ACR REVIEW 2026

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Sociedad Española de Reumatología

PATROCINADO POR: AstraZeneca · Gebro Pharma · Lilly A MEDICINE COMPANY

ACR REVIEW 2026

VASCULITIS, MIOPATÍAS Y OTRAS CONECTIVOPATÍAS

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2122: Response to Upadacitinib in New-Onset Versus Relapsing Giant Cell Arteritis: Two-Year Outcomes From the SELECT-GCA Phase 3 Trial

Anisha Dua et al. Chicago, IL



2122: Response to Upadacitinib in New-Onset Versus Relapsing Giant Cell Arteritis: Two-Year Outcomes From the SELECT-GCA Phase 3 Trial

Objective

- To evaluate continuation of UPA15 vs switch to placebo (PBO) in patients with new-onset or relapsing GCA.

Methods

- Phase 3 SELECT-GCA trial (104 weeks).
- Period 1: UPA15 + 26-week GC taper or PBO + 52-week GC taper.
- Period 2: Continue UPA15 or switch to PBO (weeks 52–104).

Key result

- 103 UPA15-treated patients entering period 2 (PBO: n=35, UPA15: n=68)
- 75/103 (72.8%) patients had new-onset disease
- UPA15 provided ≥90% reduction in risk of disease flare vs PBO in both subgroups.

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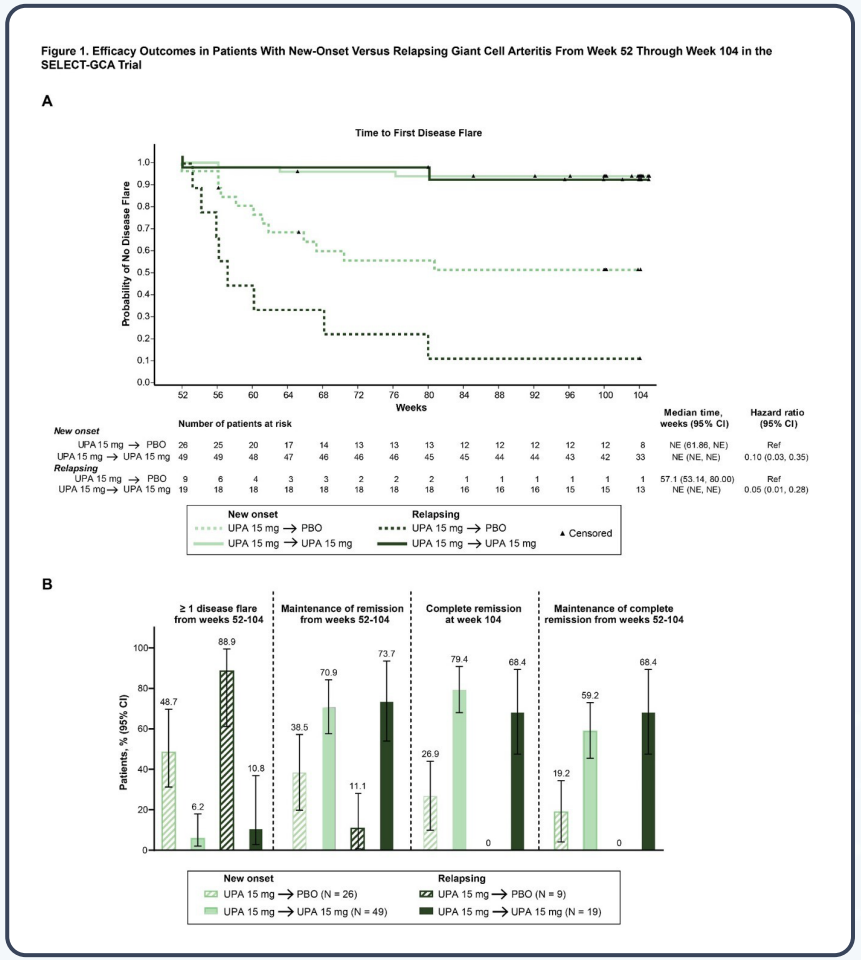
2122: Response to Upadacitinib in New-Onset Versus Relapsing Giant Cell Arteritis: Two-Year Outcomes From the SELECT-GCA Phase 3 Trial

Results

- Relapsing PBO subgroup: shorter time to first flare and numerically lower remission rates than new-onset PBO subgroup.
- Cumulative GC dose (weeks 52–104):
  - PBO: 2,297 mg (relapsing) vs 110 mg (new-onset).
  - UPA15: 0 mg in both subgroups.
- No new clinically meaningful safety risks identified.

Conclusion

- Patients with newonset or relapsing GCA benefited from continuous UPA15 treatment up to 2 years.
- Compared with the new-onset subgroup, patients with relapsing GCA switching to PBO were more likely to experience a higher risk of flare, lower remission rates, and greater cumulative GC exposure.



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2124: Secukinumab in patients with polymyalgia rheumatica: Subgroup analyses of Week 52 results of a Phase 3, multicentre, randomised, double-blind, placebo-controlled trial (REPLENISH)

Frank Buttgereit et al. Berlin, Germany



2124: Secukinumab in patients with polymyalgia rheumatica: Subgroup analyses of Week 52 results of a Phase 3, multicentre, randomised, double-blind, placebo-controlled trial (REPLENISH)

Objective

- To evaluate the efficacy of secukinumab (SEC) combined with a GC–taper regimen in PMR patients with a recent relapse, by baseline demographics and disease characteristics.

Methods

- Phase 3, randomised, double-blind, placebo-controlled trial.
- 381 patients randomised (1:1:1) to SEC 300 mg, SEC 150 mg or placebo for 52 weeks.
- All groups received a 24–week prednisone taper regimen.
- Primary endpoint: Sustained remission at Week 52.
- Subgroups: prednisone dose, age, sex, weight, race, disease duration and geographical region.

Results

- Both doses of SEC demonstrated superior efficacy vs. placebo.
- Higher proportion of patients achieved sustained remission across all subgroups.

Frank Buttgereit et al. Berlin, Germany

2124: Secukinumab in patients with polymyalgia rheumatica: Subgroup analyses of Week 52 results of a Phase 3, multicentre, randomised, double-blind, placebo-controlled trial (REPLENISH)

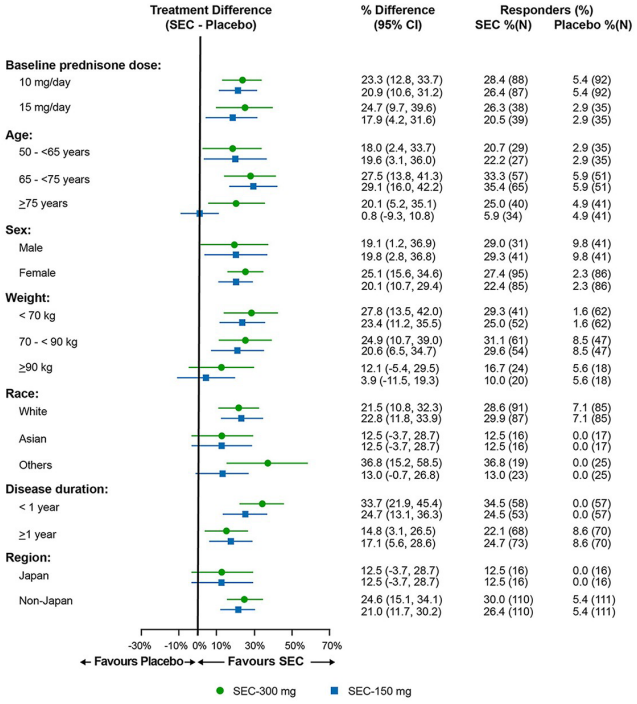
Results

- SEC-300 showed numerically higher responses vs. SEC-150 in select subgroups:
  - Baseline prednisone dose of 15 mg/day.
  - Age ≥75 years.
  - Weight ≥90 kg.
- Safety was consistent with the known safety profile of SEC, with no new safety findings.

Conclusion

- SEC achieved higher sustained and complete sustained remission rates vs. placebo, irrespective of baseline demographics and clinical characteristics.

Figure 2. Forest plot of the treatment effect (95% CI) for complete sustained remission* at Week 52 by subgroups.



*Complete sustained remission was defined as sustained remission with no elevation of inflammatory markers: C-reactive protein [≥10 mg/L] and erythrocyte sedimentation rate [≥40 mm/hr] at ≥ 2 consecutive visits.

CI, confidence interval; N, total number of patients in the treatment group for each subgroup evaluated; SEC, secukinumab

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2149: Time to Disease Relapse After Prolonged Remission in ANCA-Associated Vasculitis

Ellen Romich et al. Media, PA



2149: Time to Disease Relapse After Prolonged Remission in ANCA-Associated Vasculitis

Objective

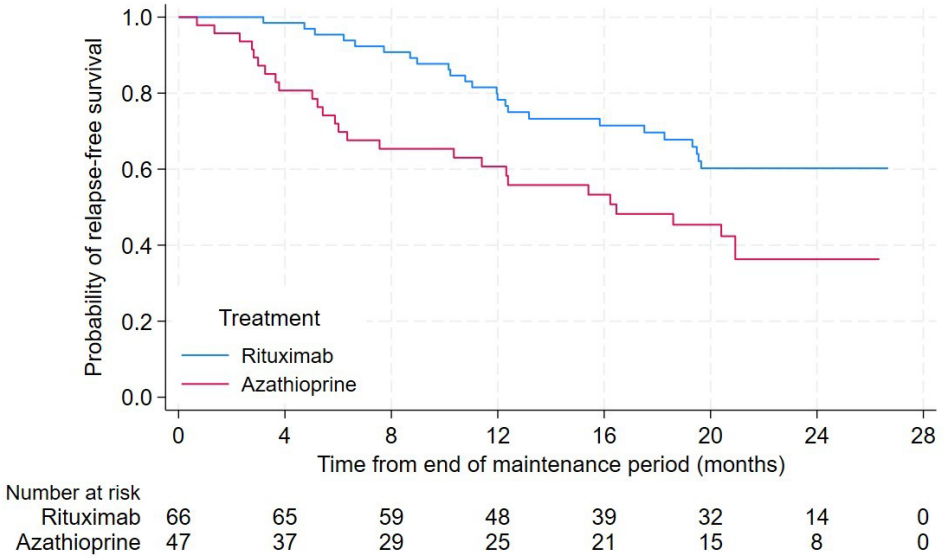
- To determine time to disease relapse after completing maintenance treatment with rituximab (RTX) or azathioprine (AZA).

Methods

- Post-hoc analysis of the RITAZAREM trial.
- 113 patients completed maintenance treatment (RTX: 66; AZA: 47).
- Time to relapse assessed after treatment withdrawal.

Results

- Relapses: 37% RTX vs. 58% AZA.
- Greater relapse-free survival with RTX vs. AZA (p=0.006).



Ellen Romich et al. Media, PA

2149: Time to Disease Relapse After Prolonged Remission in ANCA-Associated Vasculitis

Predictors of Relapse After Treatment Withdrawal

Results

- No enrollment characteristics were associated with relapse.
- RTX: B–cell presence (HR 8.2) and higher IgA levels (HR 2.9) were associated with relapse.
- AZA: Positive ANCA (HR 2.7) and higher IgG levels (HR 1.3) were associated with relapse.

Conclusion

- Patients with relapsing AAV remain at risk of relapse after treatment withdrawal, even after prolonged remission
- Risk was higher with AZA vs. RTX and is associated with laboratory markers of immune reconstitution (e.g. ANCA, B-cells, immunoglobulins) at the end of the maintenance period.

Ellen Romich et al. Media, PA

2912: Spatial transcriptomics reveals mechanism of autoimmunity driven by internalized autoantibodies

Iago Pinal-Fernandez et al. Bethesda, MD



2912: Spatial transcriptomics reveals mechanism of autoimmunity driven by internalized autoantibodies

Objective

- To investigate the mechanisms of autoantibody internalization across diseases, cell types, and tissues.

Methods

- RNA sequencing of 814 muscle biopsies (41 additional validation samples).
- Patient IgG electroporated into primary human cells.
- Immunofluorescence evaluated localization of immunoglobulins across diseases and tissues.
- Spatial transcriptomics assessed disease-specific gene expression, cellular injury, and inflammatory responses.

Results

- Anti-Mi2 and anti-PM/Scl showed reproducible, autoantibody-specific transcriptomic signatures.

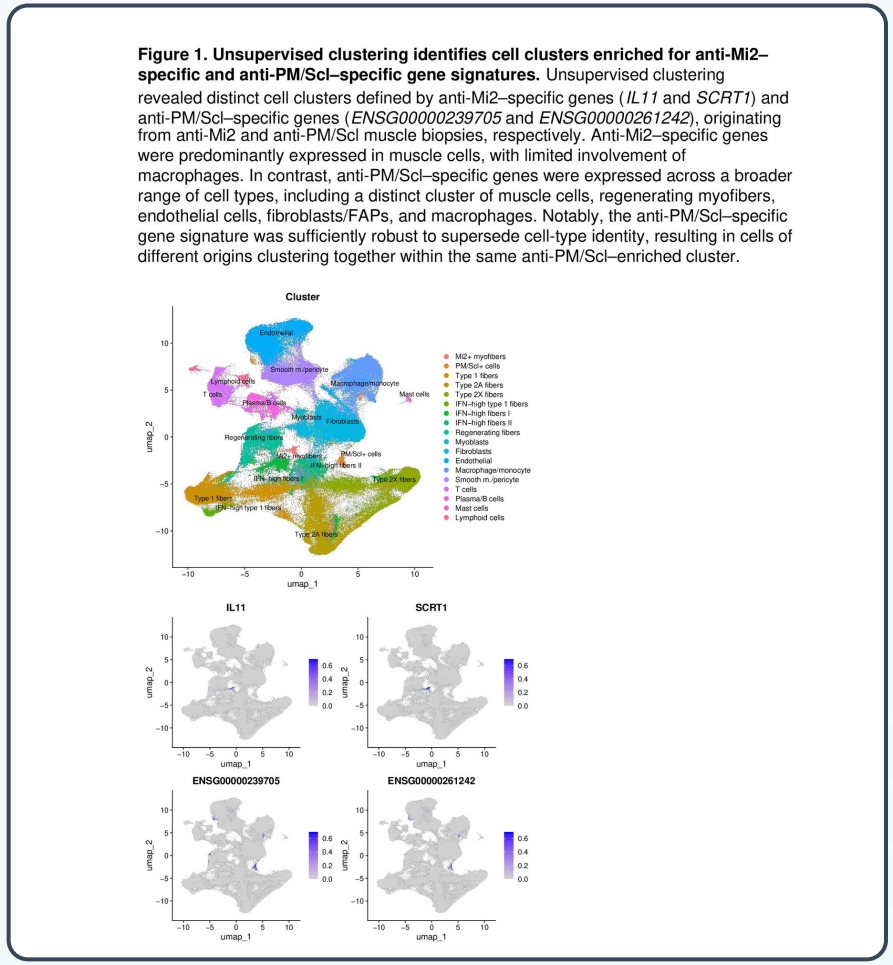


Figure 1. Unsupervised clustering identifies cell clusters enriched for anti-Mi2–specific and anti-PM/Scl–specific gene signatures. Unsupervised clustering revealed distinct cell clusters defined by anti-Mi2–specific genes (*IL11* and *SCRT1*) and anti-PM/Scl–specific genes (*ENSG00000239705* and *ENSG00000261242*), originating from anti-Mi2 and anti-PM/Scl muscle biopsies, respectively. Anti-Mi2–specific genes were predominantly expressed in muscle cells, with limited involvement of macrophages. In contrast, anti-PM/Scl–specific genes were expressed across a broader range of cell types, including a distinct cluster of muscle cells, regenerating myofibers, endothelial cells, fibroblasts/FAPs, and macrophages. Notably, the anti-PM/Scl–specific gene signature was sufficiently robust to supersede cell-type identity, resulting in cells of different origins clustering together within the same anti-PM/Scl–enriched cluster.

Iago Pinal-Fernandez et al. Bethesda, MD

2912: Spatial transcriptomics reveals mechanism of autoimmunity driven by internalized autoantibodies

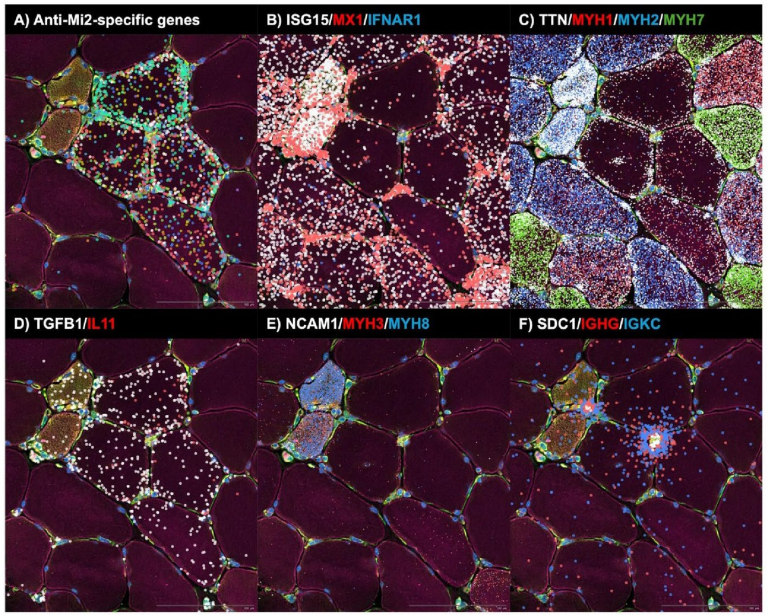
Results (Autoantibody Internalization and Tissue Injury)

- Anti-Mi2 DM: Activation of type I interferon and TGFβ signaling.
- Anti-PM/Scl scleromyositis: Activation of type II interferon signaling.
- Spatial transcriptomics linked these signatures to cellular injury and inflammation.
- Antibody internalization was also observed in skin and other autoimmune connective tissue diseases.

Conclusion

- Autoantibody internalization is a mechanism of tissue injury in autoimmunity, suggesting its broader relevance across autoantibody-mediated diseases.

Figure 2. Spatial transcriptomic analysis of a representative biopsy area from an anti-Mi2-positive patient, highlighting molecular signatures consistent with autoantibody internalization, autoantibody internalization-associated tissue damage and inflammation, and IgG-producing antibody-secreting cells exhibiting immunoglobulin RNA externalization. Colored dots indicate the spatial distribution of: (A) anti-Mi2-specific transcripts; (B) type I interferon-inducible genes (ISG15, MX1) and the interferon receptor IFNAR1; (C) transcripts associated with mature muscle fibers (TTN) and specific muscle fiber types (MYH1, type IIx; MYH2, type IIa; MYH7, type I); (D) TGFB1 and IL11; (E) markers of muscle regeneration (NCAM1, MYH3, MYH8); and (F) antibody-secreting cell markers (SDC1), immunoglobulin G heavy-chain constant region (IGHG), and immunoglobulin kappa constant region (IGKC).



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