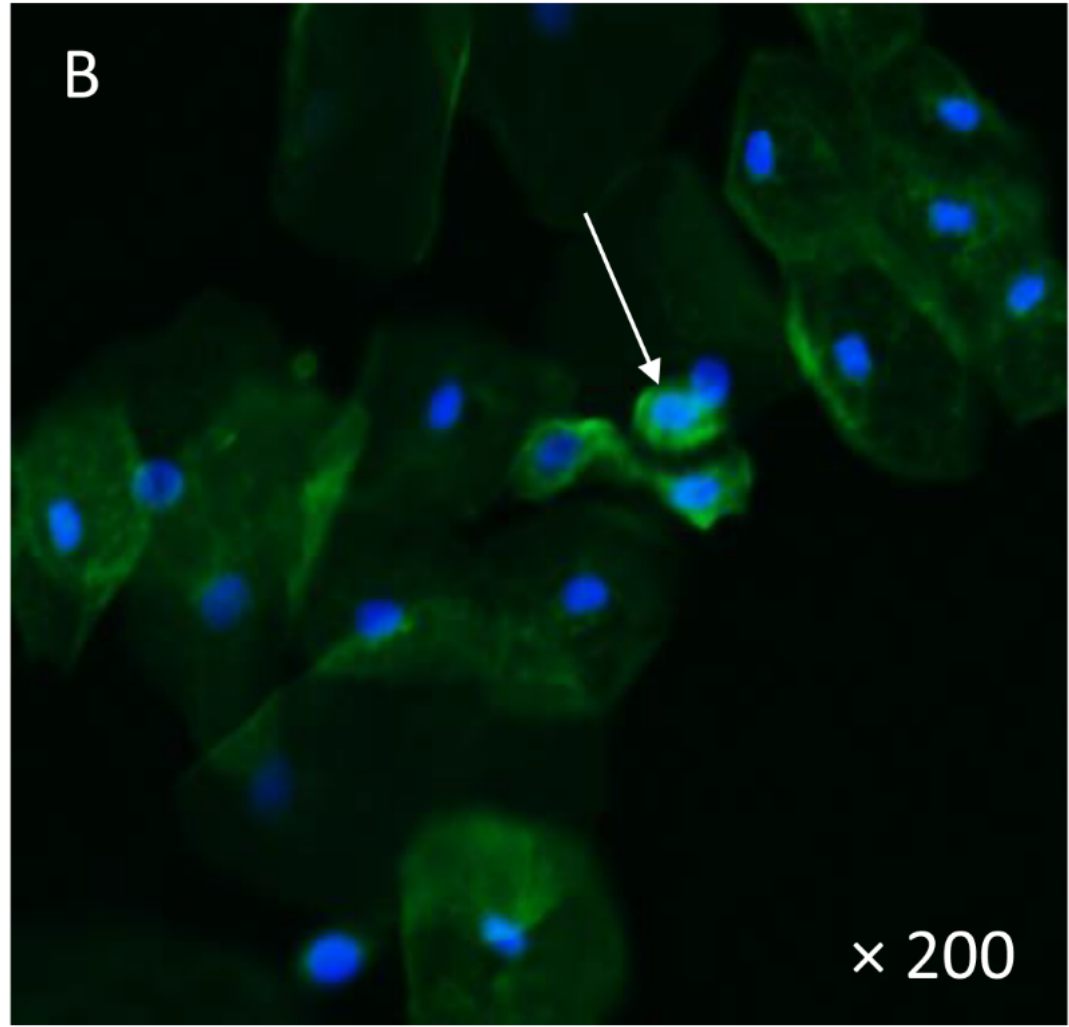
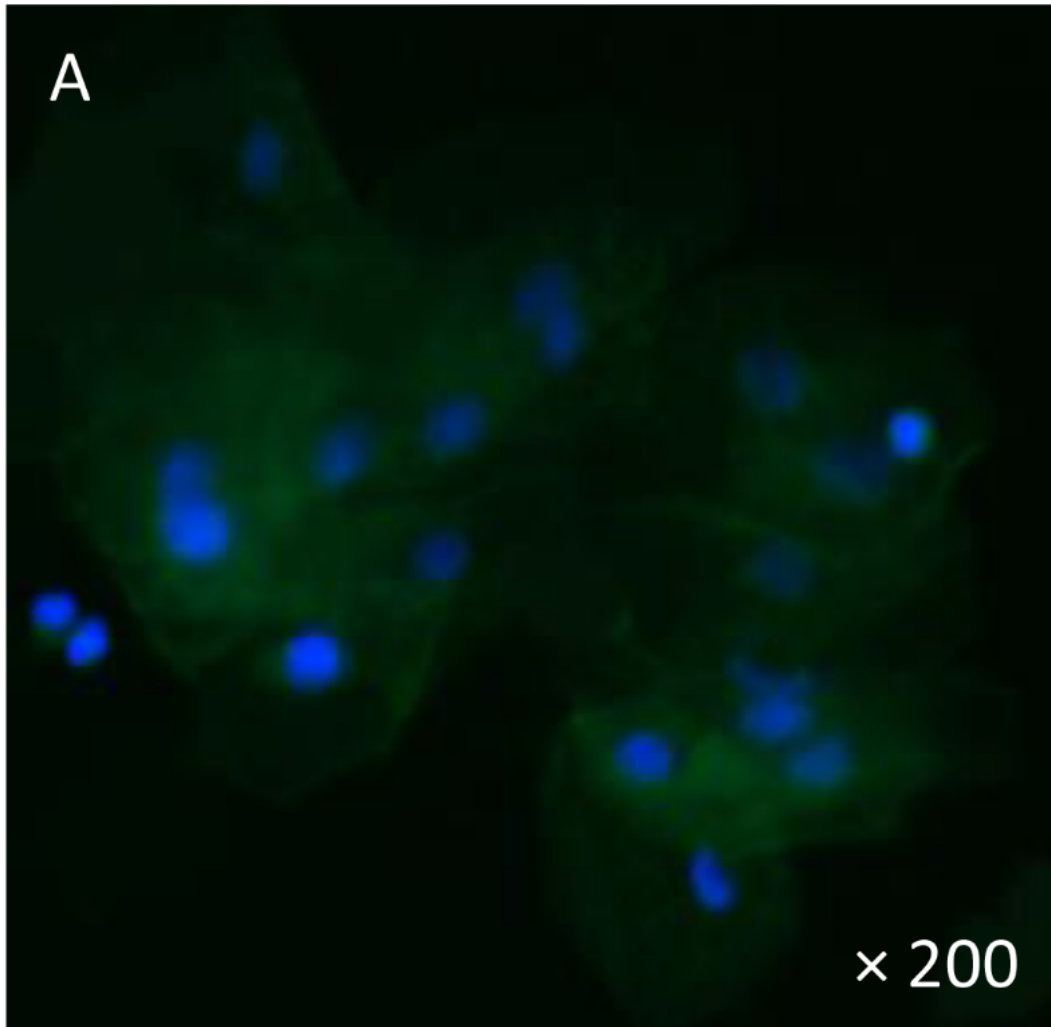
Amiloride as an Alternate Adjuvant Antiproteinuric Agent in Fabry Disease: The Potential Roles of Plasmin and uPAR

H. Trimarchi, M. Forrester, F. Lombi, V. Pomeranz, M. S. Raña, A. Karl, and J. Andrews

A novel model for stimulation of sodium reabsorption in nephrotic syndrome



Proteinuria may promote distal sodium reabsorption



Cerro Torre, glacier and lagoon, Santa Cruz Argentina



The spectrum of podocyte diseases

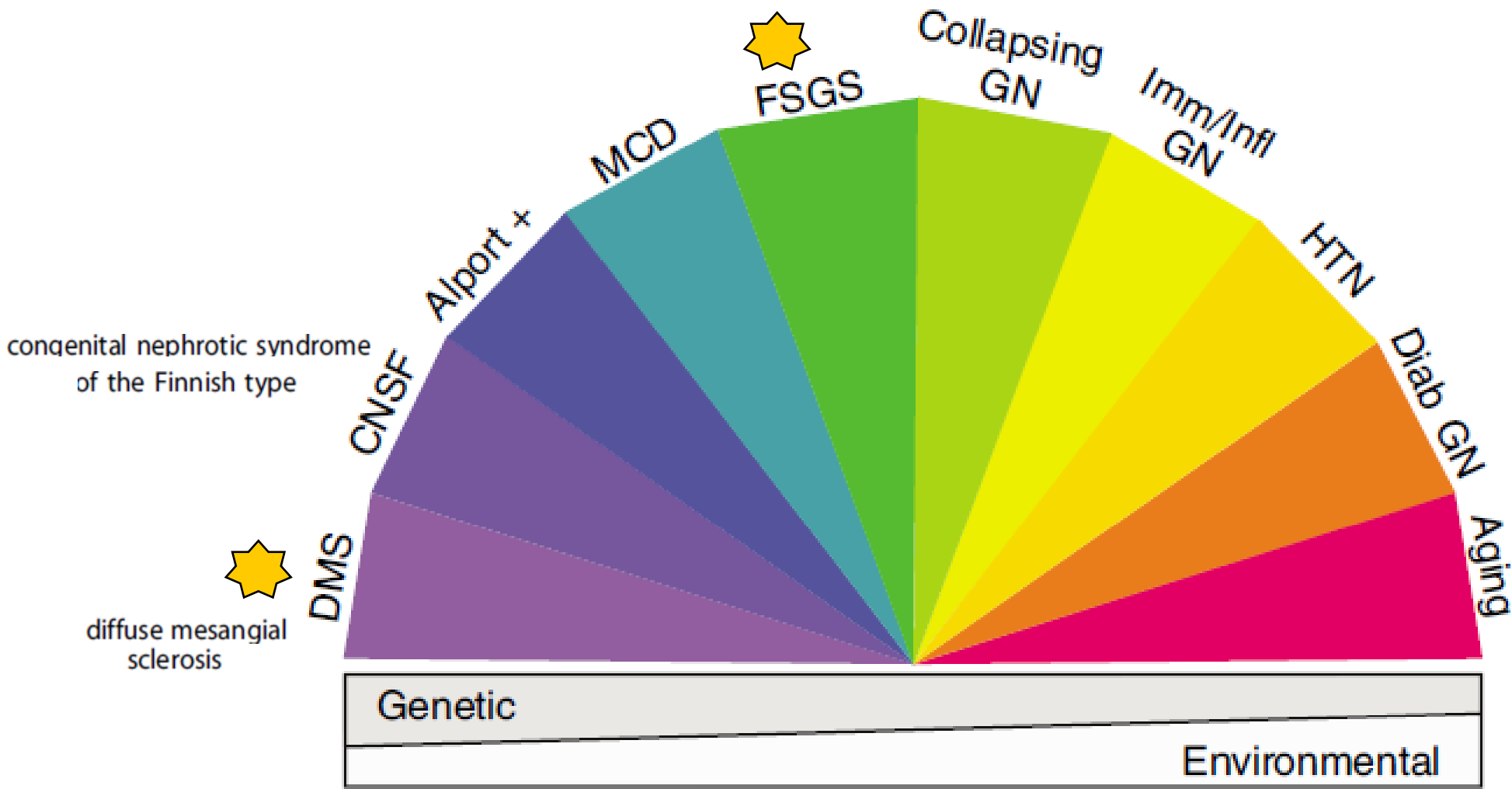
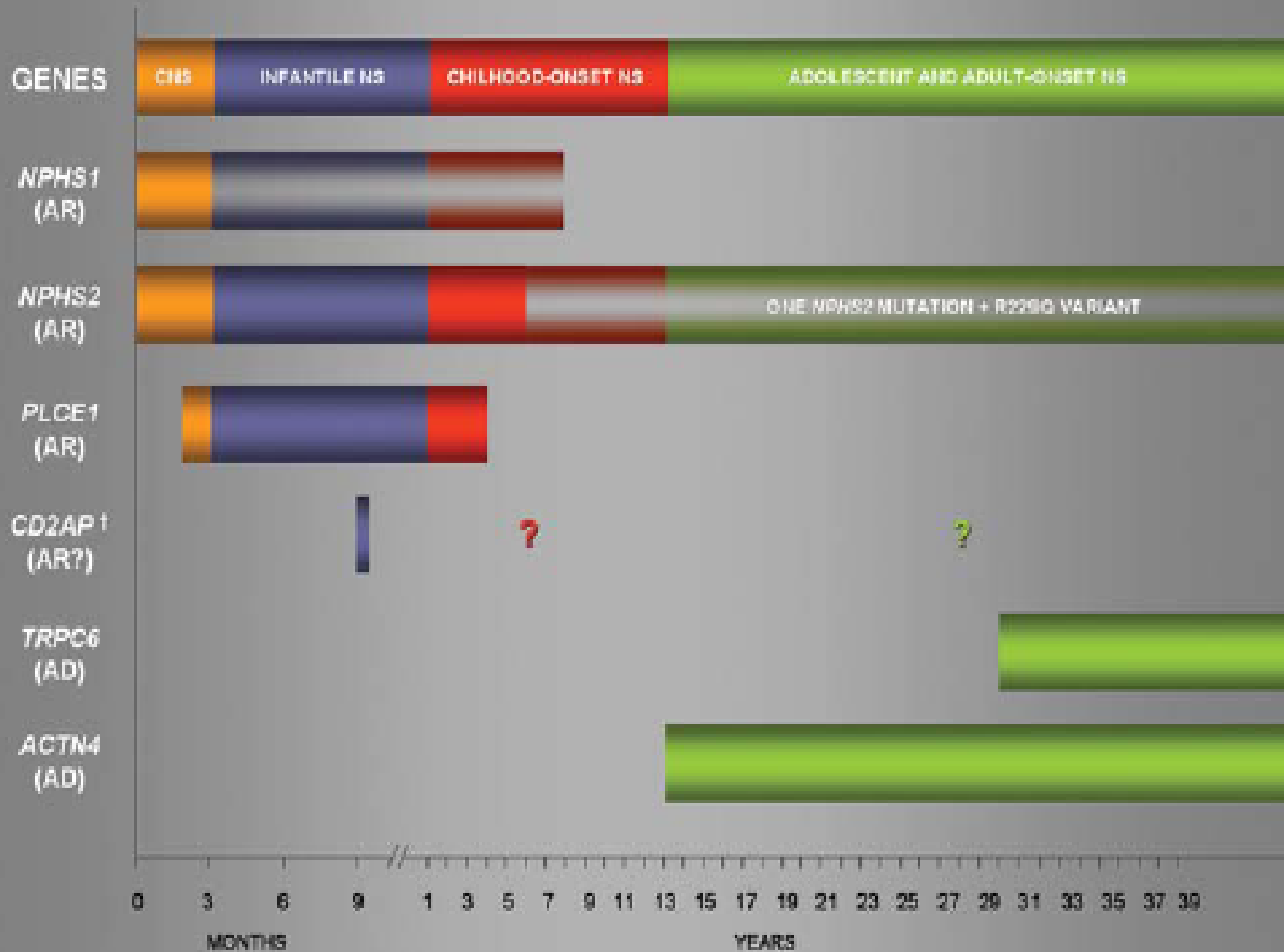


FIGURE 3. AGE AT ONSET OF NON SYNDROMIC FORMS OF NS

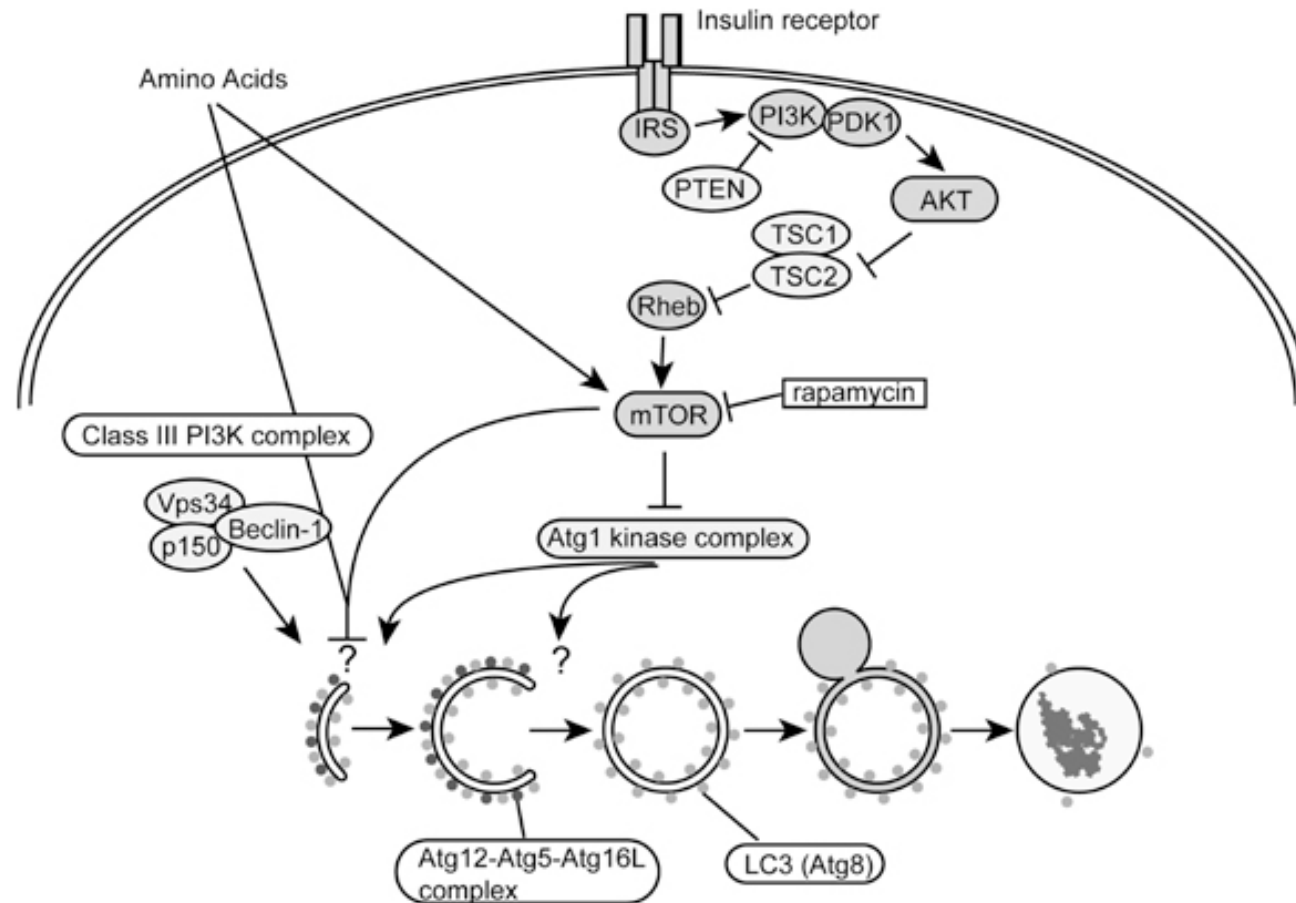


Accumulation of Gb₃ is accompanied by an increase in autophagosomes, suggesting that deregulated autophagy pathways have some involvement in the pathogenesis of glomerular damage in Fabry disease.



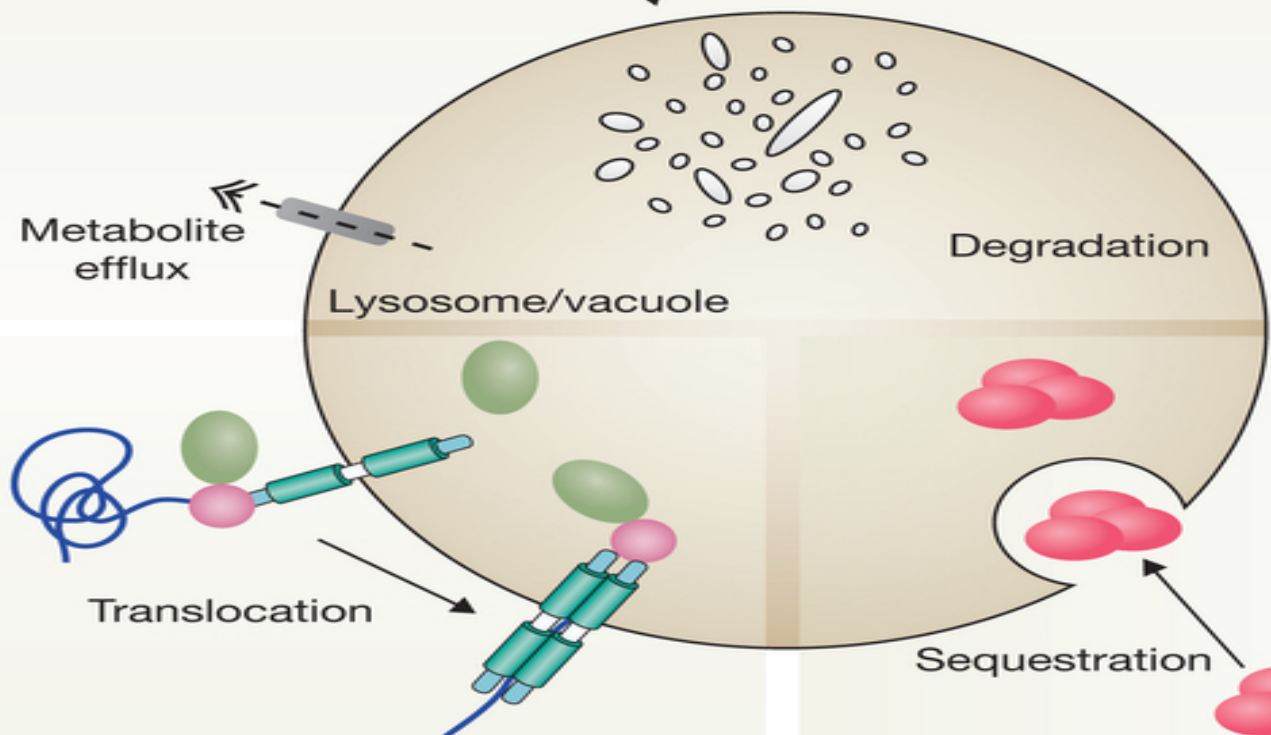
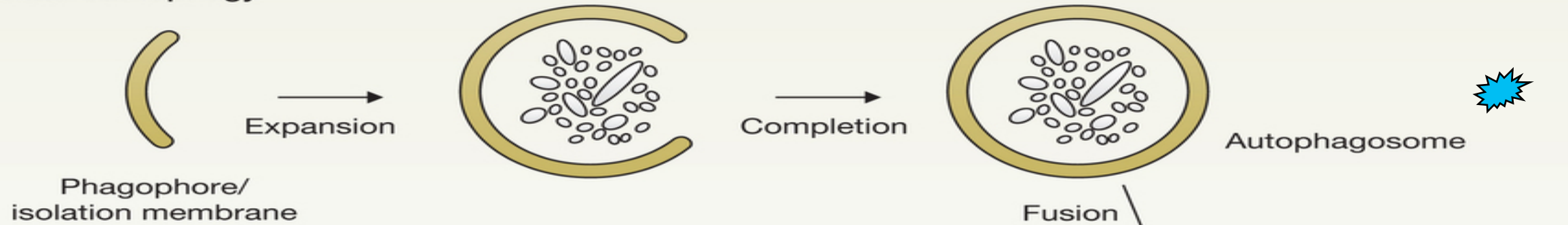
AUTOPHAGY

Autophagy enables the cell to have access to nutrients in situations of stress or starvation. Intracellular material is degraded in a lysosome dependent mechanism, and autophagy serves as an intracellular recycling system.



An isolation membrane engulfs intracellular targets to become an autophagosome containing the LC3-II isoform of the **essential autophagy protein LC3**. The autophagosome then fuses with a lysosome to form a so called autophagolysosome, which contains damaged and dysfunctional organelles like mitochondria.

a Macroautophagy



b Chaperone-mediated autophagy



c Microautophagy

 LAMP-2A

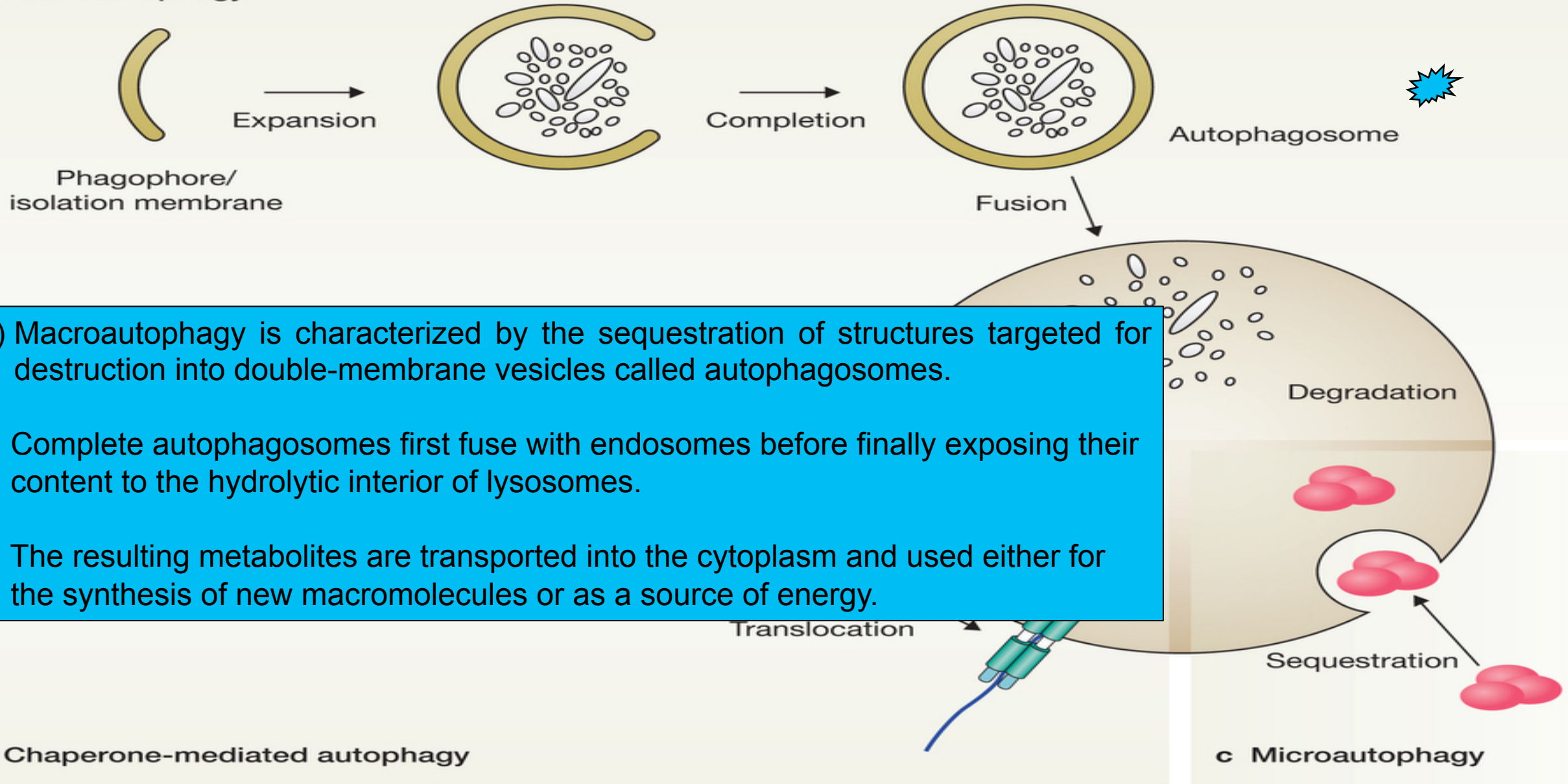
 Hsp70 chaperone

 Protein

 KFERQ motif

 Metabolite transporter

a Macroautophagy



(a) Macroautophagy is characterized by the sequestration of structures targeted for destruction into double-membrane vesicles called autophagosomes.

Complete autophagosomes first fuse with endosomes before finally exposing their content to the hydrolytic interior of lysosomes.

The resulting metabolites are transported into the cytoplasm and used either for the synthesis of new macromolecules or as a source of energy.

b Chaperone-mediated autophagy

c Microautophagy



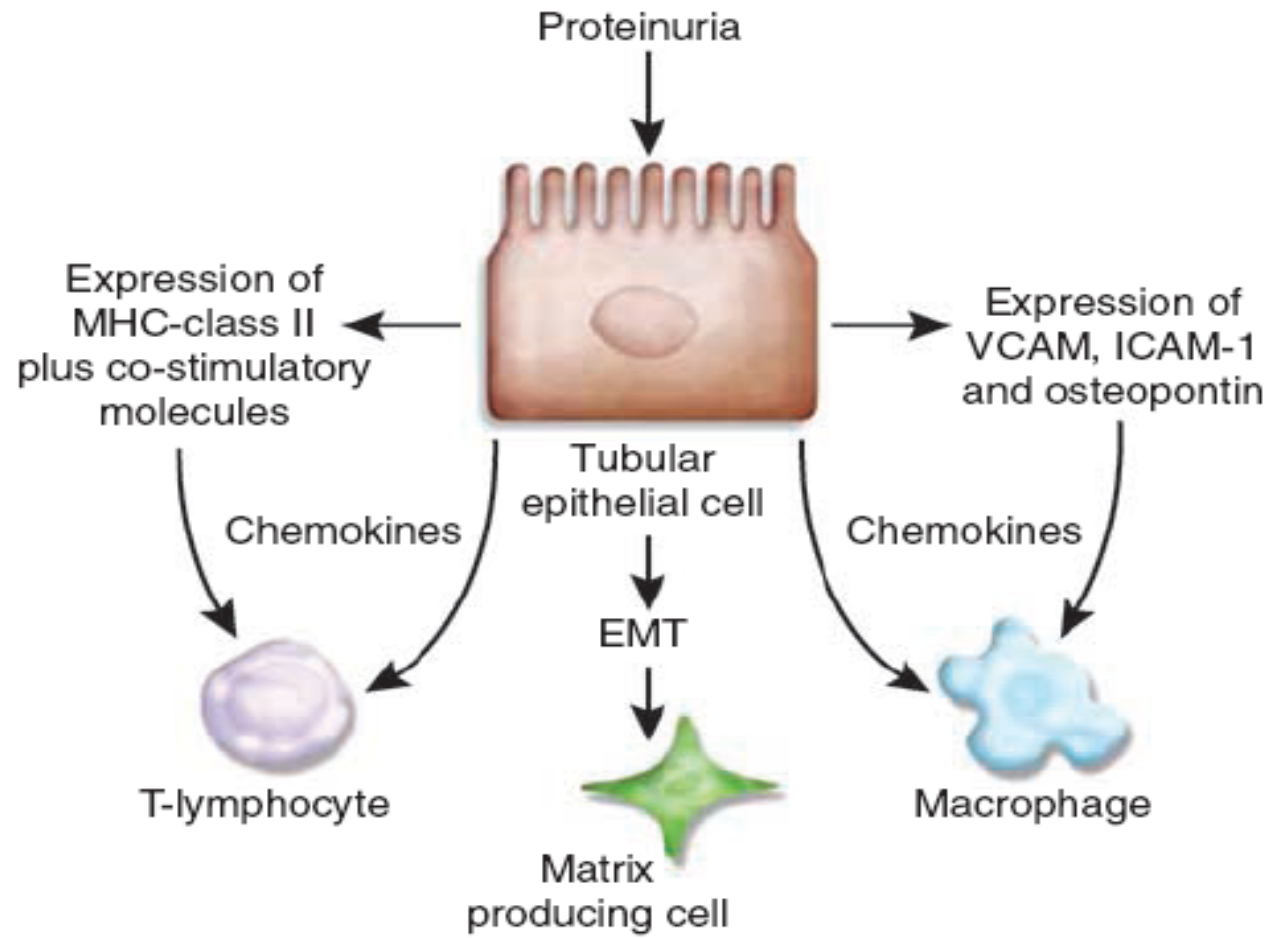
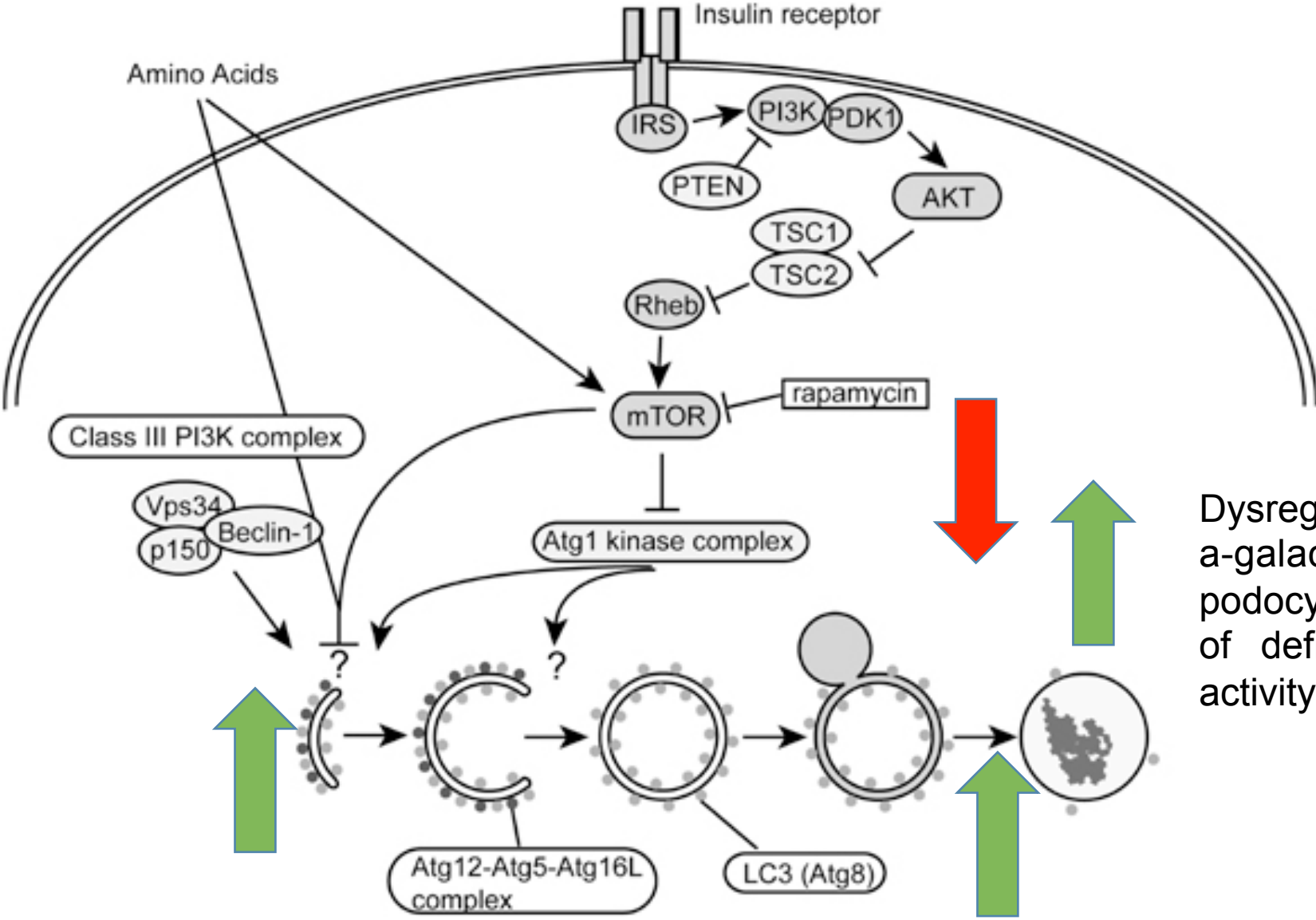
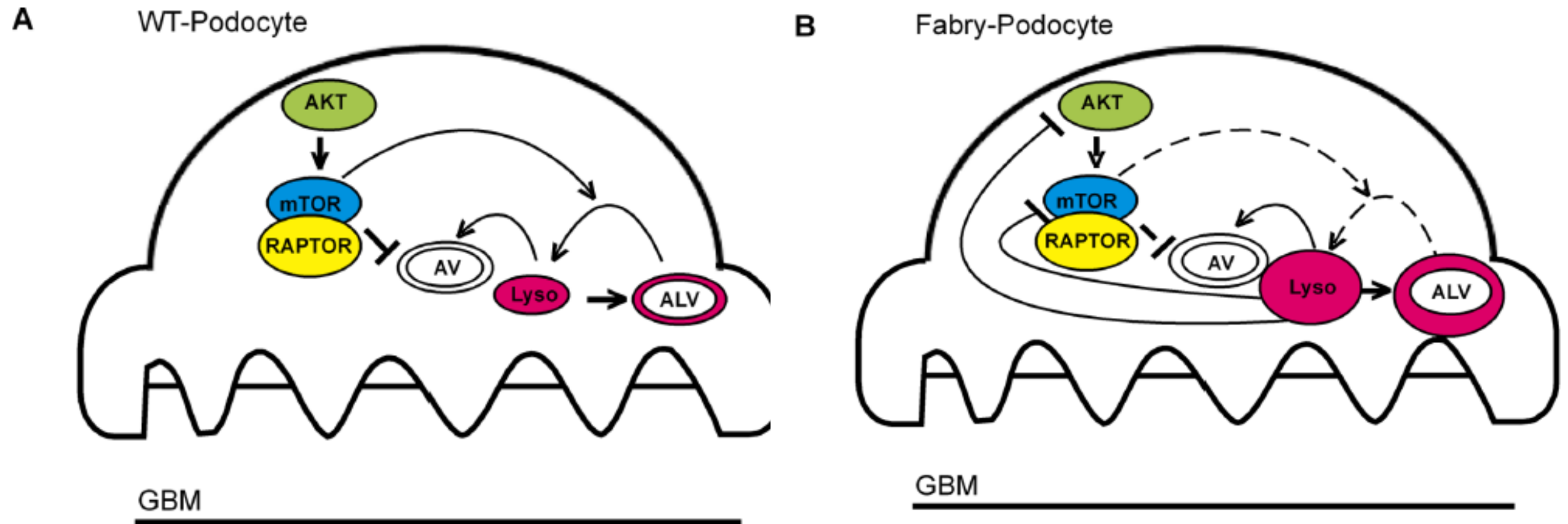


Figure 1 | Effects of proteinuria on tubular epithelial cells. Increased protein absorption by tubular cells may result in direct tubular toxicity, release of chemokines and cytokines, increased expression of adhesion and MHC class II molecules along with co-stimulatory molecules. The net effect is an increased influx of mononuclear inflammatory cells. The evidence for direct proteinuria induced EMT is weak.

Interestingly, these changes were accompanied by an increase in autophagosomes as indicated by an increased abundance of LC3-II and a loss of mTOR kinase activity, a negative regulator of autophagy.



Dysregulated autophagy in a-galactosidase A-deficient podocytes may be the result of deficient mTOR kinase activity.

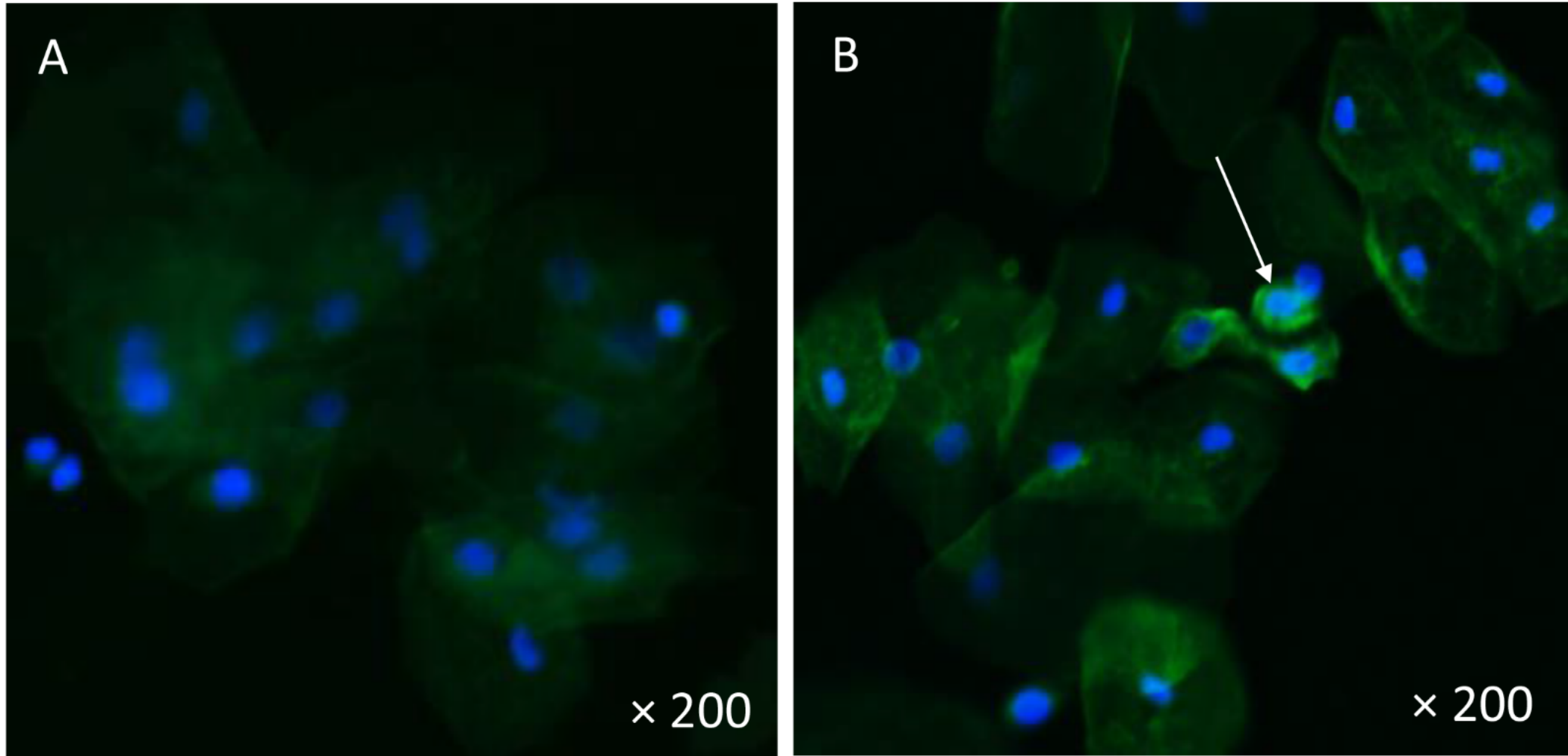


Model on the effect of a-Gal depletion in podocytes

mTOR negatively regulates the formation of autophagy vesicles and promotes the recovery of autophagosomes (AV) and lysosomes (Lys) from autophagolysosomes (ALV) in podocytes (continuous lines).

In Fabry disease a-Gal A dysfunction leads to an accumulation of Gb3 in lysosomes, an increase in autophagosomes and furthermore dysregulates autophagy signaling (dashed lines) by an inhibition of mTOR and its upstream regulator AKT (continuous line).

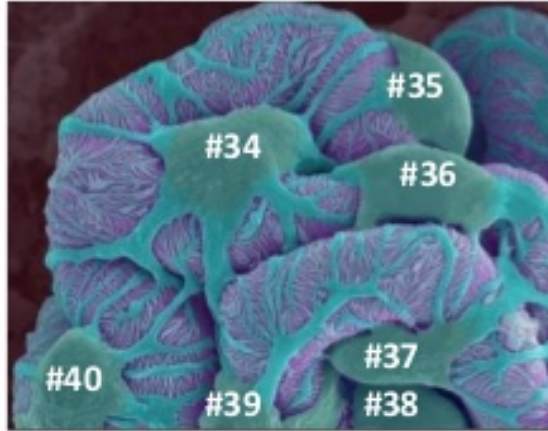
PODOCYTURIA IN FABRY DISEASE IS ELEVATED IN UNTREATED VS TREATED ADULT PATIENTS AND DOES NOT CORRELATE WITH PROTEINURIA OR RENAL FUNCTION



Each Podocyte Counts!

PODOCYTES 2%
Tryggvason 2011

1,500,000 – 2,000,000 glomeruli



Each glomerulus has 500-600 podocytes.

Podocytes do not efficiently proliferate.

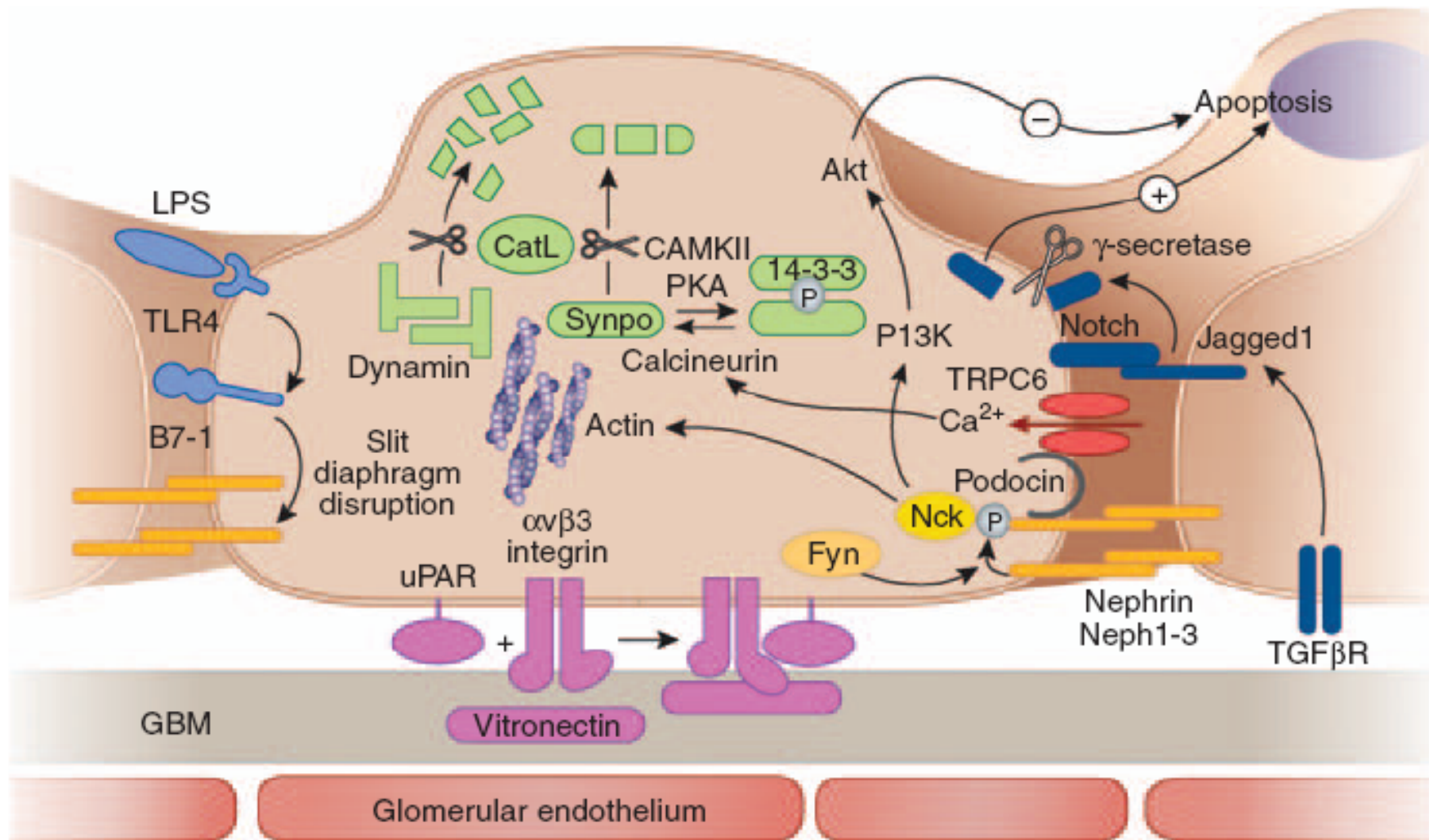
Podocyte loss is cumulative in time

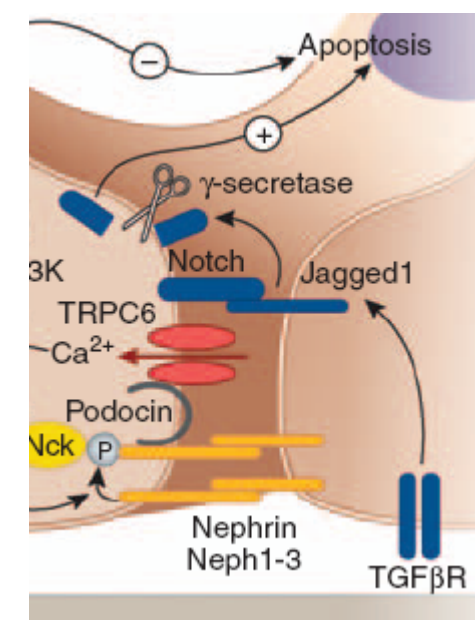
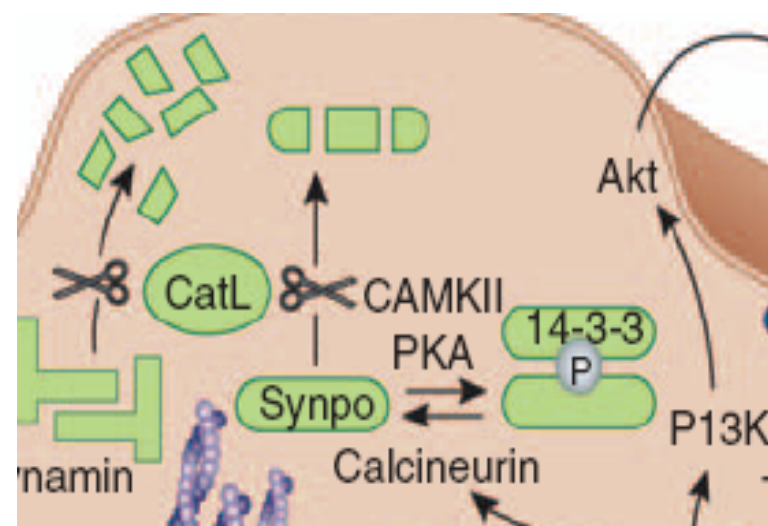
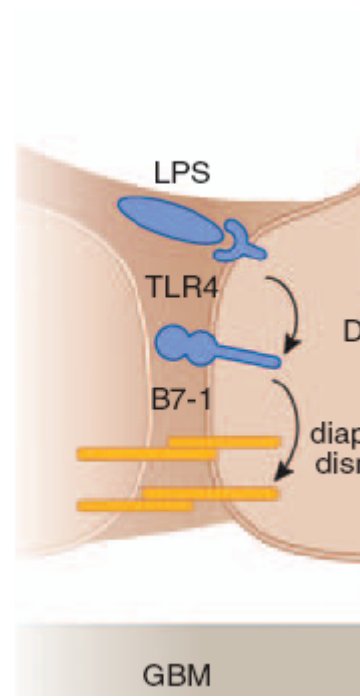
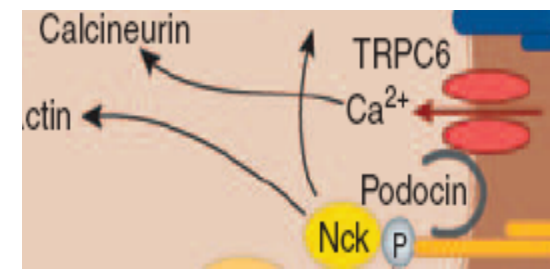
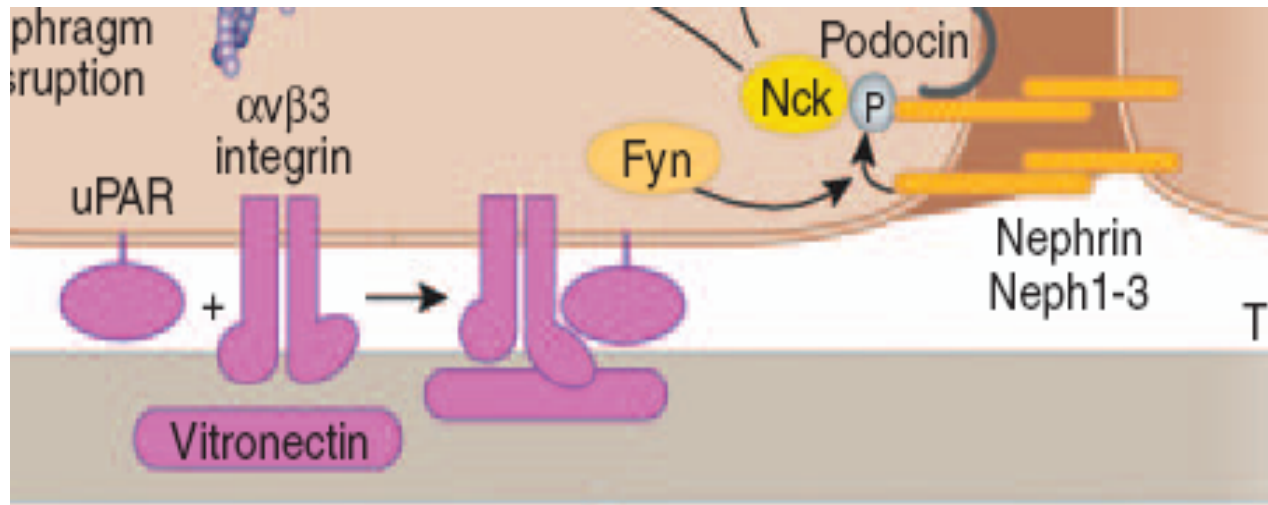
1,000,000,000 podocytes

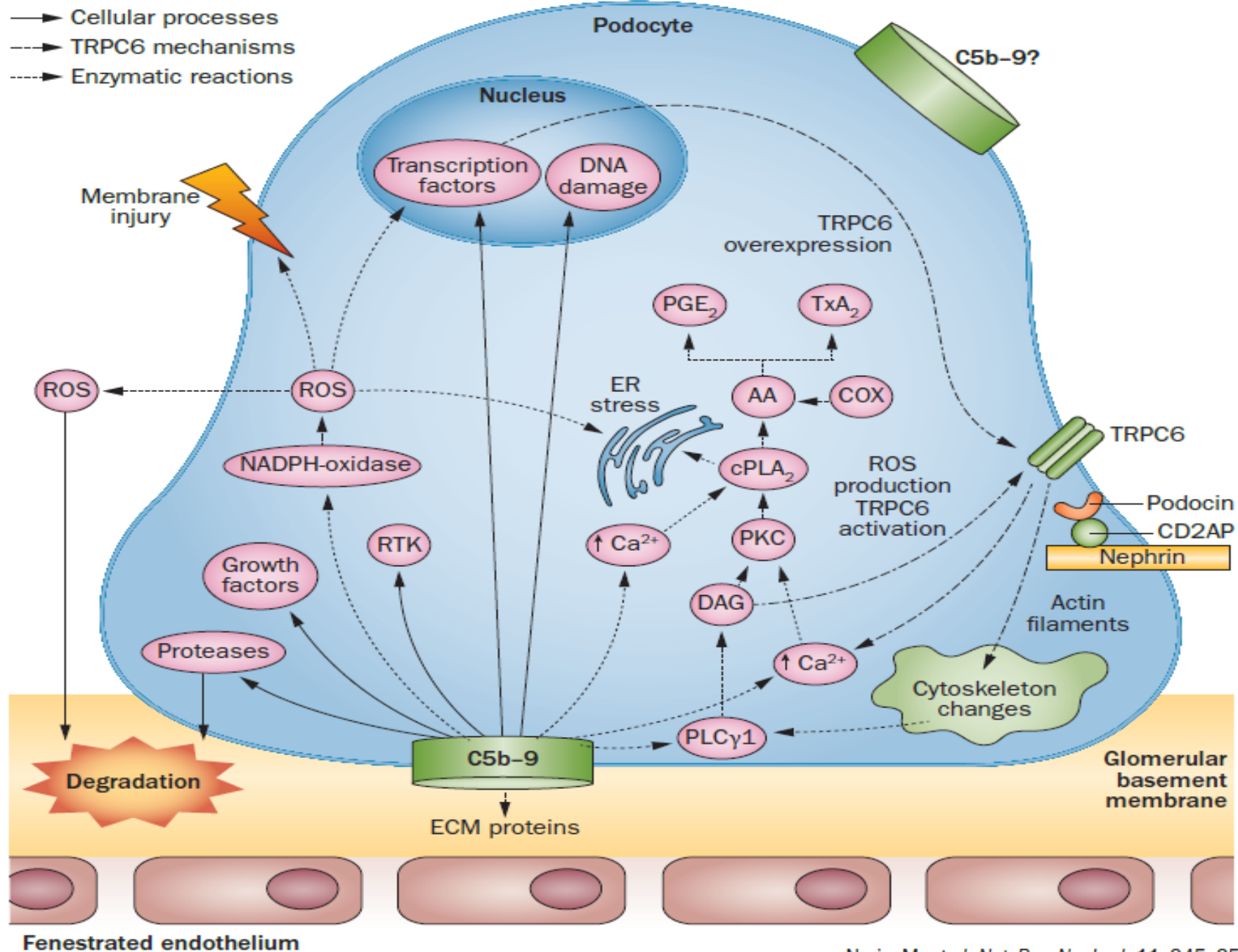
Once a glomerulus loses more than ~20% of its podocytes, it scars down. This injury is irreversible.

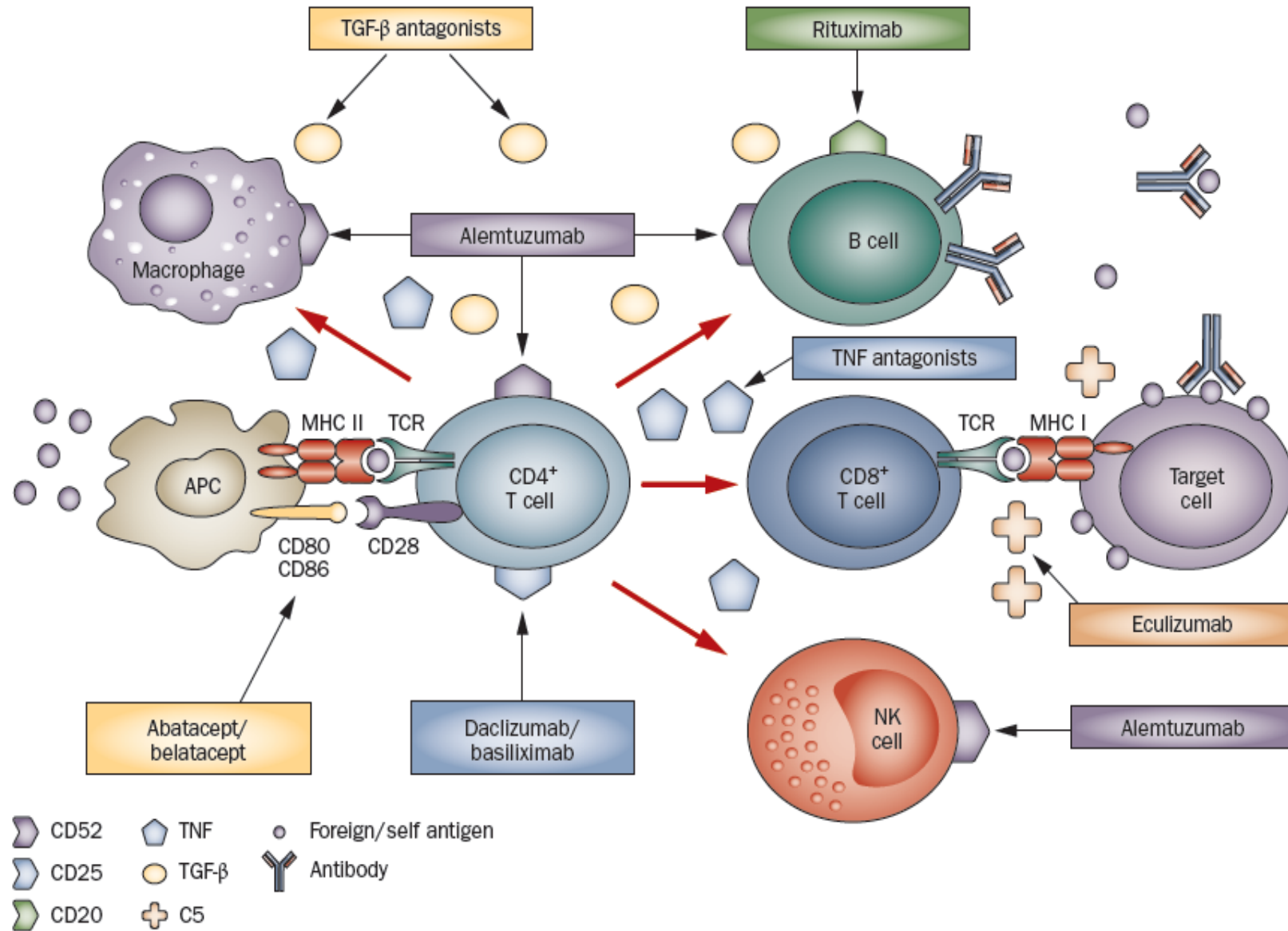
100 podocytes/glomerulus loss of 1 nephron

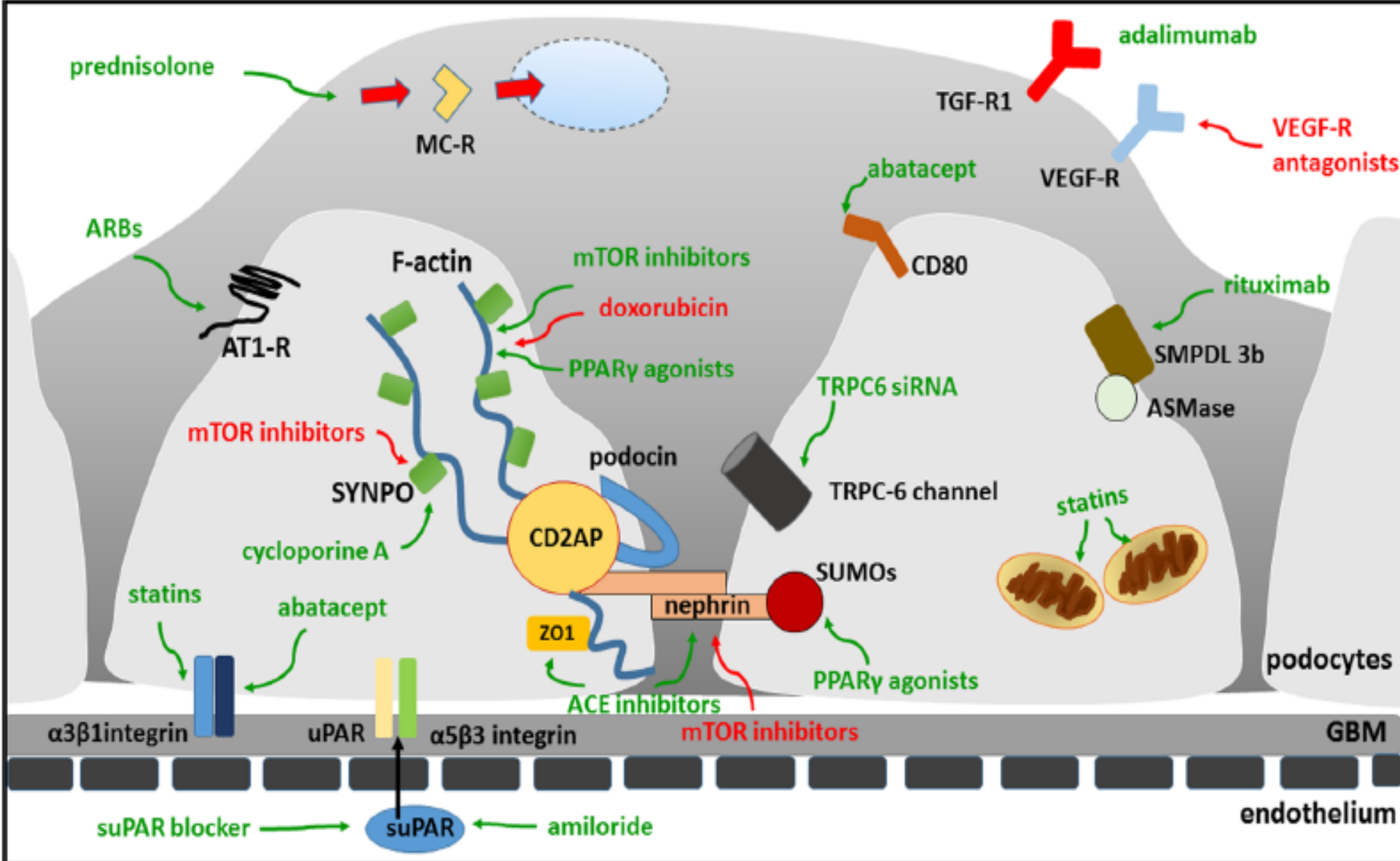
200,000,000 of podocyte losses leads to ESRD

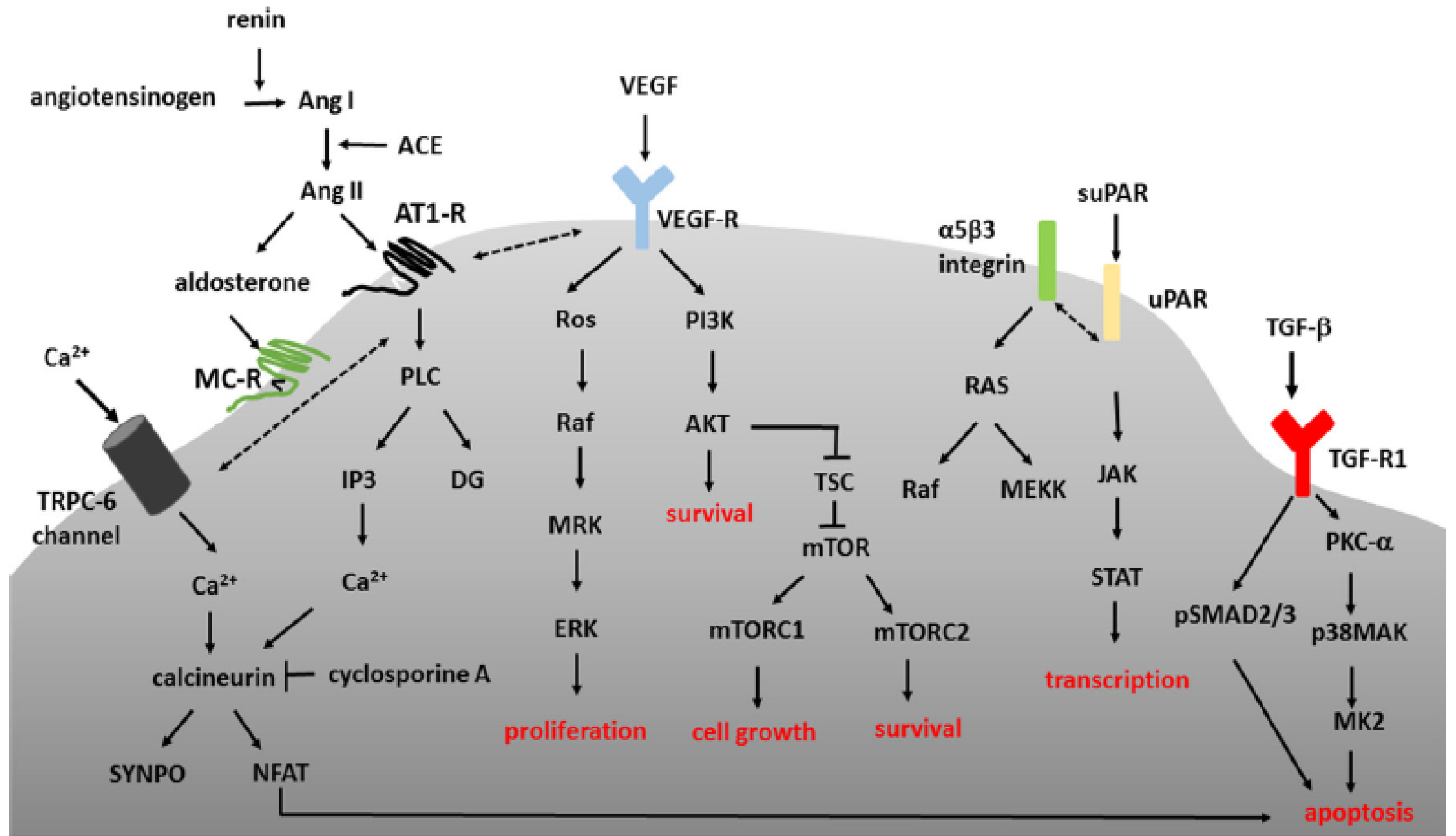








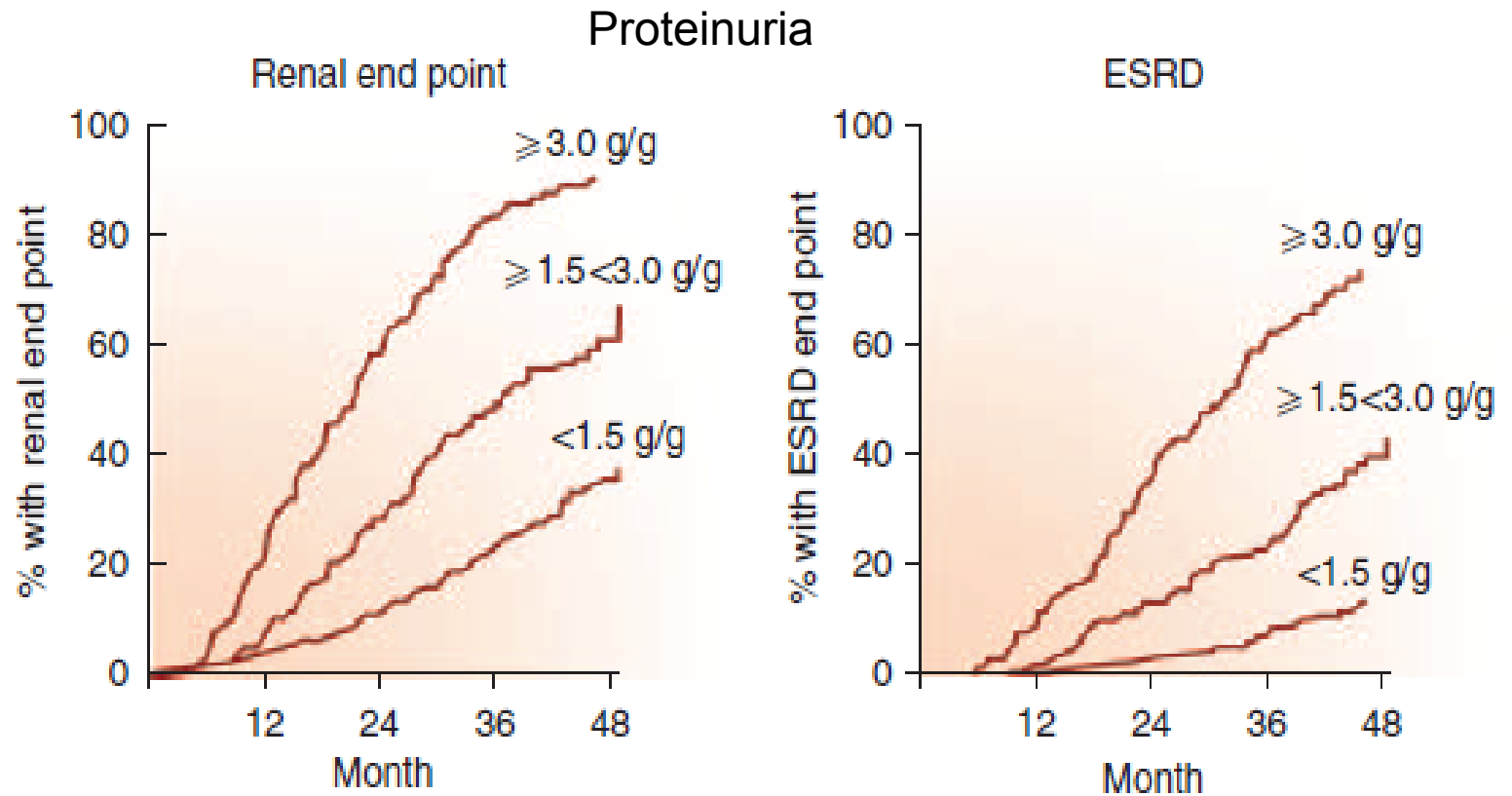




It is an early sign of Fabry nephropathy

Often the most frequent clinical manifestation

Proteinuria is an independent risk factor affecting the extent of renal decline in treated and untreated patients, and in determining the success of ERT.



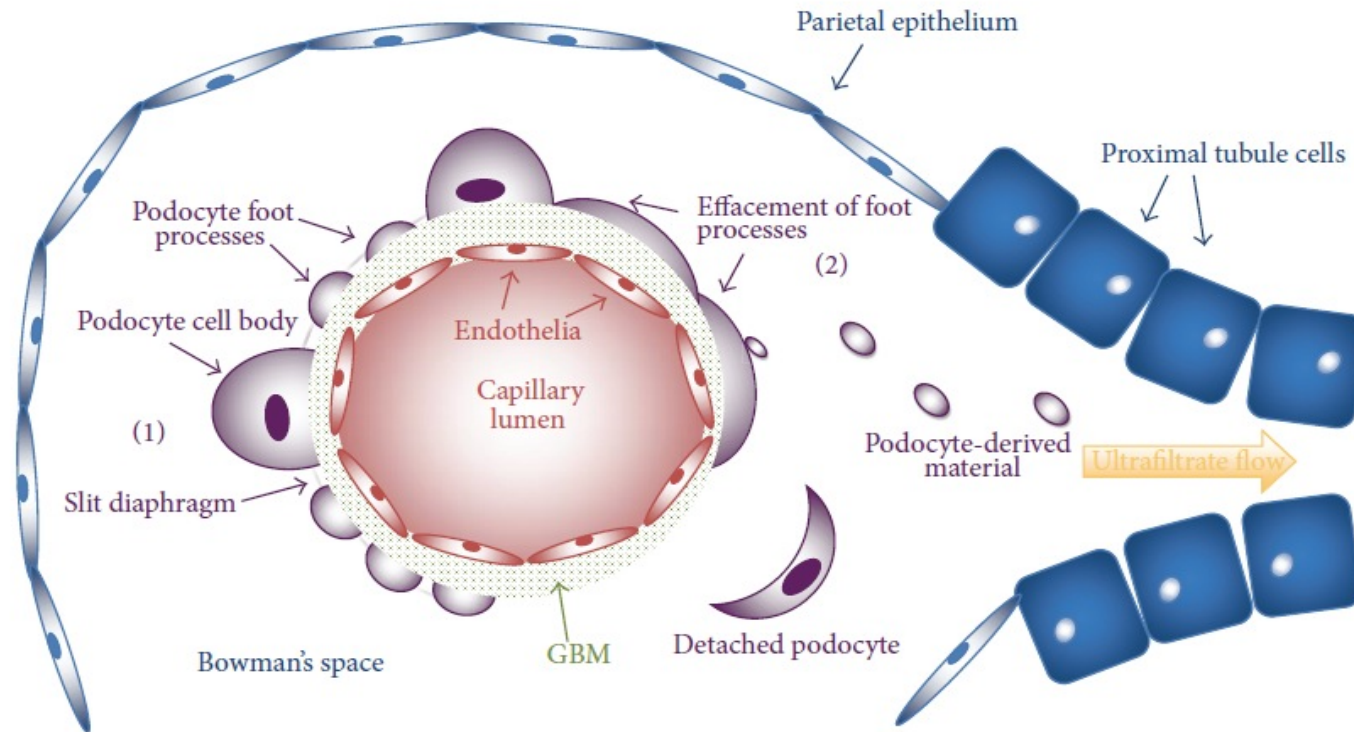
Data from 1,262 adult patients (585 males, 677 females) in the Fabry Registry demonstrated overt proteinuria (>300 mg/day) in 43% and 26% of males and females with CKD stage 1, respectively, with higher proportions in patients with more advanced kidney involvement.

Proteinuria should be monitored regularly and treated appropriately.

Podocyturia: What is in a name?

Hernán Trimarchi

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Hindawi Publishing Corporation
Case Reports in Nephrology
Volume 2015, Article ID 257628, 4 pages
<http://dx.doi.org/10.1155/2015/257628>



Case Report

Copious Podocyturia without Proteinuria and with Normal Renal Function in a Young Adult with Fabry Disease

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A. Karl,¹ F. Lombi,¹ J. Andrews,¹ V. Pomeranz,¹ T. Rengel,¹ and E. Zotta³**

2. Case Presentation

The diagnosis of Fabry disease was made in an 18-year-old male who suffered from acroparesthesias, decreased sweating and frequent episodes of diarrhea. The test for α -galactosidase disclosed decreased enzyme activity, 0.1 nmol/hour/liter (normal > 4 nmol/hour/liter). A novel mutation [c.100A>G (p.N34D)] was identified in the gene of α -galactosidase A, diagnosed by sequential analysis. The laboratory results were unremarkable, with a creatinine clearance of 115 ml/min, a negative 24-hour urinary protein excretion; microalbuminuria: 28 μ g/min. A renal ultrasound was normal.

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podocyte count was assessed by counting in urinary smears the number of cells in 10 microscopy fields of x20. The podocyte count was 1.6 cells per x20 field; the number of podocytes per gram of urinary creatinine was 133, and the number of podocytes/100 mL of urine was 8. Podocytes were identified by tagging synaptopodin (ab109560 Alexa Fluor®, Abcam, Cambridge United Kingdom) an specific marker of podocytes, to establish their identity by immunofluorescence techniques using a secondary antibody (Alexa Fluor® 488, Abcam, Cambridge United Kingdom). The smears were analyzed employing an epifluorescence microscopy, Nikon Eclipse E 200. This result was compared with a control

COPIOUS PODOCYTURIA WITHOUT PROTEINURIA AND WITH NORMAL RENAL FUNCTION IN A YOUNG ADULT WITH FABRY DISEASE

H. Trimarchi¹, R. Canzonieri², A. Muryan², A. Schiel², A. Araoz³, M. Forrester¹, A. Karl¹, F. Lombi¹, J. Andrews¹, V. Pomeranz¹, T. Rengel¹, E. Zotta³.

¹ Nephrology and ² Laboratory Services, Hospital Británico de Buenos Aires, Buenos Aires Argentina, and ³ IFIBIO Houssay- UBA CONICET, Facultad de Medicina, Universidad de Buenos Aires, Argentina

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The patient declined to undergo a kidney biopsy, but accepted enzyme replacement therapy intravenously with agalsidase beta 1mg/kg every fortnight (Fabrazyme, Genzyme Corp, Cambridge MA USA) and enalapril 5 mg/day orally.



52nd ERA-EDTA CONGRESS
UNITED KINGDOM LONDON 2015 MAY 28th - 31st
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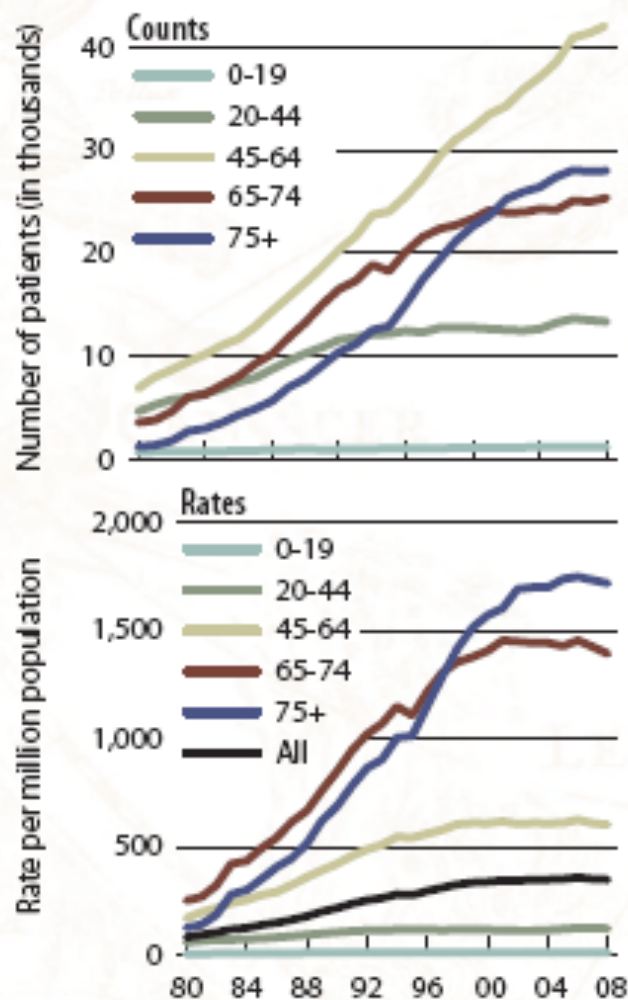


Dear Dr TRIMARCHI,

We have the pleasure of informing you that your abstract entitled **“PODOCYTURIA IN FABRY DISEASE IS ELEVATED IN UNTREATED VS TREATED ADULT PATIENTS AND DOES NOT CORRELATE WITH PROTEINURIA OR RENAL FUNCTION”** has been accepted as a **Poster Presentation** at the 52nd ERA-EDTA Congress, which will be organised in collaboration with the Renal Association in London, United Kingdom (May 28-31, 2015).

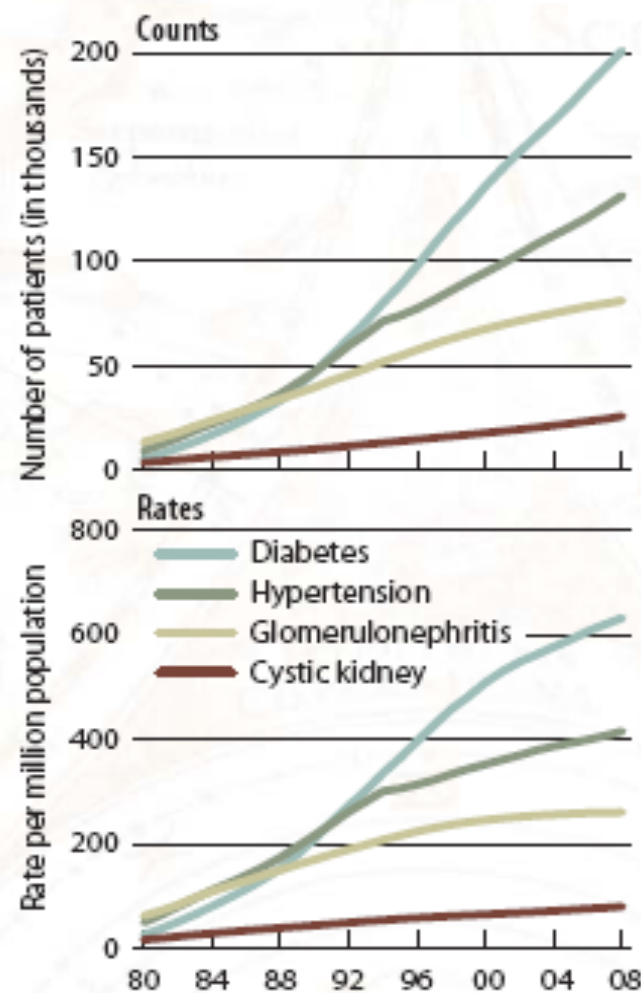
2
4th

Incident counts & adjusted rates of ESRD, by age



2
15th

Prevalent counts & adjusted rates of ESRD, by primary diagnosis





Glaciar Perito Moreno Santa Cruz Argentina